

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
6906	37274	A	6957	2	1025	WRRYQANGK*KNK/QKKAGV VILVSDKTDKPTKIKRDKEGH YIMVKGSIQEEELTVLNIYAPN TGAPRFMKQVLRDLQRDLDPH TTIMGDFNTPLSTLDRSARQKV NKDIQELNSALHQADLINIYRIL HPKSTEYTFISAPHRTYSKIDHI VGRKALLRKYKRTEIITDCLSD HSAIKLELRKIKLTQNSSTTWK LNNLLNDYWIHNKTKAEIKM CFETSENKDTTYQNLWDTCCKA VCREKFIALNAHKKQERSKID TLTSQLE/LEKQEQTHSKASRR NLEEMDKYLDITYLPRLNQEE FESLNRPTGSEIEAIINSLPTKKS SGPDGFTAKFYQ
6907	37275	A	6958	1	1661	
6908	37276	A	6959	2	1632	WRKIYQANGK/HKKAGVAIRV SDKTDKPTKIKRDKEGHYLM VKGSIQEEELTILNIYATNTGAP GFIKQVLSLQRLDSHTIIMED FNTPLSTLDSMRQKVNDQTQE LNSALHQEDLIDIRTLHPKSTE YTFFSAPHHTYSKIDHILGSKAL LSKCKRTEIITNYLSDHSAIKLE LRKLNLTQSRSTTWKLNLLN DYWVHKEMKADIKMFFETNES KDTTYQNLWDAPFAEELES LN RPITASEIVAIINSLPSKSPGPD GFTAKFYQRYKEELVPFLKLF QSIEKEGILPNSFDEASIIIPKLG RDTTKENFRPISLMNIDAKILN KILANQIQQHKKLIHHDQVGFI PGMQGWFNIHKSINVIQHINRT KDKNHMIIISIDAEKAFDKIQSF MLKTRNKLGDGTLYLKIRAIYD KPTANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLAIRQ EKEIKGIQLGKEDVKLSLFADD MIVYLENPIVSAPNPLKLSNFS KVSQYKINVQKSQAFLYTNNR
6909	37277	A	6960	1	2169	

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6910	37278	A	6961	2	1255	EGKFRENRIKRNEQSLQEIWDY VKRTNLRLLIGVPESDWENGTKL ENTLQDIIQENFPNLR*AKIQRI RSQDPSTHLTSRDTHRLKIKGW RKIYQANGKQKKA AVTILVSD KTNFKPTKIKRDNEGHYIMVKG SNQQEELTILNIYAPNTGAPRFI KQVLRLDQRDLDSHTITGDINI PLSTLDRSTKQKVNKDTQELNS ALHQVDLIDYRTLHPKSIEYTF FSAPHHTYSKVDHILGSKALLS KCERIEIITNCLSDHSAIKLELRI KNLTQNHSTWKLNNLFLNDY WVHNEMKAEIKMFETSENKD TTYQNLWDAFKAVCRGKFIAL NAHKRKQERSKIYTLTSQLKEL EKQEQTSHSKASRRQEIIRAEI KEIETQKTLQKLNESISHQLEW QSLKSQKTTGAGEDVEK
6911	37279	A	6962	1	1122	
6912	37280	A	6963	551	1536	EILSPPLPYKSS*KKH*TWKGT TGTSCC/INHAKIVTHRLKIKGW RKIYQANGKQKAGVANLVSD KTDFKPTKIKRDKEGHYIMVKG SIQQEELTTLNIYAPNTGAPRFI KQVLSDLQRDLDSHTLIMGDFN TPLLTLDSTRQKVNKDTQELN SALHQADLIDYRTLHPKSTEYTF FFSAPHHIYSKTDHILGSKALLS KCKRTEIITNYLSDHSAIKLELRI KNLTKNRSTTWKLNNLFLNDY WVHNEMKAEIKMFETNENK DTTYQNLWDTFKAMCRGKFIA VNAHKRKQERSKIDTLTSQLKE LEKQEQTSHSKASRRQEITKI
6913	37281	B	6964	28	1209	
6914	37282	A	6965	1	1284	
6915	37283	B	6966	1	1056	
6916	37284	B	6967	124	963	
6917	37285	A	6968	3	1162	
6918	37286	A	6969	1	1364	
6919	37287	A	6970	1	1003	
6920	37288	B	6971	1	1129	

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6921	37289	A	6972	1	1917	MVKGSIQQEELTILNTYAAHTG APRLIKQVLSDLQRDLDSHTIM GDFNTPLSTLDRSTRQKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFFSAPHHIYSKIDHILGSK ALLSKCKRTEIHTNYLSDHSAIK LELWIKNLTQNHSTTWELNNLL LNDYWVHNEMKAEIKMFFETN ENKDDTYHNLWDTFKAVCRGK FIPLNAHKRKQERSKIDLTSL KELEKQEQTTHSKASRRQEITKIR AELKEIETQKTQKINESRSWFF ERINKIDRLRLARLIKKKREKNQI DAIKNDKGDITTDPEIQTIRE YCKHLYANKLENLEEMDKFLD TYTLPRLNQEEVESLNRPTGAE IVAIHNSLPTKSPGPDGFTAKF YQRYKEELVPFLKLFQSIEKE GILPNSFYEASIIIPKPGRDTTK KENFRPISLMNIDAKILNKKLA KRIQQHIKKLIHHDQVGFIPGM QGWFNIRKSINVIQHINRAKDK NHMIISDAEKAFDKIQPFMLK TLNKLGIKYLGIHLTRDVKDLF KENYKPLLKEIKEDTNKWNIP CSWVGRINIVKMAILPKMCL*R RWTPLCLLTAAASLNRE*ERLV QPLLWRQMYCGPRHCRQVPQH RRLNWSPSLRLS
6922	37290	A	6973	1	2673	

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6923	37291	A	6974	261	2667	TWCSGRYMVGCR/DWHLLV/ KGLRKLTIVAEGEGGAGMSLG ESGNKKRKDEKGYIMVNGSIQ QEELTILNIYAPNTGAPFIKQV LRDLQRDLDSHTIIMRDFNTPLS ALERSTREKVNKDIQELNSALH QADLVDIYRTLHPKSTEYTFFS APHRTYSNIDHIVGSKALLSNC KRTEHTKCLSDHSTIKLELRKK LTQNRSTTWKLNLLNDYWV HNEMKAEJMMFFETIENKDDTY QNLWDTFKAECRGKFIALNAH KRKQERSKIDTLTSQKLEKQ EQTHSKASRRQEITKIRAEKET ETQKTLQKINESRSWFFERINKI DRPLARLIKKKREKNLIDAIKN DKGDITDPTEIQTIREYYKHL YANKLENLEEMDKFLDITYTLP RLNQEEVESLNRPTGSEIVAIIN SLPTKKSPPDGFTAIFYQRHT VSILISYCQGGSLMSQVYWNQQ EKPPSSSNAPGLSVNKAQHRH VCCRGEMLKRQVYHYVRAGES DSASFHCVAQGPRAFGKPLILS KENHLLTVTAIAKLNHKLCEIK SMGVFINTEPLYDSCLEQKHAL FASPPATTHSTTMISKAKVIPML SLTPGSFQTVESLAPSAGKFQG TETSSLKTLINLCCPKLPSPSPA HLGGLPGGSQERPSRQYLYESA RTTVLLGLGCPLKQIQLRSQHS SPLEYLESLPKKDRKKREKIQIN



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6924	37292	A	6975	1	1687	MLKGSIQQEELTVLNIYAPNTG APRCIKQVLSDVQRDLDSNTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLDIYRTLH PKSTEYTTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNSLSDHS AIKLELRKLNLTQNRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETKENKDTTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSQKLEKEKQEQTHSKEIQTIR EYYKHLTYTNKLENLEEMDKFL DTYTLPRLNQEEVESLNRPIIGS EIVAIHNSLPTKKSPGPDGTAEF YQRYKEEMHINRAKDKNHMIS IDA EKAFDKIQPFMLKTLNKL GIDGTYFKIIRAIYDKPTVNIILN GQKLEAFPLKTGTRQGCP LSPL LFNIVLEV LARAI RQEKEIKGIQ LGKEEVKLSL FADDMIVYVEN PLPSQPQNLL*GWLSNFSK/MSS GYKIN VQKSQAFLYTNNRQTES QIMSELPFTIASKRIKYLGIQFTR DVKDLFKENYKPLLNEIKEDTN KWKNI PCSWVGRINIVKMAILP
6925	37293	B	6976	1	2431	

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6926	37294	A	6977	1	1921	MGESVQSLTLAQRSMMIQV AVAPRTPTLKKLYKEKASKTQ LKKVNLVVQDQGSLESIEVHD HEPADTYKLLSLVKEPAEEIPR VIQNVFGHRSKKENLKDSYGLR QSSTMVATTWNNVSLMQHHSL RRPNRHILTASYPHFHQEI PVNF FHSGRDSESGWNVQHIKKDKE GHHIMVKGSIQEEELTMLNIYA PNTGAPRFINQVLSIERDLDSH KIIMGDFNTPLSLDRSTRQKV NKDTQELNSALHQADLTDIYRT LHPKSTEYTLFSAPHHTYSKIDH IVGSKALLSKWKRTETITNCLSD PRAIKLELRKKLTQNRSSIWKL NNVLLNDYWVHNEMKAEIKIF FETNENKDTSCQNLWDTFKAV CRGKFIALNAHRRKQERSKIDT LTSQLEKEKQERTHSKASRRQ EITKIRAEMKEIETQKVLQKINE SRSWFFEKINKIDRPLARLIKKE REKNQIDAIKNNKGDIITDPTET ETTIREYYKHLTYNKENLEEM DKFLDITYTLPRLNQEEVESLNR PITGSEVVAIINSLPTKKSPGPDG FTAEFHQRYKEKLISELLPMPN HTALKKQTQDLSCKAMFLYY QSVSVQTAIINYHRLRGLNRRN LFLTIVLEYSSLRSGCEHSRVL

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6927	37295	A	6978	1	1848	MSLTKMLICAALLGLFCMLLGL RWQVAELIGMTLALSSTAIA QAMNERNLMVTQMGRSAFAV LLFQDIAIPLVAMIPLLATSSA STTMGAFAALSALKVAGALVLLV VLLGRYVTRPALRFVARSGLRE VFSVALFLVFGFGLLLEEVGL SMAMGAFLAGVLLASSEYRHA LESDIEPFKGLLGAVFTPRVVV NIYSSSELRTAKNYQANGKQKK PGVAILVSDKTAF/KPTEIKRDK EGHYIMVKGSIQEEILTILNIY APNTGAPRFIKVLSLQRLDLD SHTLMMGDFNTPLSTLD\IRST QKVNKDTQELNSALHQADLIDI YRILHPKSTEYTFPSAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRKNTQSRSTT WKLNNLLNDYWVHNEMKAE IKMFFETNENKDMTYQNLWDT FKAVCRGKFIALNAHKRQERS KIDTLTSQLEKEQEQT\HKA SRRQEITKIRAELEIETQKAIQ KINESRSWGPNGCQNYRNSE SGEKSAPEGQAQHAQPTGKVV PTFLYVGKEKFPPSYLLTRKSSH LPTCGDPICGEKCRWVPTTSQG GNKADQWGGVGIGDTHDSDA
6928	37296	A	6979	1	2235	
6929	37297	A	6980	1	2955	

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6930	37298	A	6981	3	2156	KSLKDLMEIKMAQELCDEWT SLSSRCNQLLEERSVMEDEMN EMKDKHRPKIKIEWRKIYQANG QKKTRVANLVSDKTEFKPTKI KRDKEGHYIMVKGSIQQEELTI VNIYAPNTGAPRFIKVLSDLQ RALDSHTIMGDFNTPLSTLDRS TROKVNKDIQELNSALHQADLI DIYRTLHPKSTEYTFFSAPHYTY PKIDHIVGSKALLSKCKRTEIT NCLSDHSAIKLELKIKKLTQNL STTWKLNLLKDYVVKEM KAEIKMFFETNKNKDDITYQNF WDTFKAVCRGKFIALNAHKRK QEGFKIDTLTLQLEKEQEQT HSKASRRINKIDRPLARLIKRR EKNQIDTIKNDKGIDITDPTIEQ TTIREYYKLYANKLENLEEM DKFLDITYTLPRLNQEEVESLNR PITGAIEIVAIHNSLPTKKSPGPDG FTAKFYQRYKEELVPFLKLFQ SIEKEGILPNSFYEASILIPKGR DITKKENFRPISLMNDAIELNKI LASQMQQHIKKLIYHNQVGFH GMQGWFNHKSINVIQHINRTK DKNHTIISLDAEKAFDKIQQPF MLKLTNLKLGIDGMYLKIIRA IYDKPTANILHWQKLEAFPLKT GTRQGCPLSPLLFNIVLEVLR AVRKEKEIKRTQIGREEIKLSLF ADDMIVYLENPIVSAQNLLKLIS NFTKVSQGYKINVKKSQAFLYN
6931	37299	A	6982	3721	8717	MLPIKRHRLANWIKSQDP/SVC CIEETHLCRDAHRHKIKGWR KIYQANGKQNKTKQQKKQGLQ ILVSDKRDKFPKTIKRDKEGHYI MVKGPQQEELTILNIYAP/NTG APRFIKQVLSDLQRLDSHTLA MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFFSAP/HHYTSKIDHIL GSKALLSKCKRTEITNYLS/DH SAIKLKLRIKNLTQNHSTTWK LNNL

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6932	37300	A	6983	599	1074	NPRAWKQPPPTSPQEFCLVCF VVHLQKSTREALNNKNIKPLLS TFSQVPG/SINHSSCENVLAHSL AIGGVTEGICTASTPFVLLGDVL DCLPLDQCDTIFTFVEKNVATW KSGTASLPAAFMAQVEHLWLF QVNGANCQWYPSGVVWRTVAL FSQLH
6933	37301	A	6984	1	312	QSRALLWPMLVDVIQPKPWKA PGSLGLPSCISAITVQSSPGLRLC SCGQGPVNTPGTKLPQPNRPV SLSFSQMKLLTSSHWSFHCPA *INPAQSSPGWP*PQLSGCPAF QFLSFG*KSLSSGNTASSSPLW FLCWCFNLVLQAKLPDGFRLPA HRV
6934	37302	A	6985	2	484	
6935	37303	A	6986	234	405	ELKICSCDPITVRYNADDSTVSL SFSQMKLLTSSHWSFHCPA* INPAQSSPGWP
6936	37304	A	6987	1	2021	PTRPAAQWRARAAEKMSPTP PLFSLPEARTRFTKSTREALNNK NIKPLLTSTFSQVPGSENEKKCTL DQAFRGILEEEIINHSSCENVLAI NSLAMGEVTEGICTASTHFVLL GDVLDCLPLDQCDTIFTFVEKN VATWKSNTFYSAGKNYLLRMC NDLLRRLSKSQNTVFCGRJQLF LARLFPLSEKSGNLQSQFNLE NVTVNTNEQESTLQKHTED REEGMDVEEGMGDEEAPTTC SIPIDYNLYRKFWSLQDYFRNP VQCYEKISWKTFLKYSEEVLA VFKSYKLLDDTQASRKKMEELKT GGEHVYFAKFLTSEKLMDLQL SDSNFRRHILLQYLIFQYLGKQ VKFKSSNYVLTDEQSLWIEDTT KSVYQLLENPPDGERFSKMVE HILNTEENWNSWKNEGCPSFV KERTSDTKPTRIRKRTAPEDFL GKGPTKILTNGEELTRLWNLC PDNMEACKSETREHMPMLEEFF EEAIEQADPENMAENYKAMN NSNYGWRALKLLARRSPHFFQP TNQFQKSLQEYLENMVIKLAKE LPPPSEIKTGEDEDEEDNDALL KENESPDVRRDKPVTGEQIEVF ANKLGEQWKILAPYLEMKDSEI RQIECDSMDKMRKQLLVAV QDQEGVHATPENLINALNKSGL SDLAESLTNDNETNS

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6937	37305	A	6988	155	811	EFYRTGKVHRA PGVQEVETDP RDPLAQLATDRKERRGSLDH LALRVREAQLDQLVPPEVAA KDLKAPRAKPAVVPPLGSPALR APVGTQAPRAHQAKRDSPALR ALLASRDFRAPLGLGCLDLGD CQACLG YQACQAPRAPALLA HQRWCPWPCRMSQPQHRRT MAARLTGRTSQTNATIFQLRKK FLRMQSFVSKTSLHILFS*TLER NSNG
6938	37306	A	6989	91	918	
6939	37307	A	6990	199	380	CSTSSRTY*IPSRCSKG*HWRH TVNSNFGPMGNPSHPTSSAHH TVPLIESQPSSTSKK
6940	37308	A	6991	1	483	
6941	37309	A	6992	178	298	
6942	37310	A	6993	864	1298	RLQNRITLASDLSGSDRWRTY RCL*RHGPRFSSCRLSCRPFDK TCRLMCHQRLSGFPQEQTRDS RCIQLLFRQRFAAASCPTHQVH VHRWRKPMVFLILESDLKYTV LSLPEECHTGAHEQSSHCLLLSL ASVDVHCSQRP
6943	37311	A	6995	2	348	KKKRRKKIEEEEEEEEEEEEE\
						REEEGDEEQEEEEEEEEEEEE
						EEEEEEEEEDDDDDNGLLQTL
						PGLHEMRVNLTRSDGIISVWHF
						PFWHFSFLMPYEEGALLRLHLP
6944	37312	A	6996	1	192	
6945	37313	A	6997	1	507	MEKNEKEQEEEEKEKNSKKK EEEEEEEGGEEEEEEEGEGGEE EEEEEEEEEEEEEEEEEEEEEE EEE/DKEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEVVE EEDEFIWLGNL YFPFSHFA WSQPSREDEGERRLRVNSMIM DFTSNTNHVQLIVAR
6946	37314	A	6998	1	257	MGPiHKISHYVYANISKSEKVL KSEHFRSQAFQPGQSQSETVSEK/ FREDEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEI
6947	37315	A	6999	1	156	
6948	37316	B	7000	1	757	
6949	37317	A	7001	1	279	

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6950	37318	A	7002	1	1226	MPSSKGVVHVHSPPRYLAAKDF KMINKELTAATFMEVIAEDNRF IYDGDSDNFPELVLFEEFFALLS FAFICVTDQMTKSYTNVPADD VSGNKHETIYILNQDAQNKSP SAVMSHESDAAHSDSARSSSSK LELSPDVNKRKSEAMVKEKKK ADKKGEKSARSPPSSLSNDLDFS KQDGNTTTQEMSPAGVPLLGM QLNEVKPKKDRQNVQQNE/GC HPIRRVHSDQTHSGKL*RGKGS W/DCMREKASQPFKAVVPIV*V /VPFENLQEGEEGRLECECPDEP RRVHVAGRSMYEGEVVNGMR NGFGMFKCSTQPVSYIGHWCN GKRHGKVGEVATWRAEKKKK EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEKIRP
6951	37319	A	7003	3	123	
6952	37320	A	7004	2	458	
6953	37321	A	7005	239	432	CLWLFQEEEEEEEEEEED*EEE EEE/EEEEEEEEEEEEEEEE EEEEEEEEKIFLGHVRVGI
6954	37322	C	7006	7	162	
6955	37323	A	7007	39	2154	
6956	37324	A	7008	1	639	
6957	37325	A	7009	1	651	
6958	37326	B	7010	1	684	
6959	37327	A	7011	3	428	TRFQGVYLLWEQSF/CWKSPI ALGYTRGHFSALVAMENDGYG NRGAGANLNTDDDVTTITFLPV DSERKLLHVHFLSAQELGNEEQ QEKLRLREWLDCCVTEGGVLVA MQKSSRRRNHPLVTQMVEKV LDYRQIRPCTSLF
6960	37328	A	7012	2	800	

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6961	37329	A	7013	1	930	DHNSSPAMEQNWMENAFDEL T EVGFRRWVITNFSKLEHVL TQ CKEAKKLEKRLLEELLTRITS LEK NINDLMELKNTSQELREAYTTE ERISEIEDQLNEIKHEDRI REK/R/ VKRNEQSLQEIWVYVKRPNLH LT/GVPESDGENGT KLENTLQDI IQENFPNLARQANI QIEIQRTP QRYSSRRATPRHIIIR FTKVEMK EKMLRAAREKGQVTHK GKPIR LTADPLAETLQARRE WGPINIL KEKNFQHRMSYP AKLSFISVGE IKYFTDKQMLRDF VTTRPALQE LLKDALNMERN NQNSQLQKHA KL
6962	37330	A	7014	1	870	
6963	37331	A	7015	1	585	
6964	37332	A	7016	1	1032	
6965	37333	A	7017	2	770	
6966	37334	A	7018	1	2910	
6967	37335	B	7019	239	462	
6968	37336	A	7020	3	694	
6969	37337	A	7021	1	1212	
6970	37338	A	7022	1	1140	
6971	37339	A	7023	1	570	
6972	37340	A	7024	1	486	
6973	37341	A	7025	1	1476	MEVNREKQNLNELE VIGSEEQNL EEEGLMIGGVA VRLVPDDIVIP GGVNATNGTEAR DALRVKVA MSVTLLSGIIQYLL SALGWSYY TVDGVSQKNPRAL GVTA DQLH AIFTMSDEQASFR FGFVAIYLT EPLVRGFTTAAAV HVFTSMLK YLFVGVTKRYS GIFSVVYSTVA VLQNVKLN NVCSLGVGL MVFG LLLGKKEFNER FKEKLPAPIPLE FFADHNSSPARE QKWMENEF D EWTEVSFRRW VITNSSELKEHI LTQCKEAKNLEK RLEELLTRITS LEKNINDLMELK NTAQEFHEA YTSINS/RNQT EERVSEIEDQLN EI*CKDKIR EKKRMKRNEQSLQ EIWDCVKRPNLRL TGVPESDGE NGTKLENTLQDII QENFHNLAR QANSQIEIQRTP QRYSSRRATP RHIIIRFTKVEM KEKMLRAARE KGRVTHKGNP IRLIADLSADTL QARRQWEP IFNILKENFQTRISH
6974	37342	A	7026	1	1080	



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6975	37343	A	7027	1	3501	MIVYLENPIVSAQNLLKLISNFS KVSQYKIKYKIDVQKSQAFLYTN NRQTESQIMSELPFTIASKRIKY PGIQLTRNVKDLFKENYKPLLN EIKEDTNKWKNI PCSWIGRINIV KMAILPKVIYRFNAIPIKLPMTS FTELEKTTLKFIWNQKGARIK TILSKKNKVGGITLPDFKLYYK ATVTKTAWYWYQNRDIDQWN RTEASEITPPYINHLIFDKPDKN KKWGKDSL FNKWCWENWLAI CRKLLDPFLTS
6976	37344	A	7028	164	714	IGVNRHLIQESPSWNLGAPLE QIFQRKEQAIFAILQPLLVISRQ TSGSVDPPQQTADLQK/SGSDS REQNKTENEFDELTEIGCRRWV ITNSSELKEHVVTQCKEAKNLE KMLQELLTRITSLEKNINDLME LKNTAQELREAYTIINSQTDQA EERISEIEDQLNEIKGEDNIREKT VKRNE
6977	37345	B	7029	1	579	
6978	37346	A	7030	1	927	
6979	37347	A	7031	1	1362	MAAGRHLPGVADRHLIQESTG WHLAGAPLGWSFORKEQTAIF AVLQPLLVI PRQTGYGVDLQ MPADLQQRFLTVRRKTNKQKG IVSTSTKRTSSEGHQHRKVD KFTEMGGRNQHKKAENSKQN ASSP'PKDHNSLPAREQNWTE N EFDELTEIDFRRWVITNSSQTKG SMF*P'CKEAKNLEKRLDELLT RITSLEKNINDPMEKNTAREL REANKSINS*IDQGRKERVISEIE DQLNEIKREDKIREKRMQRNK QTLQEIWDYVVRPNLHLIGVPE SDRENGTKLENTLQDIIQENFP NLARQANIQIEIQRTPQRYSSR RATPRHIIVRFTK VEMKEKMLR AARKKGQVTHKGKSIRLSADFS AETLQARREWGPPIFNILKEKNF QPKISYPAKLSFISEEITSFTDK QTLRDFVTTRPALQELLKEAVN MERKNQYQPLQKHTKM
6980	37348	A	7032	1	598	
6981	37349	A	7033	3	787	
6982	37350	A	7034	61	284	RLLPEQGPLRAGSSPAGK/IGGT LERRGMPWPGP/HSEGGLSPLL LGASLAAAPHGEMPSVRVHPV RPSSRDCSSRV
6983	37351	B	7035	743	1683	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6984	37352	A	7036	1	1137	
6985	37353	A	7037	1	663	
6986	37354	A	7038	1	197	
6987	37355	A	7039	1	291	
6988	37356	A	7040	3	342	
6989	37357	A	7041	1	439	
6990	37358	A	7042	3	253	
6991	37359	C	7043	1	210	
6992	37360	A	7044	1	165	
6993	37361	A	7045	1	346	
6994	37362	A	7046	1	389	
6995	37363	C	7047	1	464	
6996	37364	A	7048	1	1806	
6997	37365	A	7049	491	1640	
6998	37366	A	7051	188	383	
6999	37367	A	7052	1	759	
7000	37368	A	7053	1	1683	
7001	37369	A	7054	1	972	
7002	37370	A	7055	1	429	
7003	37371	A	7056	3	753	DQTFWGLLETG/S/ELMLIPGDP KCHCGPPVKVGAYGGQEIKGV LAQVQITVGPVGTRTHPVPVIS VPECIIGIDILSSWQNPHTGSLTG RVRVIMVEKAKWKPLELPLPR KIVNQKQYCIPGGIAEISATIKD LKDTGVMIPTTSPFNSPIWPVQ KTDGWSRITVDYQVVTPIAAA VPDVVSLLEQINTSPGTWQHIT HLDVLLWRIYQVTQKAASFWE GPEQEALQVQAAVQA\LCH LGHMTQQIQWCL
7004	37372	A	7057	2	430	
7005	37373	A	7058	1	1515	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
7006	37374	A	7059	1	1523	MGEERRWRPSSNGKHGAFAEL DKGWL V WLEGGVIGARRSW RAHSALIKICVQQIKDLSLPGKM SKGLLQQQKPKHLLHDLYKA MSTRWGVQKARL NCTALPPTG CVTLDPFSLTEPQFPRQLSEDL LTREALEKEVQLRRQIQEKEE LLYRVLGANASPAFPLAPVTPT EVEKERELRDLDEQQRVLE GKNEEALQDPRLVDPLTSTCTVH FEKPMMLNARLWKHAGREAV ACKVRGSELPKTMGTYP LHQH DLDRHGVKGDHFGALRFDCP AGFWTCMGLAPSFWPISPIWN GPPLDISGYPATSTQKSTMCLRI IDTRLHPESRLKQSNFALNAR EKALQQVQAAVQAALPLGPYD PADPMVLEVSLADRDVWVSL WQAPIGESQQRPLGFWGKALPS SADNNSPLERQLLARYWALVE TEYLTMGHQVTM*P/ELPIMNW VLSDPSSHKVYVAWQHSIKW KIDRA*AGLAGTSKLEHEVAQ MPIVSTPATLPSCRIL
7007	37375	A	7060	1	2190	
7008	37376	A	7061	286	430	
7009	37377	A	7062	205	514	LWSLCAPVLVQVPCLRAPFVFT RRHAPSAGRGFTRSYVSAGSW TETQQGLWGLTKLGADGLLL GISKHLVEFLQIFQISGCWGHYC YLQILFFALNSISPSYHVLLFN VQFGFIFFNMVLCVP*AGTHIAPC KSSSRTRGMSSCENWKGCSKA RHLQYVSTKTPQSLSFCCGIH FVTAVCQP
7010	37378	A	7063	1	487	
7011	37379	A	7064	1	1212	
7012	37380	A	7066	140	453	
7013	37381	A	7067	1	3341	MGKKQNRKTGNSKNQSA PPP KERSSSPATEQSWMENDFDEL EEGFRLSNYSELPEDIQTGKGE VENFEKNLEECITRITNKRNFKP TKIKRDKEGHYIMVKGSIQQUE LTILNIYAPTGA PRFIKQVLSDR QRDLDFHTLIMGDFTNPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHKSSTEYRFFSA PH HTYSKIDHLLGSKAFLSCKCRT EHTNVLSDHSAIKLELRINKLTQ NRSTTWKLNN
7014	37382	B	7068	1	1785	

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7015	37383	A	7069	I	1141	MVTWNFIQERNRSGMDQCDD GGGKILDPVYILTVELTGFAKG WKMFVSVDQSVNVLGFAGYPL ITQTARKGAGKIPTWASLRQYQ KGLGSKYQLRRALRPDCALGN GQGVRYCNSLDEEEKRELKLF SQRKRENLGRGNVRPFVPTMT GAICEQCGGQINGGDIASFASR AGHGVCVHPPCFVCTVCNELL VDLIYFYQDGKIYCGRHHAECL KPRCAACDEIIFADECTEAEGR HWHMKHFCFECETVLGGQRY IMKEGRPYCCHCFESLYAEYCD TCAQHIGHAGSFIKEC/SRLLP GEAEI/SRRATVLCVLRVSVRPE AASKSPNMRRKRKRKGACPLS SVGPVPSVP*NTQRT*RPQSRP LGAPWNPWPCLMQ
7016	37384	A	7070	I	2388	VHQYYSCLPEEKVPYVNSPGEK LRIKQLLHQLPPHDNEVRYCNS LDEEEKRELKLFSSQRKRENLG RGNVRPFVPTMTGAICEQCGG QINGGDIASFASRAGHGVCVH PPCFVCTVCNELLVDLIYFYQD GKIYCGRHHAECLKPRCAACD EIIFADECTEAEGRHWHMKHFC CFECETVLGGQRYIMKEGRPYC CHCFESLYAEYCDTCAQHIGID QQQMTYDQGHWHATETCFCC AHCKKSLGRPFPLPKQQQIFCS RACSAEDPNGSDSSDAFQNA VGRSPGA VPKLARTRARRGAH AEPAQPAASEF*PAVSRRRPPVT ADGHAQPVQPDTPQPGPHILE EPGRALPLWEQDGAEPDPEPSA APARQCNIRTSYSPGGQGAQAQ PEMWGKHFSNPKRSSSLAMTG HAGSFIKECREDYYPGRLLRSQ SYSDMSSQSFSETRGSIQVPKYE EEEEEEGLSTQQCRTRHPISSL KYTEDMTPTQTPRGSMSLAL SNATGLSADGGAKRQEHLSRFS MPDLKSDSGMNVSEKLSNMG LNSSMQFRSAESVRSLLSAQQY QEMEGNLHLQSLNPIGYRDLQSH GRMHQSFDFFDGGMAGSKLPQG EGVRIQPMSETRRRRATSRDDN RRFRPHRSRRRSRSDNALHL ASEREISRLLKDRPPLRAREDY DQFMRQRSFQESMGHGSRRDL
7017	37385	A	7071	I	807	

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7018	37386	A	7072	500	2666	YCLRLAQVGIFAPSRRAWVPDL DPESRLCCFPSSLGSLANPTAVG LEEDREQDVGTSSRGGAWDTRI KRELEKMSSEKCGGQINGGDIIV FASRAGHGVWCWHPPCFVCTVC NELLVDLIYFYQDGKIYCGRRH AECLKPRCAACDEIIFADECTEA EGRHWHMKHFCCECTEVLGG QRYIMKEGRPYCCHCFESLYAE YCDTCAQHIGEAIFGSQLGPSV MRSPLFWGVGIAAALDAVLIR AHQRTQGCHELSALLAFEKG SEKKEEEGGQVSRSSSLKVQA QELSATEDKGHSPPFWA VYH YASGECRGP GPYPYSHSLRLYSQ QALPTGRGPSSSQPFCQFYCC YKKSLLCDCLSKSPA LEKAMR GIDQGMITYDGGHWHATETCF CCAHCCKSLLGRPFLPKQGQIF CSRACSA GEDPNGSDSSDAFQ NA\GPRSPGAVPKLARTRARR/G AHAEPAQPAASEF*PAVSRRRP PVTADGHAQVPQPDTPQPGP HLEEPGRALPLWEQDGAEPDPE PSAAP\RQCNIRTSYSPGGQGAG AQPEMWGKHFSNPKRSSSLAM TGHA GFSIKECREDYYPGR LRS QESYSDMSSQSFSETRGSIQVPK YEEEEEEGGLSTQQCRTRHPIS SLKYTEDMTPTETPRGSMESL ALSNA TGTKTCSVTFQAKETCR YQDAQFGKVKARVKERQSLWS
7019	37387	A	7073	1	2239	
7020	37388	A	7074	1	282	
7021	37389	A	7075	2	430	GFGAQDPKSLALRTHCQTSGW/ SLTEQDPYNNVIRTIEALAAATL GGTQSLHTNVFDEALGLPTDFS ARIARNTQIIIQEESEL CRTVDPL AGSYGGAIQQIDVAGGLAKRI EAGLSKRMIEASAREQALIDQ GKRIVVGV T

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
7022	37390	A	7076	1	1561	MVTLILYFRFYRLNGDTLRRRIQI HLLDKYRKVPPEPVHADIPVGA RRFSRPSWFLRITKRGYRRTV HAMAGQKEKLLGAGMSDYLA KPIEEERLHNLLRYKPGSGISS RVVTPEVNEIVNPNATLDWQ LALRQAAGKTDLARDMLQML LDLPEVRNKVEEQLVGENPEG LVDLIHLHGSCGYSGVPRMK NLCQLIEQQLRSGTKEEDLEPEL LELDDEMDNVAREASKILGDPK THLRRIRRDVLATDPRPARDRR KACLHACVLRTPPLGAARAIQ QIDEAGGMAKAI EAGLPKRMIE EASAREQSLIDQGRVIVGVNK YKLDHEDETDVLEIDNVMVRN EQIASLERIRTRDDAAVTAAL NALTHAAQHNNENLAAAVNA ARVRATLGEISDALEVAFDRYL VPSQCVTG VIAQSYHQSEKSAS EFDAIVAQTEQFLADNGRRPRI LIAKMGQDGHDRGAKVIASAY SDLGFDVDLSPMFSTPEEJARLA VENDVHVVGAISSLAAGRSR
7023	37391	A	7077	1	354	
7024	37392	A	7078	1	1116	
7025	37393	A	7079	1	450	
7026	37394	A	7080	1	252	
7027	37395	A	7081	1	242	
7028	37396	A	7082	1	242	
7029	37397	A	7083	1	9228	
7030	37398	A	7084	3	664	
7031	37399	A	7085	3	718	
7032	37400	A	7086	380	1038	WTRWRASAADNLAHGRWGEQ KLVTGTGASGAPDRQAARCAA SAKISWYRSKSGSKIHLTPKEVE KTGWGLKIP/MGQQQLPERV KEAARILELDGLKKRRPRELSG GQRQRVAMARAIVRDPVFLF DEPLSNLDAKLRVQMRLELQQ LHRRDQVEAMTLAQRVMVMN GGVAEQIGTPVEVDGDDTLEIL GADNLAHDAGRAEAGGDWRI RSARRSSTCAH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
7033	37401	A	7087	380	920	WTRWRASAADNLAHGRVGEQ KLVVTTGASGAPDRQAARCGC IWRKISWYRSKSGKSHPLTPKEV EKTGWGLKIPG/MGQQQLPERV KEAARILELDGLLKRPRRELSG GQRQRVAMARAIVRDPVAVFLF DEPLSNLDAKLRVQMRLELQQ LHRRDQVEAMTLAQRVMVMN GGVAEQIGTPVE
7034	37402	A	7088	1	258	
7035	37403	A	7089	3	208	
7036	37404	A	7090	34	125	
7037	37405	A	7091	1	393	
7038	37406	A	7092	1	690	MVAPVYIRDQYSALITNIGKGD HTTFVKPNIPATGEFGVGFLF APRGMLSHWMVIKDGHSNYQ AVVPSTWNSGPRNFNDVGPY EQSLVGTVPVADPNKPLEVVRTI HSFDPDMAWVGNILLTDEAIGV RIVEALEQRYILPDYVEILDGGT AGMELLGDMANRDHLIADAIV SKKNAPGTMMLRDEEVPALFT NKISPHQLGLADVLSDLRFTIGE FPKLPWVQA
7039	37407	A	7093	82	224	
7040	37408	A	7094	1	239	
7041	37409	A	7095	1	1062	
7042	37410	A	7096	1	221	
7043	37411	A	7097	1	1067	
7044	37412	A	7098	1	1545	
7045	37413	A	7099	1	2820	
7046	37414	A	7100	1	1223	
7047	37415	A	7101	1	3087	
7048	37416	A	7102	1	1182	MDKFLDTYTLPRLNQEEVESLN RPITGSEIVAIINSLPTKKSPGPD GFTAIFYQRYKEELVPFLKLF QSIEKEGILPNSFYEAHILIPKG RDITTKENFRPISLMNIDAKILY KILAKRIQQHIKKLIHHDQVGFI PGMQGWFNIRKSINVQHINRA KDKNHMIIISDAEKAFDKIQPF MLKTLNKLQANLLKLISNFNKV SGYKINVQKSQAFLYTSNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWSVGRINIVKMAIL PKVIYRFNAIPIKLPMTFFTELE KTTLKFIWNQKRAHIAKSLSQ KNKAGGITLPDFKLYYKATVT KTAWYCYQNRHIDQWNRIPSEI TPHIYNYLIF

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
7049	37417	B	7103	1	1722	
7050	37418	A	7104	1	3513	
7051	37419	A	7105	1	2546	MSELPFTIATKRKLYLGIQLKSD VKDLFKENYKPLLNEIREDTYK WKNTPCSWIGRINIMMAILPK VIYGFNAILIKLPLTFFTELEKTT LKFTQSLKRAHIAKTILSKKNK AGGIMLPDFKLYYKATVTKTA CTIHNSKDLEPTEMPSNDTLDK ENVAYIIHHGILCSHSGRVHIL CRDMDEAGNHHSRQTNTGTEN QTLHLVTHKWELNDENTWTQ GGEHHISGPVRTNNKNHMIISIG AEKAFDIQPPMLKTLNLQGLI DGTYLKIIIRDIFDRPIANILLNGQ KREASPLKTGTROGCPLPPLLF NIVLEILARAIKKEIKGIQLG KEEVKLSLFADDMIYLENPIVS AQNLKLSISNFSKVSGYKINVQ KSQAFLYTNNRQTESQILSELPP TIASKRIKYLGLQLTRDVKDLFK ENYKPLLNEIKEDTNKWKNIPC LSIGKINIMKMAILPKVIYRFNAI PIKLPMTFFTELEKTTLKFIWNQ KRARIAKTILSQKNKDDGGITLPD FKLYYKATVTKTAWYQYQNR DIDQWNRTEPSEIIPHYVNHIF DKPDKNKKWGKDSLFNKWCW ENWLAICGKLLDPFLTPTYTKI NSRWIKDLNVRPKTIKTEENL GNTIQDIGMGKDFMSKIPKAM ATKAKIDKWNLIELKSFACTAKE TTISVNRQPTWEKIFAICLSDK GLISRIYKELKQRHKKKTNNPIK
7052	37420	A	7106	1	2575	
7053	37421	A	7107	1	875	
7054	37422	B	7108	1	3421	
7055	37423	A	7109	1	3790	MELKTKARELREECRLSRRRN QLEERVSADEEMNEMKREG KFREKRIRKNEQSLQEIWDYVK RPNLRLJGVPESDAENGTKLEN LTQDIHQEDFPNLRQANVQIQE IQRTQRYSSRRATPRHIIIVRFT KVEMKQKMLRAAREKDFKPT KIKRDKEGHYIMVKGSIQQEEL TILNIYAPNTGAPRFKQVLSDL QRDLDSHTLMGDFNTPLSTLD RSTRQKVNKDQELNSALHQA DLIDIYRTLHPKSTE
7056	37424	A	7110	134	307	



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7057	37425	A	7111	2	173	RPPRSEVPGPLSPGRPPAAGLRGR*PAGVRGLREPRAFSGVRVER RSLFIGKDMFDS
7058	37426	A	7112	888	1016	VPGEIHALHSAADROQHENA*NAR TRWQHAQSGRSPLFLALSRE
7059	37427	A	7113	573	872	SPSLLPDPDAHVGC*SRSRKRDP RIRRFDSR*NLFCYCRKTS*PFH *G*MCQ*YQTDPRNSAQCHPVL LRLWWPGDEYDFLCRSGSVGS VRQSGRASGL
7060	37428	A	7114	1	654	
7061	37429	A	7115	71	2776	
7062	37430	A	7116	31	1016	TVLPERPYNRKSSRRNRRCGNP PARSFCPSSGSRSSSPATGP/ HTAIASALPRIAFGKISDSTQH TGPQDMAKAAT*NSLRGSMRY SFKPMVGRWIKSCLRPVWC
7063	37431	A	7117	279	1243	SVLLMCAADYLPRPDDVQTCN AVRVWLRYHRSNHGTPPDFSP GPVSAWYYAH/QPKIPIWSQ/QR GFTD/R*TRHKCPQRFVAPDK*I SSPD*AMNYRKHHRPAPRHTA PTQKARLMADKSSLRHRHNSA NKRRSASPLSSAGYP/GKRJRAQ NLIPASTTNGQLRIRQRRISQAR **TKRMARKGSIPISAVSNSLN SS*ASIIVSSCIRCALSPLSNIHK S*TAGPWGASSRKTNIGLSRQRI FPAWQSPCSRRTVKSSRQCAVT AAISSVAFRNAAFNPEGISVAS SNSLRGSMRYSFKPMVGRWIKS CLRPVWCIRPK
7064	37432	B	7118	1	726	
7065	37433	A	7119	1	138	
7066	37434	A	7120	56	133	
7067	37435	B	7121	1	1524	
7068	37436	B	7122	1	1521	
7069	37437	A	7123	1	1494	
7070	37438	B	7124	4	1698	

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7071	37439	A	7125	1	1725	MELKTKARELREECRSLSRSCD QLEERPNNRLIGVPESDGENGT KLENTLQDIIQENFPNLAKQVN VQIQEIQRTQPRYSLRRATPRHII VRFTKVEMKEKMLRAAREKGR VTLKGKPIRLTADLSAETLQAR REWGPIFNILKEKNFQPRISYPA KLSFISEGEIKSFIDKQMLRDFV TTRPALQELLKEALNMERNNRS WFFEKINKIDRPLARVIKKKRE KNQIDAINKDKEDITTNPTETI IREYYKHLYPNKLENLEEMDTF LDITYTFPRLNQEEVESLNTSITG SEIVAIISIAYPKKVQDQMDPQ PNSTRVLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASKRIKCLGIQLTRDVK DLFKENYKPLLKEIKEDTNKW KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTDLEKTTL NFIWNQKRARITKSILSQKNKA GGITLPDFKLYYTATVTKTAW YWYQNRWYWYQNRDIDQWN RTEPSEITPHVYNYLIF
7072	37440	A	7126	1	2478	

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7073	37441	A	7127	1	1746	METQKTLQKINESRSWFFKEKIN KIDRPLARLIKKEKNQIDTIK NDKGDITTDPTIEIQTITREYYKH LYANKLENLEEMDKFLDITYTL PRLNQEEAESLNKPIGTPEIEAII NSLPTKKIPGPDGFTAIFYQRY KEELQHKKLIHHDQVGFIPGM QGWFNIHKLINVIQYINRTKDK NHMHSIDAEEKSDKIQQPFMLK TLNKLIGDGYLKIRAIYDKPT ANIILNGQKLEAFPLKTGTROG CLLSPLLFNIVLEVLAIRQEK EKKCIRLGKEEVKLSLFADDMI VYLENPIVSAQNLLKLISNFSKV SGYKINVQKSAFLYTNNRQIE SQIMSELPFTIASKRIQYLGILQ RDVKDLFKENYKPLLEIKEEDT NKWKNI PCSWIGRINIMKMA LPKVIYRFDIAPIKLPMTFFTELE KTTLKFIWNQKRARIAKSILSQ KNKAGGITLPDFKLYYKAIVTK TAWYWYQKRDVDQWNRIEPS ETIPHICNHLIFDKPDKNKQWG KDSL FNKWCWEIWLAIGRKRK LDPFLTPTYTKINSRWIKDFNIRP KTIKTEESLGNIQDISMGKKFTS
7074	37442	A	7128	1	1908	
7075	37443	A	7129	1	1494	
7076	37444	A	7130	2	1562	
7077	37445	B	7131	1	1569	
7078	37446	A	7132	1	1593	
7079	37447	A	7133	1	1520	
7080	37448	B	7134	1	2796	

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7081	37449	A	7135	101	1686	SIAYQPKRVQDQMSQPNSTR ANIILNGQKLEAFPLKVTGTRQF SKENFEPVSPLLFNIVLEVLAARA IRQEKIKGIQLGKEEIKLSLFA DDMIYVLENPIVSAQNLLKLISN FSKVSGYKINVQKSQAFLYTNN RQTESQIMSELPFTIASKRIKYL GIQLTRDVKDLFKQNYKPRLKE IKEDTNKWKNI PCSWVERIYIV KMAILPKVIYRFSAIPIKLPMTFF TELEKTTLKFIWNQKRARIAKSI LSQKNKAGGITLPDFKLYYKDT VTKTAWYWYQNRDIDQWNRT EPSEIMPHIYNILFIDKPEKNKQ WGKDSL FNKWCWENWLAICR KLKLNPFILPYTKINSRWIKDL NVRPQTIKTLEENLGITIDIGM GKDFRSKTPKAMATKAKSDK WDLIKLSFCTAKETTIRMNRQ PTKWEKIFATYSSDKGLISRIYN ELKQIYKKKTNNPIKKWAKDIN RHFSKEDIYAAKRHMKKCSSSL AIRQMOKITTMRYHLTPVRMAI IKKSGNNRDMDEIGNHPSQ
7082	37450	A	7136	1364	3024	TEPKTKTT*LSQ*MQKRPLTKF NNASC*KLSIN/IVLEVLARAIQ EKEIKGVQLGKEEVKLSLFADD MIIVYLENPIVSAQNLLNLISNFS KVSQYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNER KEDTNKWKNI PCSWVERINIVK MAILPKVIYRFSAIPIKLPMTFF TELEKTTLKFIWNQKRARIAKSI LSQKNKAGGITLPDFKLYYKAT VTKTAWYSYQNRDIDQWNRT PSEILPRIYNILFIDKPEKNKQW GKDSL FNKWCWENWLAICRKL KLDPFKLPYTKIKSGWIKDLNV RPKTIKLEENLGITIDIGMGK DFMSKTPKAMATKAKIDKWDL IKLKSFTAKETTIRVNRQPTER EKIFATYSSDKGLISRIYKELKQI YKKRTNNLIK VVKDMNRHFS KEDVYAAKKHMKCCSSSLAIR EMQIKTTMRYHLTPVRMAIHK SGNNRITIVLLPGSLIVRSFHVTL NAILLHPGLTLFSPSAGRRDIPR VAFSYLAFSAQPSHNTPVN
7083	37451	A	7137	1	2274	
7084	37452	A	7138	2	2348	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
7085	37453	A	7139	1	2202	
7086	37454	A	7140	1	2823	
7087	37455	A	7141	1052	3831	RHKKPFKKSMPGAGFFERINK IDRPLARLTKRKREKNQIHAIK NDKGDITTDPTIEIQTIREYYKH LYANKLENLEEMDKFLDTYTL PRLNQEEIESLNRPIGTAEIVAIL NSLPTKKSPGPDGFTAEFYQRY KEELVPFLKLFQSIEKEGILPNS FYEASINLIPKPGRDTTKKENFR PISLMNIDAKILSKILANRIQQHI KKLIHHDQVGFIPGMQGVFNIC KSINVIQHINRTKDKNHMHISID
7088	37456	A	7142	1	327	
7089	37457	A	7143	1	446	
7090	37458	A	7144	382	1485	
7091	37459	A	7145	1	378	
7092	37460	A	7146	2	217	
7093	37461	A	7147	1	483	
7094	37462	A	7148	1	1260	
7095	37463	A	7149	1	891	
7096	37464	A	7150	5	182	RQGLLVSPRLVQKGEIRTPGLK RSSRLDLQKC*DYRHEPSSLAS EAPSVWVLLPPWRQS
7097	37465	A	7151	1	1914	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 9,540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
7098	37466	A	7152	1	2200	MKLTTHRENMALTNFGCHHIA AQQLNYTNTLLAARIKQRLTEQ FELMLRQAQIDFAGKAHSLTEA QANTTQVSAERDRLFKNYQRY LKGSQAAVNPFSERDIDDARQN FLAQDALAQISQLDSL VNGEQ SQIVSLKAQLAEAKYNLEQTIV RAPSNQYVTQVLIRPGTYAASL PLRPVMVFIPDQKRQIVAFQFRQ NSLLRLAPGDDEEVFNALPG KVFSGLAAISPAVPGGAYQST GTLQTLNTAPGSDGVIAITLDE HTDLSALPDGIYAQNPKNLKIV ELKAPQLPRSLDDAQIALAVIN TTYASQIGLTPAKDGIFVEDKES PYVNLIVTREDNKDAENVKKF VQAYQSDEIPCTRSKHCTPAE SGACKTESAARHAGPNLYQCR RIRSANRSAISVKGWRTPCIPDS LPAAEWLTYGSGYLAGMKLGD TPLVEYTRDRLHRETRLSFGRY ELTTAYTPAGQLQSOHLNLLS DRDYTWNDNGELIRISSPRQTR SYSYSTTGRLTGVTHTAANLDI RIPYATDPAGNRLPDELHPDST LSMWPDNRIARDDNLYLYRDR HGRLTEKTDLIEGIVRTDDERT HRYHYDSQHRLVHYTRTQYEE PLVESRYLYDPLGRRVAKRVW RRERDLTGWMSLSRKPVQVWY GWDGDRLLTIQNDRTRIQTIVQ PGSFPTLIRVETATGELAKTQRR
7099	37467	A	7153	719	1575	
7100	37468	A	7154	1	239	
7101	37469	A	7155	1	735	FNDSPSEARKITRRWRIGEAAD LVGVSSQAIRDAEKAGRLPHHP DMEIRGRVEQRVGYTIEQINH MRDVFGTLLRRAEDVFPVIGV AAHKELNNDYTSKKVMKPLIT SNTVTDEIERANVLKMNKGWY LFTDSRGSKMTIDGINSNDIYM LGYVSNLSLTPGYPLNKTGLVL QMALDPNDVTFYSHFAVPQT KGNVNVITSYMTNNGFFEDKK ATFAPSFLMNIKGKNTSVVKNS ILEQQQLT
7102	37470	A	7156	1	4368	
7103	37471	A	7157	1	1452	
7104	37472	A	7158	1	516	
7105	37473	A	7159	1	743	

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7106	37474	A	7160	3	1743	DSPEARKITRRWRIGEAADLV GVSSQAIRDAEKAGRLPHPDME IRGRVEQVRVGYTIEQNHMRDV FGTRLRRAEDVFPFVIGVAAHK GNDPQGTASMYHGWVPDLHIH AEDTLLPFYLGKEDDVYAIKP TCWPGLDIIPSCALHRIETELM GKFDEAQPNLIGITINVVCAAD VLIVPTPAELFDYTSALQFFDM LRDLLKNVDLKGFPDVRILLT KYSNSNGSQSPWMEEQIRDAW GSMVLKNVRETDEVGKGQIR MRTVFEQAIDQRSSTDLSLSTP AAPMVDSLIARVGVGMARGNAI TLPVCGRVDVKFTLEVLRGDSVE KTSRVWSGNERDQELLTEDAL DDLIPSFLLTGQQTAFGRRVSG VIEIADGSRRRKAAALTESDYR VLVGELDDEQMAALSRLGNDY RPTSAYERGQRYASRLQNEFAG KYFLRWLMRKIFHIITRCINTAK LPKSVVALFSPHGELSARSQDA LQKAFDTKEELLKQASNLHE QKKAGVIFEAEVITLLTSVLKT SSASRTSLSSRHQFAPGATVLY KGDKMVLNLDLRVPTECIEKI EAILKELEKAP
7107	37475	A	7161	1	438	
7108	37476	A	7162	1	3216	MKLMETLNQCNAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQVRVGYTIEQI NHMRDVFGRTRLRRAEDVFPFG FGDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLARQVSR/VKRAPTC WPGLDIIPSCALPRIETELMGK FDEGLPTDPHMLRLAIETVA HDYDVIVIDSAPNLG
7109	37477	A	7163	1	513	

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7110	37478	A	7164	1	2027	MRGHREKAAACKPRTRASEGT TPASTFILDFQPPNCNYITSGDNH TLRDPHYVEDKGHKYL VFEAN TGTENGYQGEESLFNKAYYGG GTNFFRKESQKLQQSACKRDA ELANGALGIELNNDYTLKKVM KPLITSNTVTDEIERANVFKMN GKWYLFITDSRSGSKMTIDGINSN DIYMLGYVVSNSLTGPYKPLNKT GLVLQMGLDPNDVTFTYSHFA VPQAKGILCEEDNYTAGDNHM MRAPHCEEDRAHKFVVFDANA GTESGHQGEESLFNRACGGGGT FFFSKESQKLQQSACKRDCINA GHIENTKAIAIAQFNDDSPARK ITRRWRIGEADLVGVSSQAIR DAEKAGRLPHPDMEIRGRVEQ RVGYTIEQINHMARDVFGTRLKR AEDVFPPIGVAAHKGGVYKT SVSVHLAQDLALKGSLLLPKND FLFKLGLLEGHPLGKIHSPTGA DVARGSSGLPKSELFLPERNTQ ELQQDSEEGPLALQVLQSNLM DFADFGTTIKQDFRLLGQTSVD RLQLSQGQAVKGNQLLPVSL VKRKTTLPNTQTASPRALADS LMQLARQVSRLESGQNNDGIC EIHVAKYVEIFGLTSAEASKDIR QALKSFAGKLVVFYRPE/VGCR R*KRL*IFSLVYQTCAQSIQRAL CQTYQPIHSLLYRVTEPVYAV
7111	37479	A	7165	1	750	
7112	37480	A	7166	1	723	
7113	37481	B	7167	1	1156	
7114	37482	A	7168	1	999	
7115	37483	A	7169	1	529	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFVAGDEKGYESFPWF IKTCA\HPSRGLYSVHINPYLIPS LSGYRTGLRSFGLVKQKKSPIR MPCVYTNPCVSIYSRMAQASSL
7116	37484	A	7170	1	1038	
7117	37485	A	7171	1	1098	



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7118	37486	A	7172	1	838	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGLRLRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGTE TMYHGWVPDLHHIAEDTLLPF YLGEKDDVTYAIAKPTCWPGLDI IPSCIALHRIETELMGKFDEGSL PTDPHLMYYQAPCMKSNAL IVILGTVTLDVAGIGLVMPVICR ASCGISSIPTASPVIMACC
7119	37487	B	7173	1	1212	
7120	37488	A	7174	1	738	
7121	37489	A	7175	1	654	
7122	37490	A	7176	1	448	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGLRLRAEDVFPPVI GVAAHKAGNLSQCLH**IGQR AGRGGLRIGRQGGFSFHQ
7123	37491	B	7177	1	753	
7124	37492	A	7178	1	345	
7125	37493	A	7179	1	516	
7126	37494	A	7180	1	1989	
7127	37495	B	7181	1	1191	
7128	37496	A	7182	1	669	
7129	37497	A	7183	1	574	
7130	37498	A	7184	1	934	
7131	37499	A	7185	1	1281	
7132	37500	A	7186	1	324	
7133	37501	A	7187	3	817	
7134	37502	A	7188	1	587	
7135	37503	B	7189	1	610	
7136	37504	A	7190	1	882	
7137	37505	A	7191	1	1077	
7138	37506	A	7192	1	418	
7139	37507	A	7193	1	840	
7140	37508	A	7194	1	337	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRNVFGSLRRPTAELKCA SQT
7141	37509	A	7195	1	1142	
7142	37510	A	7196	1	1080	
7143	37511	A	7197	1	1170	
7144	37512	B	7198	1	1296	
7145	37513	A	7199	1	1179	

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7146	37514	A	7200	1	507	
7147	37515	A	7201	1	411	
7148	37516	A	7202	1	793	
7149	37517	B	7203	366	1502	
7150	37518	A	7204	1	1107	
7151	37519	A	7205	1	2388	
7152	37520	B	7206	1	2260	
7153	37521	A	7207	1	1067	
7154	37522	B	7208	563	1467	
7155	37523	B	7209	1	1272	
7156	37524	A	7210	1	1722	
7157	37525	B	7211	1	1917	
7158	37526	A	7212	1	2679	
7159	37527	A	7213	1	1207	MKLME TLNQINAGHEMTKAI AIAQFNDDSP EARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRV EQRVGYTIEQI NHMRDVF GTRLRR AEDVFPPG FGDFAHFGNHHQNRIFALLGQ TSVDRLLQLSQGQAVKGNQLL PVSLVKRKTT LAPNTQTASPR A LADSLMQLARQVSRL ESGQAIR DAEKAGRLPHPDMEIRGRVEQ RVGYTIEQINHMRDVF GTRLRR AEDVFPPVIGVA AHKGGVYKT SVSVHLAQDLAL KGLRVLLVE AARGLKKRGLAGTAQGPGE PG EAPKGGKKGKTEPGHERKGNWT GKGPQIREGTS PNP PREHGGE C APPPPSAKRKOPKAQKRKANSN AHPRQPKPKKRPRKRTNSRTN TRSGKRQNKQPEEPK
7160	37528	A	7214	1	2757	
7161	37529	A	7215	1	2984	

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7162	37530	A	7216	1	2387	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRD AEKAGR LPHDPMEIRGRVEQRVGYTIEQI NHMRDVFGRRLRKAEDVFPPI GVA AHKAKGLTALSPQTDWNR KRNSKPLAQVQEEDSAWHPE CLQKTRQAWCDNLKTCHTSHG SVMETA VINHKKRKNSPRJVQ SNDLTEAAYSLSRDQKRMLYL FVDQIRKSDGTLQEHDGICEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVFYRPEEDAGDEK GYESFPWFIKRAHSPSRGLYSV HINPYLIPFFIGLQNP LTQFRLSE TKEITNPYAMRLYESLCQYRK DGSIGVSLKIDWIIERYQLPQSY QRMPDFRRRFLQCINAGHEMT KAIAIAQFNDDSPARKITRRW RIGEAADLVGVSSQAIRD AEKA GRLPHDPMEIRGRVEQRVGYTI EQINHMRDVFGRRLRKAEDVFP PVI GVA AHKGGVYK/TLISVHL AQDLALKGLPGLLR/EGNDPQG /TTS MYHG WVPDLHIAEDTLL PFYLG EKDDVPYAIKPTCWAG AWHFFLPCRALHRIETELMGKF DEGKLPTDPHMLRLAIETVAH DYDVIVIDSAPNLGIGTINVVCA ADV LIVPTPAELFDYTSALQFFD MLRDLLKNVDLKGFE PDVFIRD KLMERRNRRTGRTEKARIWEV
7163	37531	A	7217	1	917	

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7164	37532	A	7218	I	1862	MKLMETLNHCINAGHEMTKAV AIAQFNDDSPSEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVGFTRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAY DLALKGLRVLVVEGNDPQGT SMYHGWVPDLHIHAEDTLLPF YLGEKDDVTYAIPKTCWPLDI IPSCALHRIETELWGK/FDEGR SFMPGPP/HHHPLGRSSQ*QVSN SLDRAAKGN*KPLCHCPCSGTT HATLRLIKEQRPYVPPYHLQQA VVDPRRGHMLV/LNVVRVTG DVGKGQIRMRTVVEQAIDQRSS TGAWRNALSIEWPVCNEIFYRL IKPRWEIRWGWKRAPIPKHTLN TQPVEDTSLSTPAAPMVDSLIA RVGVMARGNAITLPVCGRDVK FTLEVLRGDSVEKTSRVWWSGNE RDQELLTEDALDDLIPSLFTTGQ QTPAFGRRVSGVIEIADGSRRR KAAALTESDYRLVVGELDDQ MAALSRLGNDYRPTSAYERQ RYASRLQNEFAGNISALADAEN ISRKIITRCINTAKLPKSVVALFS HPGEAICPVRMFRMKLMTLN QCINAGHEMTKAI AIAQFNDD PGSEENNPALENR
7165	37533	A	7219	I	2724	
7166	37534	A	7220	I	3252	FNDDSPSEARKITRRWRIGEAAD LVGVSSQAIRDAEKAGRLPHPD MEIRGRVEQRVGYTIEQINHMR DVGFTRLRRAEDVFPPFNDDSP EARKITRRWRIGEAADLVGVSS QAIRDAEKAGRSTATRILEIRGR VEQRVGYTIEQINHMRDVGFTRL LRAEDVFPPVIGVAAHKGGV YKTSVSVHLAQLALKGLRVL LVEGRSFPQTEACLLQYSSWDV SSEKPAALNKNKSEMRGDFAD FGTITIKQDFRLLGQT
7167	37535	A	7221	I	465	
7168	37536	A	7222	I	291	

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7169	37537	A	7223	1	1710	MLCTKWDLGLEKNAGKNKN AYKWYGPANAPDEPHIEQLV GECRVMRQLKRLISRIAPSSV MVVGESGTAIPVVSHEAFKGGF ADIGVHYLDWTSRTTEKSSTKS HKDDDFGYLEFEGGANFSWGEM YGFDFWENFYNGRHNKPGSEQ RYTFKNTNRIYLGDTGFNLYLH AYGTYGSANRVNFHDDMFLA GFGQF*PAGGW/WGSNPFFAK RYTRSKPYTGDNGYVAGWV AGYNFMLGSEKFTLTWNEYE FDRDATYAADFLPLYDVCQD NGNLEYDTYSQPEWKHNFH YLAVLYRFKDESGKEQFSGAV VKTREATPGKIEAITRRMLDFS PRLKKLADCPSPRVFEALCICS MLDALLLCPLDYHASCNYS YALLDPQGFPLPHRRLWGPYID VDVPMHLHIQHAWAQDALLSC LYSDLLYMSSFYPYAGTLRLM GVTSYNHKNLTLLTYCITLMSTI RFAYDGDDEEIAMKYTDFLKGE LSMNIRPLHDRVIVKRKEVETK SAGGIVLTGSASAKSTRGEVLA VGNGRILENGEVKPLDVKIGDI VFFNDGYRGEI
7170	37538	A	7224	678	1588	RTQHKASLHGRASAFCPPLFA PQAPRLFDRGFLTFSANFAA VAFCPPLFPPTGAAAVCPLPLF APRRFLPPPPRLFRCHGFFPPC LGFLTSAAFFLPPPLFALRRRG FLPFAAAAFPPTRLFAPPPTQL FAPSPWWLFAAAAFCPWWLAP TPPRLFVPAAAAFCCRDPLPSP PLFRHRDFLPPPRIFVPAAL RAGAADSAAGSTGVLGQDLWS RCVVGTMGEAPGSRGGGGGLR EDIPLPEFPSPGALSSCR*GNRR PEGEMTCQEPLLS/CSWIP*VKE FETNPNDIVRPH

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7171	37539	A	7225	1	1627	MTKQLELPQSPGEVPGSDYPLL IACAYIGFLTWGGGFGSGMPLL AATPGNPVEHIALGPLVGDLTFLS GFNIFITVALIVVMPFITRMMMP KPSDVVSIDPKLLMEEADFQKQ LPKDAPPSEERLEESRILTLIGAL GIAYLAMYSFSEHGFINITNTVNL MFMIALGLLLHKTPMAYMRAIS AAARSTAGILVQFPFYAGIQLM MEHSVTGIEAAMLDDLGGHLLG VNVASLLGDGQQRSEVEMLGY LFFVGNRKATPLPYQSQPDDSC DWYRLRHEEAMTPDAVVRLEAE AAYEKYGFNDFKLKGGLVAGE EEAESIVALAQRFPQARITLDPN GAWSLNEAIKIGKYLKGSLAY AEDPCGAEQGFSGREVMAEFR RATGLPTATNMIAITNWREMGH AVIAQSVSDIPLADPHFWTMQG SVRV AQMCHEGLTWGSHSNN HFDISLAMFTHVGAAAPGNPTA IDTHWVQEGDCRLTQNPLEIK KGKIAVPDAPGLGVELDEWQV QKAHEAYKRLPGGARNDAGP MQYLIPGWTFDRKRPVFGRH
7172	37540	A	7226	3	655	
7173	37541	A	7227	1	633	
7174	37542	A	7228	1	630	
7175	37543	A	7229	362	1491	PTLSVIHESMRFFIRHQPENLTL VVLRSNLPQLALPICVFVINCW KLA VSNWHLPISTGC AVTKDG RWSPEFTITGQA/WDLPVVG YR NGVAQPLRLWQATHAHPDLT KFNDGDFLRAEQQGGINAEKLT VLYPNDNHTAGKKLRLMQQYF QCACSVADILRRHHLA GRKLLH ELADYEVIQLNDHTHTAIPELL RVLIDEHQMSWDDAWAITSKT FAYTNHTLMPEALERWDVKLV KGPLPRHMQIINEINTRFKTLDL QDAEHRPLKMRGCLLCQCHTL FQKGHRFFT GAGGNRQNNVIE HLVAASRYRFTTASRRPLFTAG FTLLTAFLFHSNFAEGVNSLMF MKNLTISGGFLLLAITGPGAYS IDRLNNKKW
7176	37544	A	7230	1	660	

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7177	37545	A	7231	545	1322	KHAEHLGQATHAHPFILTKFNP GYFLRRQTTRGINAEK/LAKIFF \PKANHFAAGKKLRLMQQYFQC ACSVADILRRHHLAAGKRLHEL ADYEVIQLNDTHPTIAIPELLRV LIDEHQMSWDDAWAITSKTFA YTNHTLMPREALERWDVKLVKG LLPRHMQIINEINTRFKTLVEKT WPGDEKVWAKLAVVHDKQVH MANLCVVGGA VNGVAALHS DLVVKDLFPEYHQLWPNKEHN VTNGITPRRWIKQCNPAALL
7178	37546	A	7232	641	874	KYPTPGRDLRMFITGLSERL*EI TSLLKRSITGDKYSLRPLTANSV TSVTHFSFGRVALKSLSSVRAV SLDLNRCFK
7179	37547	A	7233	1	693	
7180	37548	A	7234	980	1305	TWLKICIRHKSLLTSL/HVLH SDQGWQYRMRRYQNILKEHGI KQSMRKGNCCLDNAVVECFFG TLKSECFYLDEFNSISELKDAVT EYIEYNSRRISLKLKGSDSN
7181	37549	A	7235	1	3219	
7182	37550	C	7236	1	7521	
7183	37551	A	7237	1351	2117	CDRILCSACCAEPQPVSHLHRL RRSFSEKQPDNGSQNPASRDR/ DVVDVTVIAWIEHRGGHEAPS GPGEDGMDAPAIAAGTFSPREA STLPVQVS*VCLNCCSRDVPK ATRVPL/EKLAGPLRHPLFMLF QTCLHLSLFTHHFADDSRRLQIF SVGFVAGLKQYRRDLLQGDV NPRMATAVGNDQVWFQSGNG FQARLRARSDGLPRFQVRTHFG QDAFCIVIGNTDRDDVHGGQ RIGEREFQHINPLWRFEC
7184	37552	A	7238	690	868	

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7185	37553	A	7239	2607	3692	TWLRICSIHRSKSLILTSI/HVLHSDQGWQYRMRRYQNLKEHGIKQSMRSRKGNCLDNAVVECFFGTLKSECFYLDEFNSISELKDAVTEYIEYYNSRRISLKLGLTPIEYRNQTYMPRVNCPLEDTLRIPDIGGVVRARAIAKLLNDTDMAIIDKRRPRANVSQVMHIIGDVAGRDCVLVDDMIDTGGTLCKAAEALKERGAARVFAYATHPIFSGNAANNLRNSVIDEVVCDTIPLSD EIKSLPNVRTLTSEKYTAARFT RDLIAGITVGIIAIPALMALAIGSGVAPQYGLYTAAVAGIVIALTGGSRFSVSGPTAAFFVILYPSVQ QFGLAGLLVATLLGLDFSDG
7186	37554	A	7240	1326	3930	NVLRGISAAFVG*AKAPRNGTQ
7187	37555	A	7241	3	195	RVDDFVGAGAPASPL*QCGQLQKLIGISIGSLRGLGTICAVSNDLTEQEIRLTLEHCPNSFF
7188	37556	B	7242	75	402	
7189	37557	A	7243	1	309	
7190	37558	A	7244	3	187	
7191	37559	A	7245	383	1778	
7192	37560	A	7246	2	447	IREKLIRLQHENKMLKLNQEGSDNEKIALQLSLDDANLRKNEL ETE/Q*VLVPINFPLTTAFVSHRFRLVNRLLLEVQSQVEELQKSLQDQGSKAEDSVLLKKLEEHLEKLHEANNEQLQKKRAIHEDLEPRFNNSSSLKIEELQEALR
7193	37561	B	7247	80	1042	
7194	37562	A	7248	1	192	
7195	37563	A	7249	3	62	
7196	37564	B	7250	219	230	
7197	37565	A	7251	246	594	
7198	37566	A	7252	1	316	
7199	37567	A	7253	1	1059	
7200	37568	A	7254	1	516	EDALEQEKELQIQVEHYEFQTRQLELKAKNYADQISRLERES EMKKEYNALHQRHTEMIQTYVEHIERSKMQQVGGNSQTESSLPGRSRKERPTSLNVFPLADGT/CTCTDRGQARACGGPLAPE*PRPA AVQLQLPGFVAVPWSERLLPVAGVPRSLGREPRLQAALHGS
7201	37569	A	7255	1	1176	
7202	37570	A	7256	1	749	
7203	37571	A	7257	1	691	



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7204	37572	A	7258	2	810	VMMTGYNNGRCPRNSLYSDCII EEKTVVLQKKDNEGFGFVLRG AKADTPIEEFTPTPAFPALQYL ESVDEGGVAWQAGLRTGDFLI EVNNENVVKVGHQVVMNIR QGGNHFLKVVTVTRNLDPDD TARKKAPPPPKRAPTTALTLRS KSMTSLEELVDKASVRKKKD KPVEIVPASKPSRAAENMAVEP RVATIKQRPSSRCFPAGSDMNS VYERQGLA VMTPTVPGSPKAPF LGIPRGTMRRQKSIGKKCGTTP QKLPLGFQTQP
7205	37573	A	7259	1	1416	
7206	37574	A	7260	2	1142	
7207	37575	A	7261	1	576	
7208	37576	A	7262	21	289	
7209	37577	A	7263	2	372	
7210	37578	A	7264	170	655	VRRRLGALFTWICSVTRESTSK PLSSALLSAKLLHRARSRTGLS GRNPKTISQDLQFAAIGSPLTES LNLHSRQALRDCCWHTHTIPPNP *ICTHARR/WRDCCWHTHTIPPNP DTVWRFP.LSSPVSAPKQERAS SEPCSWSHWCRCSLSWLSIIPTE GCTPVCSSICLLMATFPMFSLIK IVR
7211	37579	A	7265	1	1725	
7212	37580	A	7266	307	686	PRRTPMKSKCKIEVPIFVPLRT TRENCLRPKGYAIYEKAPRSIL KDVHLTRNQCVPIPDTRYK WWS WQVCRPKQWGWTOGPVAPK RSAEFFAAHA*KRRRVMLNLR GLDVDSLVIHQVNKAP
7213	37581	A	7267	1	276	
7214	37582	A	7268	1	726	
7215	37583	A	7269	3	231	
7216	37584	A	7270	1	217	
7217	37585	A	7271	3	283	KRKTEGDAKGDKAKVKDESQR RSARLSAKPAPPKPEPKPKAP AKKGEKVPKGGKKRKADAGKE REGYWRSSQVKCIHFL*LYFW*L YSLKYYFI
7218	37586	A	7272	1	1188	
7219	37587	A	7273	5	365	
7220	37588	A	7274	1	453	

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7221	37589	A	7275	1	441	RQPAHPTGSSAAAAPKRKSA HAGVAVAASARLPPCAGCLR AAPPLASSARLRALRRP/GGL WAAGCAPAAGQLCTAAGSAAP GALQRCGGRHGIRPWCAEIAS AG*GSGGSRWGCWPCFLLR CTSHPLSSPLPTHGSLQASFS LTRDCVSTKTLWVWLEVQR
7222	37590	A	7276	2	1957	
7223	37591	A	7277	1	678	
7224	37592	A	7278	1	720	
7225	37593	A	7279	190	2947	QALQRGLLSR/DRAPCSSKLSW RS/SPRRRAGTGPVQEEVALKP VLLRHPVQPVIRVKLPRLCLLE AGQLRGVHRLESVEEYYEADG AEWGPPDTAMLESLPEMAGKH SLPQLLSSASQPGAIIQIYSIL YQIHYLKHLSSYWGASQWKH TRITHYFESLW*EHLPS*KYQK REKWADLTRSLENP/GQQPRDS WEPGFWALPQAGDSCQTSQSP RKPTGPPKSPPPPEEGRLLR/CPT MPVMRKSLTE
7226	37594	A	7280	3	439	
7227	37595	A	7281	1	273	
7228	37596	A	7282	2	1664	
7229	37597	A	7283	1	7511	
7230	37598	A	7284	1	5046	
7231	37599	A	7285	42	8716	
7232	37600	A	7286	2	201	
7233	37601	A	7287	2	797	CS/GSPPTCRQAQTSLEVALYM FLQNPDTAEAVLVAMSCFHLCE EADTQCGVDESVHNLNPN TFMEFACQCDVNSPPVGPVSE HKGSMISVMSSEGNADTPVSK YMDQLLSLMVCNLEKVG LQIP TNDKDLVLLTDINTQFVEQTL DIMKNLLDNHTEGSPHELEQAS IETMMLNLVRNKMVEYLT DW VMGTSNQAADDDVKCLTSR/D HPGGTLL*GQPRPELPA GLPRQ PASPGPRHPGASCGWPR APPDS APGGPGRER
7234	37602	A	7288	56	8669	
7235	37603	B	7289	278	2333	
7236	37604	A	7290	1	423	

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7237	37605	A	7291	2	1688	PLYFHSPPAWLCSPSPPSARLYL ELRKLPA TL PWSSVTD TGSYSA GRRERGGEGEGRRVRVADH RSALPRTGPGQSEELANMQGL VERLERAVSRLESLSAESHRPP GNVCGEVNGVIA/GVAPSRGKPL HKLMDSMVAEFLKNSRLSGD VETLAEIVHSAFQAQRAFLMA SQYQQPHENDVAALLKPISEKI KEIQTQRE/RTRGSNMFNHL VSESIPALGWIAVSPKPGPYVK EMNDAA TFYTNRV LKDYKHSD LRHVDVWKS YLNIWSELQAYI KEIHHTTGLTWSKTGPVASTVS AFSVLSSGGLPPPPPLPPPGPP PLFENEGKKESSPSRSALFAQL NQGEAITKGLRHVTDQKTYK NPSLRAQGGQTQSPTKSHTPSP TSPKSYPSQKHAPVLELEGKKW RVEYQEDRNDLVISETELKQVA YIFKCEKSTIQIKGVNSIINDNC KKLGLVFDNVV GIVEVINSQDI QIQVMGRVPTISINKTEGCHIYL SEDALDCEIVSAKSEMNILIPQ DGDYREFFPIPEQFKTAWDGSKL
7238	37606	B	7292	44	355	
7239	37607	A	7293	1	3623	SEKEKEELERLQKEEBEERKKRL QLYVFMRCIAYPFNAKQPTD MARRQKQKSKQQLQTVKDRFQ AFLNGETQIMADEAFMNAVQS YYEVFLKSDRVARMVQSGGCS ANDSREVFKKHIEKRVRLPEID GLSKETVLSSWMAKFDIYRG EEDPRKQQARMTASAASELILS KEQLYEMFQNLGIKKFEHQLL YNACQLDNPDEQAAQIRRELD GRLQMADQIARERKFPKFSVKE MENMYIELKSSVNLLMA
7240	37608	B	7294	1	1555	
7241	37609	A	7295	1	1056	
7242	37610	B	7296	54	2173	
7243	37611	A	7297	1	984	
7244	37612	B	7298	95	1350	

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7245	37613	A	7299	1	2569	MDGAKAFFSAVAAGFVILTCQ LQWQWQHGGVHAHQWLWLA SGYRDACFCVSTYSSGPSEFP TLGLTNELAIIDLEERKRRKAK VWKGEGGGLRSPRQSLAFA VLASRGTRSCHVSPYLGVS SSPNPHPTTGAIPPVQRWGL PQINQKNREIAIPLTLGMSTH RGCKNMSRFSPLHCCTTPIST FTDPGSHCKGAHGDIQLLIQNL KGALPMSINRSYFNAHPLLQISE AVTFKDVAVVFTEELGLDPA QRKLYRDVMLENFRNLLSVGN QPFHQDTFHFLGKEKFWKMK TSQREGNSGGKIQIEMETVPEA GPHEEWSCQIWEQIASDLTRS QNSIRNSSQFFKEGDPVCQIEAR LSISHVQKPYRCNECKQSFSD VSVFDLHQQSHSGEKSHTCGEC GKSFYCSPALHIHQRVHMGEK CYKCDVCGKEFNQSSHLQTHQ RVHTGEKPFKCGQCGKGFHSRS ALNVHCKLHTGEKPYNCEECG KAFIHDSQLQEHQRIHTGEKPF KCDICGKSFRVRSRLNRHSMVH TGEKAFCRDTCKGNFRQRSAL NSHSMVHIEEPYKCEQCGKGF ICRRDFCKHQMVTGEKPYNC KECGKTRWSSCLLNHQVHS GQKSFKEECGKGFYTNRRSS HQRSHNGEKPYNCEECGKDYK RRLDLEFHQRVHTGERPYNCK
7246	37614	A	7300	2	326	
7247	37615	A	7301	166	443	

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7248	37616	A	7302	1	2692	MDPGTLQSASQGP TAINPCDYV LKRRNIQTWSQRLTPIKWHVYI LMIGPGEKEAGRN LGIFGK WTP FPKIPAKRLRESNCPVDAQEIW LPQAFREYLGRRGNFGPGRRTC EFWEVESICSVESWELWLRQA DSGDSGKCSPDACGHIDTSLR AGHCYLTRLWHVSGRIPPSFKL HHPGVCKFPKVGGKMTTFKEA VTFKDVA VVFTEELGLLDPAQ RKLYRDVMLENFRNLLSVGHQ PFHQDTCHFLREKFWMMGT ATQREGNSGGKIQTOMETVPE AGTHEEFSCQIWEQIASDLTR SQD TTISNSQLFEQDDNPSQIKA RLSIHVKTETSEGRCKKSFSD VSVLDLHQQLQSREKSHTCDEC GKSFYSSALRIHQRVHMGKEL YNCDCVCGKEFNQSSHQIQRI HTGEKPFKCEQCGKFSRRSGL YVHRKLHTGVKPHICEKCGKA FIHDSQLQEHQRIHTGEKPFKC DICCKSFRSRANLNHRSMVHM REKPFRCDDTCKGSFGLKSALNS HRMVHTGEKRYKCEECGKRFI YRQDLYKHQIDHTGEKPYNCK ECGKSFRWASGLSRHVRVHSG ETTFKCECGKFYTNQRYSH QRAHSGEKPYRCEECGKG YKR RLDLDFHQRVHRGEKPYNCKE CGKSPGWASCLLNHQRIHSGEK PFKCEECGKRFTQNSQLYTHRR
7249	37617	A	7303	1	585	KRTAISPKDAFETRQDLNEEEA AQVHG VKDPAP/ASTQSVLADG TDSAGN*ARQEPHKAAL*PIQN YQANLVNTFPYSNNSGGRG/RL MKTV/TQGSQQPSLADPASHLP VGDHLTYSNETEPVRALLPDEK KEVKPPALSMNLEHATMPVL LDHLRETRADKKRLRKALREFE EQFFKQTGRSPQKEDRIPMADE YY
7250	37618	A	7304	1	366	

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7251	37619	A	7305	1	1265	R Y R P G I G S T I S S L V E E H A P P S W E P Q H Q N V E A T V L V D S V L R P S M G N F K S R K P K S I F K A E S G R S H G E S Q E T E H V V S S Q S E C Q V R A G T P A H E S P Q N N A F K C Q E T V R L Q P R I D Q R T A T S P K D A F E T R Q D L N E E E A A Q V H G V K D P A P A S T Q S V L A / D G T D S A D P S P V H K D G Q N E A D S A P E D L H S V G T S R L L L / Y H I T D G D N P L L S P R L F P L S G S Q R F N L D P E S A P S P P T Q Q F M M P R S S S R C S C G D G K E P Q T I T Q L T K H I Q S L K R K I R K F E E K F E Q E K Y R P S H G D K T S N P E V L K W M N D L A K G R K Q L K E L K L K L S E E Q G S A P K G P P R N L L C E Q P T V P R E N G K P E A A G P E P S S S G E E T P D A A L T C L K E R R E Q L P P Q E D S K V T K Q D K N L I K P L Y D R Y R I I K Q I L S T P S L I P T I V S Q D T C M L L L C
7252	37620	A	7306	797	1390	P R M G A R P R A P A Q P P P A A A Q R P P A R P A T P T A C G S S A H R A P S P A R S R R S P C T P R A A P A A P G P K A A R Q W A G T A T R S S R P Q R S A R R S P R D S S R C W A I S S R S K R A A T A C T P G A K R R V A T K A R G A L W S K P K S K A M R L W P W C L S G R L G S * K A Q E V A Q D P G S D E G R G R L V E S G L Q D E G W V P Q G G E G G V A G Q D A S H R G S F R G A L K
7253	37621	A	7307	605	697	
7254	37622	A	7308	1	1263	
7255	37623	A	7309	257	1190	
7256	37624	A	7310	394	485	
7257	37625	A	7311	21	674	
7258	37626	A	7312	277	396	G L L P G W K I * C S R V F V T S A I H V E V A E L A N L P C T K V H F P D P N K L H C F Q L T V T P D E G Y Y Q G G K F Q F E T E V P D A Y N M V P P K V K C L T K I W H P N I T E T
7259	37627	C	7313	74	316	
7260	37628	C	7314	211	390	
7261	37629	A	7315	1	2601	
7262	37630	A	7316	1	1365	
7263	37631	A	7317	358	760	S I P L L F R K S S L S R K * C S A A S I F S G S S K F K R S V N K E F N P Q T T S F N V L V G A Q P V P S I E C S L N K L R H I S P V S V I V G V P D S L V Q A F H F G R H H V V R I R E L Q F Q T E I F H P G S N P H L G L L L A E N N E A C L D Q E N A L Y M Y K V
7264	37632	A	7318	1	1728	
7265	37633	A	7319	1	558	

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7266	37634	A	7320	2	1884	PAGAGPGQEAGAGPGGAVAY ATGAEEGEMKPVAAGAAVPPG EGISAAPTVEPSSGEAEGGEAN LVDVSGGLETESSNG\KDTLEG AGDTSEVMDTQAGSVDEENGR QLGEVELQCGICTKWFTADTFG IDTSSCLPFMTNYSFHCNVCHH SGNTYFLRKQANLKEMCLSAL ANLTWQFRTEEHPTMFSKD KDIIFFIDKYWECMTTRHRPGK TTWPNNIVKTMskerDVFLVK EHPDPGSKDPEEDYPKFGLLDQ DLSNIGPAYDNQKQSSAVSTSG NLNGGIAAGSSGKGRGAKRKQ QDGGTTGTTKKARSDFLSAQOR LPPHGYPLEHPFNKDGYYILA EPDPQAPDPEKLEIDCWAGKPIS GDLYRACLYERVLLALHDRAP QLKISDDRLLTVVGEKGYSMVR ASHGVRKGAWYFEITVDEMPP DTAARLGWSQPLGNLQAPLGY DKFSYSWRSSKGTKFHQSIGKH YSSGYGQGDVLFYINLPEDTE TAKSLPDTYKDKALIKFSYLY FEEDFVDKAEKSLKQTPHSEI FYKNGVNVQGVAYKDIFEGVYF PAISLYKSCTVSINFGPCFKYPP KDLTYRPMDSMDGWGAVVEHT LADVLYHVETEVDGRRSPPWE
7267	37635	A	7321	1	267	
7268	37636	A	7322	60	888	RGAALARTLSVRVPGAGTRR SHALGPRPGARSSFLRCELRR CMCGNNMSTPLPAIVPAARKA TA AVIFLHGLGDTGHGWAEAF AGIRSSHIIYICPHAPVRPVTLN MNVAMPWF\DIIGLSPDSQED ESGIKQAAENIKALIDQEVKNGI PSNRILG/GFSQGGALSLYTALT TQQLAGVTALSCWLPLRASFP QGPIGGANRDISILQCHGDCDPL VPLMFGSLTVEKCLKLVNPNAN VTFKTYEGMMHSSCQEQEMMD VKQFIDKLLPPID
7269	37637	A	7323	1	1182	

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7270	37638	A	7324	1	2469	MVDRARPTVLVTEVPLKSKHT AQMGVLVTANESQPLVHETAL KNKKPQSWFNPFCVSYNRKPG LQD*GRAERPELGEQATEAALL KAPAESVRQEHRSNT/PQTRSC CPQYFPRAGCLPSRGHDVEPQH EAGDGPCRGIRNG*KLLSSFFG QQVRT**R/CSELTPEKQEFFKGS ESSNRTSGGLFGVVPGA AETGD VCVYTFKELEGQTSDEEGSRLE NDFLEITDEDKKKSTKDRYDKY KEVGEHPPLSSSPVEHEGVKLG QKSYRCDECGKAFNRSSH.LIGH QRIHTGEKPYECNECGKTRFQT SQLIVHLRTHTGEKPYECSECG KAYRHSSHLIQHQLHNKEKPY KCNECAKAFQSSRLTDHQR HTGEKPYECNECGEAFIRSKSL ARHQVLHTGKKPYKCNECGRA FCSNRNLIDHQRIHTGEKPYECS ECGKAFSRSSGLISHHRVHTGE KPYSCIECGKAFNQNSQLIEHQ RMHRGKKVYKCECGKAFGLS KCLIRHQRLHTGEKPYKCNECG KSFNQNSHLIHHQRIHTGEKPYE CNECGKVFSYSSSLMVHQRT TGEKPYKCNDCKGAFSDSSQLI VHQRVHTGEKPYECSECGKAF SQRSTFNHHQRTHTGEKSSGLA CQEGNKEISKGPQKPPGYRLCP LQAVGGGEFGPTRVHISFSLSD LKQIKVFFPGGLMLEKQKKKS
7271	37639	A	7325	1	1596	
7272	37640	A	7326	2	3394	MAHAGGSGSGSAGGPGPAGRG LSGARWGRSGSAGHEKLPVHV EDALTYLDQVKIRFGSDPATYN GFLEIMKEFKSQSIDTPGVIRRV SQLFHEHPDLIVGFNAFLPLGY RIDIPKNGKLNQSPQTSQENSH NHGDGAEDFKQQVPYKEDKPKQ VPLESDSVFNNNAISYVVKIKTR FLDHPEIYRSFLEIHTYQKEQL NTRGRPRFRGMSEEEVFTEVANL FRGQEDLLSEFGQFLPEAKRSLF TGNGPCMHHSVQ
7273	37641	A	7327	1	738	
7274	37642	A	7328	1	399	
7275	37643	A	7329	3	223	
7276	37644	A	7330	1	1040	
7277	37645	A	7331	1	465	
7278	37646	A	7332	1	288	



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7279	37647	A	7333	109	4770	
7280	37648	A	7334	109	4687	
7281	37649	A	7335	109	4860	
7282	37650	A	7336	1	336	
7283	37651	A	7337	1	441	
7284	37652	A	7338	305	446	
7285	37653	A	7339	2	461	
7286	37654	A	7340	59	620	FQKIGL**/FIDLKDLFTIPLAE QDCEWFAFTIPVNNLQPAKRF HCFDTGSGNNGKASYSGSKNV FQMSYTSAQKAEVAVIELIEN AQLRFHTDEQLMTLFTQLQTA VRSRMHPFYITHIRAHPLPGPL TEGNQMADRLVANAISSARHF QQHLL/THSHPPGDRSRSCRHW RKKLEESGTSSHE
7287	37655	A	7341	1	1410	
7288	37656	A	7342	1	1740	MGQVWALVHSTLETFTHTDEEE GEYNEVTEQVCLPAKAGSAAV DLCTKA VSLLPGESPPQKVPTG AGGPLPAGMTGLLLGRSSLNIK AVQVQTGVTDSDYNGEIQVITS TSVPWKAKPGDHIAQLLVIPKK FIEGLKEPLQVERQSSCQGLGY/ PFLMAAIVKPEPIPLKWLTDKP IWTEQWPLSKEKLEALEDLITQ QLKKGHIAPTFSPWNSPVFIKK KSAEQDCEWFVFTILAVNNLQL KPAKRFHWKVLPGPNQPIWI PSRYLKYHKPDACEEIEPGSQ GFPVAAMSRLTLRRTPTVTSNT HRTQPPTWGQIEKLPMQAEENL RKAGQPVTSISNWILPRITKFKPI EGAENVFTDGSNGKASYSGSK GPLTEGNQMADRLVAKVISNA RHFHNLTHVNASGLKRRYSIT WKEAKAIQRCPTCQVMLSAAE QHLQKSAAKTEAEKLVWWRD PITKSREIGKIITWGRGYACVSP GPNQQPIWIPSKHLKPYHKPDA GEKIPGESRGPPVAAMSRLTLR RMPTVMSNTHRTQPPTWGQIK KLSQMAEENLRKAGQPVTMNN LMIAVITTA FNKG
7289	37657	A	7343	1	1239	

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7290	37658	A	7344	1	777	MPQNSLEECALGLGKKSLQEN VNNFPKTKLQFLKLTNWLPKI TKFKPIEGAENVFDGSSNGKA SYFGLKGKVFQTPYTAQKVE LVAVIEVLTAFDMPVMSIDST YVVHSTQLTENAQLRLHTDEQ LMTLSQLQTAVR/CFAVMGIP ASTTT/DNAPGYTSQALATFFS MWNIKRITGIPYNSQQAIVER MNLCLKQQLQKQTEGDREYGT PQMQLNLALLTLNLSLPGQG MLSAAEQHLQKPAVKTEAEQLI
7291	37659	A	7345	1	1307	
7292	37660	A	7346	1	2040	
7293	37661	A	7347	1	1898	MAGAPPPAWLPHCSSISDCCAR NERGSGVGVPASKPARSAAVDL CCTKAVSLLPGEPPQKVPARVC GPLPAGTVGLLGRSSLKKEV QIHTGVIDSDYKVEIQVVSSTV PWKAEPGERIAQLLVPPYVGT GKSEIKQTEGFGSTNKQGKAAY WVNOITDKHLTCEITQGGKFK GLVDTGADVSIISLQHWPSMW IQSTQFNIVGVDGSSNGKASYF GSKCKVFQMPYTSQKVELVA IIEVLTTFDMPINVISDSSYVVHS TQLIENALQFHTDEQLMTLFT QLQTAVRSRMHPFYITHIRAR/H TPLPGPLTEGNQMADCLVATA VSNARHFHNLTHVNASGLKCR YSNTWKAAKAIQRRPTCQMV HSSSFTGGVNPQGLEPNSLWQ MDVTHVPSFGRLAYVHVCVDT FSHFVWATCQSGESSACVKHH LLQGFVVMGIPASIKTDNVPGY TSQALATFFSMLNKRITDIPYN SQDVEADANADVGVDDVDADA DVEDAEVFTDADADAEDVDV EDADAERLCNADSDLDLDL VDAEMDADVDTNLDVDAADV VDVDADADVADIDVDVDTG LNLEADLDLDVADVDVTDADV DRDADVEVADADATVNADV DYVDVDTDS
7294	37662	A	7348	2	565	
7295	37663	A	7349	1	996	
7296	37664	A	7350	18	260	
7297	37665	A	7351	1	594	
7298	37666	C	7352	232	603	
7299	37667	A	7353	1	1236	
7300	37668	A	7354	568	1370	

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7301	37669	A	7355	1	1800	
7302	37670	A	7356	1	498	
7303	37671	A	7357	1	3400	MDCSEKWRDPLDAVCVLPATE EPVVQGSALYLVAHDDYCV WYSLQRTSPEKNERVRQMRPV CDCQAHLWNRPRFGEINDQD RTDRYVQALRTEIPLTLKGAKL QREEKEGDMPCRANILVTELF TELIGEGALPSYEAHRHLVET SLGEQVIVPPVDVESC PGAPSV CDIQLNQVSPADFTVLS DVLPM FSIDFSKQVSSAACHSRREPEL TSGRAQVVLVSWDIEDMPEGK IKCTMAPFWAHSDEEMQ
7304	37672	A	7358	1	687	
7305	37673	A	7359	1	660	
7306	37674	A	7360	112	474	
7307	37675	A	7361	352	441	
7308	37676	B	7362	1	831	
7309	37677	A	7363	460	612	
7310	37678	A	7364	251	496	LFVSI/VQVFH*GRRGFLVRN DCVQIWCEMISHSGFDLHFS DGQ*/WMSISSC/DFLAA*MSSFEK CLFMSFAHFLMGLVFVFL
7311	37679	B	7365	1	729	
7312	37680	A	7366	1	774	
7313	37681	B	7367	1	516	
7314	37682	A	7368	10	504	
7315	37683	C	7369	520	1656	
7316	37684	B	7370	1	1206	
7317	37685	A	7371	677	1126	AVTLTTKVCSTPEASETTNPPG GTNNSRRTALRAVALTAKVRS FTPRGSAASFLKSVRPRTHQFRT Q*HVHQIEFSPGGLWESCPRAS SSTGDPGRPPERRGAAARKTVG VQGVGYSLPRKLCPLFSRTTYP HTSLRKDCLESDDTAE
7318	37686	A	7372	2	394	HLFIYLLVLLWCPGWQPTAG LKGSCLSLSNWNYRPPL*AL LLGTQKLPRVWNFIMVRRIQDG VKPSVIAEREMSKRKAASLL SQRDHEPTRRKKLRTHPNIRRN KLQTRHLKSCNTHCEGPWRHS
7319	37687	A	7373	1	204	
7320	37688	A	7374	1	879	
7321	37689	A	7375	139	4488	
7322	37690	A	7376	1	933	
7323	37691	A	7377	335	582	VLQLLRQHVVSCSFLLVGSWS HWLQERSCRSSQ*VLQLIKAV WTQRTQEPSWLHLVDPAPGLQ VELPASPTRYAHTPQPLGG

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7324	37692	B	7378	1	3101	
7325	37693	A	7379	365	625	VAKIFSHVVGCLFTLMVVSFAV QKLFSLIRSHLSILAFVIAAFGLV DMKSLPTMS*MVMPRFSSRVF MVLGLKFKSLIHLELIFV
7326	37694	A	7380	994	1167	NKGGHKQMEEHSMMLMDRKNQ YRENGHTAQGNL*IQCHPHQAT NDFLHRJGKNKLASNM
7327	37695	C	7381	143	3529	
7328	37696	B	7382	54	1158	
7329	37697	A	7383	1662	1919	LLNVFALAFLVLLIEMLGCFW IFPAFSCRHLVL*ISLYTLL*MRP RDSGMWCLCSRWFQRTSLFLA SFERYVPSHSGAGCSVSM
7330	37698	A	7384	63	1650	SPGHI*SSV*REIYSTKCPQEA GKI*NSHPNITIKRTGEARANTF KS*QKARNN*DQSRTEGDRDT KNPSKNQ/CNPGAGFLKRSTKLI DR*QD*RRK*RRIK*T**KMIK GI/VTDPTEIQTITREFYKHFYA NRLKNLEEMDEFLETYTLPLRN QEEVESLNRPTGSEIAIINSLP TKKSPGPDGFTAIEYQRTNDKN HMIISIDEKAFDKIQPFMLEM LNKLGIYGYMIKIJRTIYDKSTA NIILNVQKLEAFPLKTGTTRQGPC LSPLLFNIVLEVLARAIRQEKEI KGIRLRKEVFKMFLFADDMIVY LENPIISAPNLLKLISNFSKVS GYKINVQKSQAFLYTNNRQTESQI MSELPFTIATKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTNK WKNIPCSWIGRINIVKMAILPKV IYRFNAIPIKLPMTFFTELEKTTL KFIWNQKRALNAKTILSQKNK AGGIMLPDFKLPYKATWYWNQ NTEIDQWNKTEASEITPHIYNHL VFDNPDKNKK
7331	37699	A	7385	392	493	
7332	37700	A	7386	1	1223	
7333	37701	A	7387	386	553	KMIKGISLIPQRYKLPSSENTINT STQIN*KI*KKWHHSHTHTPSQD* TRKKLNL
7334	37702	B	7388	285	1581	
7335	37703	A	7389	1	1473	
7336	37704	A	7390	755	1042	SSYATKKEPALPSQSEAKKTKL ETSCYLTSNYTRTLQ*PKQHG GTKEI*ANGTEQSPQ*YHTA TTIWSLTNLTKTRNGERIPYILN GVGKTG
7337	37705	C	7391	1	2334	

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7338	37706	A	7392	1	1539	
7339	37707	B	7393	1	2361	
7340	37708	A	7394	5071	5535	GTAFLWRRRGALRFRVSSFSVL FFPHLCGFYFWSLMMVMYRC VFGVDVLVVC*FSF*QTGPSAA GLLEYPAV*GVSVPLLGGASQL GCSGVRGQGPT*GGSPLVLRSP AACWENHCSLQSCQTGTFKSA EVTAVFLFVCALPPEVEPTEAG
7341	37709	A	7395	1	459	
7342	37710	A	7396	3	1063	
7343	37711	A	7397	39	895	
7344	37712	A	7398	2	277	
7345	37713	A	7399	34	845	
7346	37714	A	7400	1	3399	
7347	37715	A	7401	1	3126	
7348	37716	A	7402	1	387	
7349	37717	A	7403	1	3578	RDLVVGCGGFVKSDVEINYSLI EIKLYTKHGTLKYQTDCAPN GYFMIPLYDKGDFILKIEPLGW SFEPTTVELHVDGVSDICTKGG DINFVFTGFSVNGKVLKSGQPL GPAGVQVSLRNTGTAKIQSTV TQPGGKFAFFKVLPGDYELAT HPTWALKEASTTVSVTNSNAN AASPLIVAGYNVSGSVRSDEP MKGVKFLFSSLVTKEDVLGC NVSPVPGFPQDESLEYLYCYTV SREDGFSFYSPLPSG
7350	37718	A	7404	34	460	
7351	37719	A	7405	105	245	VSSEKVLGVPCPAASAAASGD ASR*MATGRGGGGGVAALPE SAP
7352	37720	A	7406	1	1289	
7353	37721	A	7407	462	5250	
7354	37722	A	7408	714	887	
7355	37723	A	7409	1	109	PLRQLLCVKRGFC*HH*HEGCQ SRLLRLCLLCSTAI
7356	37724	A	7410	1	1845	
7357	37725	A	7411	192	1507	
7358	37726	A	7412	2	688	
7359	37727	A	7413	1	518	
7360	37728	A	7414	1	276	

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7361	37729	A	7415	984	3112	MWQETFFRMENLQLIILILGSP SQLHFPVIRNNQGWTLYHQWP HFLNRFSSRLSNSLLNLQKFTC ANCKKPLQKGQTAYQRKGS LFCSTTCLSSFHKKPAKKLCV MCKKDITTMKGTI/VLAQVDSS ESFQEFCSVTSCLISL/YEEQNP TKGALNKSRTCIGKLTETIRHE VSFKNMTHKLCSDHCFNRYRM ANGLIMNCCEQCCEYLPSKGA GNNVLVIDGQKRFCCQSCVSE YKQVGSHPFLKEVRDHMQDS FLMQPEKYGKLTCTGCRTOC RFFDMTCQIGPNGYMEPYCSTA CMNSHKTAKYAKSQLGIIHCF KRNSLPQYQATMPDGKLYNFC NSSCAKQFQALSMQSSPNQGFV APSDIQLKCNKYCKNSFCCKPEIL EWENKVHQFCKTCSDDYKKL HCIVTYCEYQEEKTLHETVNF SGVKRPFCEGCKLLYKQDFAR RLGLRCVTCNYSQCLCKGGAT KELDGVVRDFCSEDCCKKQFD WYYKAARCDCKSQGTLKERV QWRGEMKHFCQDQCLLRFYCQ QNEPNMTTQKGPENLHYDQGC QTSRTKMTGSAPPPSPTPNKEM KNKAVLCKPLMTKATYCKPH MQTKSCQTDDBTWRTYVVPVPI VPVPIPVPMHMSQNPVPTTV PVPVVPVFLPAPLDSSEKIPAAI EELKSKVSSDALDTELLTMD
7362	37730	A	7416	1	1071	
7363	37731	A	7417	88	2118	
7364	37732	A	7418	2	2930	
7365	37733	A	7419	1	1677	
7366	37734	A	7420	172	13329	
7367	37735	A	7421	2	946	
7368	37736	A	7422	255	933	WIEAAPQAQEVQGDGLWLPCG AAGAGGLQARSYGTVGEASY AEHPW/CAPGGCMAGCGSLAA AASPLGVPGHLP/QPTAAPSHPH RASLRVALLSGQWGLTCGQLL ASAPLLQSWAWDTRLLMCRRLL SCSSEEGERIAQLLLPYLKLGS STVKRTGGFGNTNPAGKAVYW VNQVSKDRPICTVAIQGKDFEG LVDTEADVSIHAINQWQPHWPK QKASIGIVGVGAA
7369	37737	A	7423	718	2385	
7370	37738	A	7424	1	180	

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7371	37739	A	7425	1	1713	
7372	37740	A	7426	1	774	
7373	37741	A	7427	2	158	
7374	37742	A	7428	1	174	
7375	37743	A	7429	252	1245	ELGECGCRQGSVSHCGRGRPL LPRVRGKRHLPRARLARCQEAL SPWGFRCRFRNHHQTGFSLAGA NQRGPLAATLSGPGGEGQSAV ARLMGEKKNHPGAQYATRLSP RVGRFINAAGTTGFTGKRAPT CWPGADNIPSCCLALPRIETELM GKFDEGKLPTDPLMLGLAIET VAHDYDVVIDSAPNLGIGTINV VCAADVLIIVPTPAELFDYTSAL QFFDMLRDLKKNVDLKGFEPP VRILLTKYSNSNGSQSPWMEEQ IRDAWGSMLVKNVRETDEVG KGQIRMRTVFEQAIDQRSSTGA WRNALSIEWPVCNEIFDRLIKPR
7376	37744	A	7430	1	1113	
7377	37745	B	7431	56	1234	
7378	37746	A	7432	667	1048	LLLFRDLGIGTINVCAADVLI PTPAELFDYTSALQFFDMLRDL LKNVDLKGFEPPDVRILLTKYSN SNSQSPWMEEQIRDAARFPV GKPVVPAALMNRPTRRGEAVC VLGARVVFLFTSETGNS
7379	37747	A	7433	1	1428	
7380	37748	A	7434	1	1125	
7381	37749	A	7435	1	756	SDRRYEWDRGPSLIIRPTIRVGP WSQTNNQTDTSGTVV/RRFPF PVIGVVFHKGGVYKTSVSVHL AQDLALKGLRVLLVEGNDFQG TASMYHGWPDLHIHAEDTLL PFYDPLMLRLAIETVAHDYD VVIDSAPNLGIGTINVCAADV LIIVPTPAELFDYTSALQFFDMLR DLKKNVDLKGFEPPDVRILLTKY SNSNGSQSPWMEEQISDALRIS QRRNISSKFIQSACITLTFIST CWAIIVTQSG
7382	37750	A	7436	1	1329	
7383	37751	A	7437	1	1185	
7384	37752	A	7438	1	1065	
7385	37753	B	7439	67	1033	
7386	37754	A	7440	1	1192	
7387	37755	A	7441	1	1413	
7388	37756	A	7442	1	1176	
7389	37757	A	7443	1	1302	
7390	37758	B	7444	1169	3356	
7391	37759	A	7445	14	3974	

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7392	37760	A	7446	677	1033	RATASSISTTRPCESTSNAPSCN SPIRSRSPLIPIRPASITLILVSM MRMVRAATISCAILVSRCPAISP PLCTAFFRPICAAAGVPVFTLFTT TP*SLPLLLISAPSMPLKMELES T
7393	37761	A	7447	1558	1748	CSNASARFFAAVNPSSGLGMILM *SRFIVFTKLSAIPPLSGLRTAVF FGSSPNIRANWRVSLAR
7394	37762	A	7448	1	595	LKNSKPQVVMMAAGIFLIMCG VWLFGGGVLDPTKSSGYLIVDI YNEIICMLSNRIAGLGLSIMAVG GYARYMEGTPASRAMVSLLSR PLKLIRSPYIILSAT*VIGQIMP/Q FITSASGLGMLLMVPLFPTLVSL GVSRLSAVAVIATTTMSIEWGIL ETNSIFAAQVAGMKIATFFCHA HNPVASRVILSVAISGTRAR
7395	37763	A	7449	1	978	
7396	37764	C	7450	32	316	
7397	37765	A	7451	1	2465	
7398	37766	A	7452	1	1416	MIILIDAEKAFDKIQPFMLKTL SKLGTDTGYLTKIIRAIYDKPTAN IILNGQKLEAFPLKTGTTRQGCPL SPLLFNIGLEDLARAIRQKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVS KINVQKSQAFLYTNNRQTESQI MSELPTTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPR DIDQW/NRTEPSEIMPHTYNYLI FDKPEKNKQWKGDSLFFHKWC WENWLA VCRKLKLDPLTPYT KINSRWIKDLNIRPKTIKTLEEN LGITIQDIGVGKDFMSKAPKAM ATKAKIDKWDLIKLSFCTAKE TTIRVNRQPTTWEKIFATYSSD KGLISGIYNELKQIYKKKTNNPI KKWAKDMNRHFSKEDIHAAK KHMKCCSSSLAIREMDIKTTMR YHLTPVRMAILKKSGNNRCWR GCGEIGTL



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7399	37767	A	7453	3	2272	RSTRQKVNKDITQELNSALHQA DLIDIYRTLHLKSTEYTFSSAPH HTYSKIDHILGSKALLSKCKRTE IITNYLSDHSAIKLELRKLNLTQ NRSTTWKLNLLNDYVWHN KMKAEIKMFFETNENKDTTYQ NLWDTFKAVCRGFIALNAHK RKQERSKIDTLTSQLEKEKQE QTHSKASRRQEITKIRAELEKE TQKTLQKINESRSWFFERINKID RPLARLIKKKREKNLIDAIKND KGDITDPTETIQTIREYYKHL TNKLENLEEMDKFLDITYLPR NEEEVESLNRPTGAIEIVAINSL PTKKSFGPDGFTAIFYQRYKEE LVPFLKLQFQIEKEGILPNSCY EASILIPKPGRDITKKENFRPIS LMNIDAKILNKILAKRIQHHKK LIHHDQVGFIPGMQGWFNIRKS INVIQHINRAKDKNHMISIDAE KAFDKIQQFFMLKTLNKL/DIGR NYCKVHMEPKKSPHRQVNPKE KEQSWRHHTT*LTQILQGSYNQ NSMVLVPKQRYRSMQNRALR NNAAYLQLSDL*QT*EKQAMG NGFPI**MVLGKLASHM*KAET GSLPYTYLKNQFKMD*RLKR*T *NHKNPRKRPRHYHSGHRHGG GLHV*NTKSNNGNKSQN*QMG N*TKELLHSCRNYHQSEQATY KMGENFHNLLI*QRANIQLQ* TQTNLQEKKNQPHQKVGKGHE
7400	37768	A	7454	1	3020	
7401	37769	A	7455	1	3046	MVKGSIQEEILTINLIYAPNTG ALRFIKQVLRDLQRDLDSHTIM GDFHTPLSTLDRSTQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFSSAPHHTYSKIDHIVGSK ALLSKCKRTEITNCLSDHSAIK LELRKLNLTQNRSTTWKLNLL LNDYVWHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQ LEKEKQEQTHSKASRRQEITKIR AELEKEITQ
7402	37770	B	7456	197	1917	
7403	37771	B	7457	1	1954	

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7404	37772	A	7458	1	1947	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGRQGWFNICKSIN VIQHINRAKDKNHHMISIDA EKA FDKIQQLFMLKTLNKLIGDGT FKIIRAIYDKPTANIILNGKKLEA FPLKTGTRQGCPLSPLLFNIVLE VLARAIQEKEIKGIQLGKEEV KLSLFADDMIVYLENPVSAQN LLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDANKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELEKTTLKFIWNQK RAHITKAILSQKNKARGITLPDF KLYYKATVTKTAWYWYQNRD IDQWNRTPQSEITPHIYNILIFD KPDKNKQWKGSLFNKWCWE NWLAI CRKLKLDPLTPYTKIN SRWIKDLNVRPKTTKTLEENLG ITIQDIGMGDMFMSKTPKAMAT KDKIDKWDLIKLSFCTAKETT IRVNRQPTKWEKIFTTYSDDKG LISRIYNELKQIYKKKTNNPIKK WAKDMNRHFSKEDIYA AAKKH MKKCSPLAIREMQIKTTMRYH LTPVRMAIHKSGNNRCWRGC GEIGTLLHCWWINWMKKTWH IYTMEYYASIKKNEFMSFAGA* MKLETII
7405	37773	A	7459	1	1713	

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7406	37774	A	7460	281	2882	KPRLNEMKNAEASRADAINW KKGY/LVMEDKMNMKREGKF REKRIKRNKQSLQEIWDYVKRP NLRLISVPESDRENGTKLENTL QDIHQENFPNLRQANIQIEIQ RTIPQRYSSRRATPRHIVRFSKV EMKEKMLRAAREKEIQTNIREY YKHRYANKLENLEEMDKFLNI YTLRRLNQEEVESLNRPIRGSEI VAIINSLPTKKSPGPDGFTA EYY QRYKEELVPFLKLQFSIEKEGI LPNSFYEASIIIPKGRDITTKKE NFRITSLMNIDAKILNKILANRI QQHIKLLIHHQVGFIPGMQ WFNIRKSINVIQHINRTKDKNH VIISIDAEKAFDKIQQLFLLKTL NKLIGIDGTYLKIKRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLARAIQKEKEI KGIQLGKEEVKLSLFADDMIVY LENPIVSAQNLLKLISNFSKVS YKINVOQSQAFLYTNNRQTETQ IMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTKK WKNIPCSWVGRINIMKMAILHK VIYRFNAIPKLPMTFFTELEKTT LKFTWNQKRARIAKSILSQKNK AGGIMLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIT PHIYNILIFDKPEKNKQWGKDS LFNKWCWENWLAIRWKLKLD PFPTPYTKINSRWIKLDNVRPKT
7407	37775	B	7461	1	2633	
7408	37776	A	7462	3	1336	

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7409	37777	A	7463	2	2458	SWFFEKINKIDRPQARLIKKKRE KNQIDITIKNDKGDITDPTIEQIT IREYYKHL YANKLENLEEMDK FLDITYTL PRLNQEEVESVNRPT GSEIEAITNSLP TKKSPGPDGFT AEFYQRYKEELVPFLKLFQPIE KEGILPNSFYEAIIIPKGRDT TKKGNFRPISLMNIDAKILNKIL ANQIQHHIKLHHHDQVGFIP MQGWLEVLARA/IRQEKEIKGI QLGKEEVKLSLFADDMIVYLEN PTVSAQNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLNEIKEDTNKW KNIPCSWIGRINIVKMAILPKVI YTFNAIPIKLPMTFFTELEKTTL KFIWKQKRSHIAKSILSQNKKA GDITLPDFKLHYKATVYKTAW YWYQNRDIDQWNTTEPSEIML HIYNHLIFDKPKNKQWGNDS LFNKWCWENWLAICRKLKLD FLTSTYTKINSRWIKDLNVRPKTI KTL EENLGNTIQDIGMKDFMS KTPKAVATKAKIDKWDVIKLE SFCTAKETTIRVNRQPTWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWAKDMNRHFSKED IYAAKRHMKKCSSLAIREMQI KTTMRYHLTPIRMVIAKKSGNN RAPGGRGGCGCSFGRLKRSVCP ALKRVADLPAQRSSSAKGETAS
7410	37778	A	7464	2	2101	
7411	37779	A	7465	196	792	GILSFAKDMNRHFSKEDIYAAK KHMKKCSSLAIREMQIKTTMR YHLTPVRMAIKKSGNNRCWR GCGEIGTLLHCWL DCKLVQPL WKS VWRFLRDLELEIPFDPAIL LGIYPNEYKSCCYKDTCTRMFI AALFTIAKTWEPPKCSNMIDWI K/KMWH/IYTRDTMRPKNDEVQ SLVG/TWVNWETTFSVTIAVQK PTRLSH
7412	37780	A	7466	3	610	
7413	37781	A	7467	1	1986	

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7414	37782	A	7468	965	4421	TWKGITTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDY RTLHTKSTEYTFSSAPHTYSKI DHILGSKALLSKCKRIEITNYLS DHSIAKLELRIKNLTQSRSTTW KLNNLLNDYVWHNEMKTEIK MFFETNENKDTTYQNLWDAFK AVCRGKFIALNAYKRKEERSKI DTLTSQLKELEKQEQRHSPSR RQEITKMRAELKEIETQKTLQKI NESSSWFFERINKIDRPLARLIK KKREKNQIDT
7415	37783	A	7469	1	1674	MGQLQRNARDLQESVMSIRM MPMEYVFSRYPRLVRLAGLK GKQVELTLVGSSTELDKSLIERI IDPLTHLVNRNSLDHGIELPEKRL AAGKNSVGNLILSAEHQGGNIC IEVTDDGAGLNRERILAKAASQ GLTVSENMSDDEVAMLIFAPGF STAEQVTDVSGRGVGMDEVVKR NIQKMGGHVEIQSKQVTGTTIRI LLPLTLAILDGMSSLLTHGIGQF ADVACAGPLLAELDALGKAL KEPARPMVAIVGSKSVSTKLTV LDLSKSIADQLIVGGGIANTFIA AQGHVDVGSLYEADLVDEAKR LLTTCNIPVPSDVRVATEFSETA PATLKS VNDVKADEQILDIGDA SAQELAEILKNAKTILWNGPVG VFEFPNFRKGTEIVANAIDSEA FSIAGGGDTLAAIDLFRIADKNS YISTGGGAFLEFVERLTTLTQLL HDQGYVTQAIGKWHMRETTPEP QPQNVGFDDFRGFNSVSDMYT AWRDVHVNPEVALSPDRPAYI NQSPLSKDDVHALRGDQQA ADITPKYMA LDLQRC TEYGAQ LLDKMAKSA
7416	37784	A	7470	1	3360	
7417	37785	A	7471	2	543	
7418	37786	A	7472	1387	1805	QAIAFDVQPGRGDYAGNQRHH NQYNQHQAHS*SWQRCIGIGDL ARFARHNATKANKPGETGDR FNHQKNHGGQDPVLHQLIEV MLVGRGGDQAVGQATLGIDTN VGLHAKV/LTDCLSWSDASPD VAALCSWSSWVPO
7419	37787	A	7473	4088	4228	SPPSA*VKALPGPKHHGGLKPV HPIPGASLVLARRWSMFRRWG LIT
7420	37788	A	7474	332	538	

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7421	37789	A	7475	1	1983	
7422	37790	A	7476	856	964	
7423	37791	A	7477	1	1563	
7424	37792	B	7478	1	1086	
7425	37793	A	7479	372	886	
7426	37794	A	7480	2028	2368	RPPGNSLNVSRMGTRSSYSCRR HSPAFLSWKGGRCHLCNK AHL LAGA*HYSFLSGSAPY*N*VNG QI**R*TAHRSTPDAPIGH*NCC S*L*CHSY*QRA*PGYRHD*CR MCC
7427	37795	A	7481	146	402	LGFLRLLEMPRKQGDYRTR/C EIRGRVEQRVGYTIEQINHM RD VFDRRYEWDHGPRLIIRPTIRVG PWSQSDYQTDDTSGTVVVD
7428	37796	A	7482	3	149	
7429	37797	A	7483	5	753	ARKVVVAARHKCPA/CISFSA SHRLYRYWEEEMNPAPVEAMR TFQFIDEGNYTSGDTHTLRDP HYVEDKAHKYLVFEANTGTEN GYQGEESLFNKAYYGGGTNFF RKESQKLQQA AKKRD AELANG ALGIHLENNDYTLKKVMKPLITS NTVTDEIERANVFKMNGKWYL FTDSRGSKMTIDGINSNDIYML GYVSNSLTGPYKPLNKTGLVLQ MGLDPNTNIQTDDTSGTVVQT NNQTADTSGTMVVD
7430	37798	C	7484	182	709	
7431	37799	B	7485	1	1488	
7432	37800	A	7486	2	1034	YLIQSRGLIRRSKISLQTSQIER AFLQAPVEER*SMACSK/YSSH DLTFTNFIRFTYNIF*NHASP GIP NLLLHPRGLRAITIAVFGKQNT YIRLEPFKINVLEQITKHIEKLQC G/ECSQTTOQAWEQSAHQQHIR H*SCRYPG*ARCQ*VHQARTL* DQRS*ADHEAYRKTA VRRC SQ TTQQAWEQSAHQQHIRH*SCR YPG*ARCQ*L*IHSHSEQQFQWP VG/CIRCGSVGSLPSSICPLTQF QYGAEPDRKE*QCAPASKWAL LHK*HRFPQDRKAGECLLHEY EDLVPIRDLRLFPGGRYLPRA KHVAPSEPDPTIRVG/PWSQSDY QTDDTSGTVVVD
7433	37801	A	7487	2	426	
7434	37802	A	7488	138	346	RWRLQNLSCSSC/SRIWL*RGY VFCSWKPREQSSQSPACSAAC LTLRTQSCCLGTAGQTDDTSGT MVQY

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7435	37803	C	7489	1	1290	
7436	37804	A	7490	48	439	HHHSGGLDD/HRRKILNTAYRSR KLQASC*KSAERA WKTKASLT VNGWMKKIRCKTPMCRPTVR* SIRILIIITPLPRVPSRS*LKPPTS CT*CIPTQPTRC*KMITCWRCRS TSRKSSGHVCVSPGSVAVTI
7437	37805	A	7491	1126	1340	KARWMLQTRKRAVRRSNWRK RNIWCAPAAICKRSTLTITSF*K PVKMACPFICAMLRRLARRC AGALPN
7438	37806	A	7492	12	960	
7439	37807	A	7493	1	1806	
7440	37808	B	7494	1	1318	
7441	37809	A	7495	1	1385	MLQIPKQQQNEKYQVPQFDQS TIKNIESAKGLDVWDSWPLQN ADGTVAEYNGYHVVFALAGSP KDADDTSIYMFYQKVGDNISIDS WKNAGR VFKDSKFDANDPIL KDQTQEWSSGATFTSDGKIRLF YTDYSGKHYGKQSLTTAQVNV SKSDDTLKINGVEDHKTIFDGE RKTYQNVQQFIDEGNYSGDN HTLRDPHYQNTYIRLEPFKINV EQITKHIEKLQCGGVVKQLSRR GNNQHISSTYDINRADTQVRR VNNYDIIVMSNSFNGQSEHQV WIDRKAGECLLHEYEDLVPIRD TLRLFPGGRYLPRAKHVAPSEP DPEQDEQKLSCTYRKRYRVL VGELGDEQMAALSRLGNDYRP TSAYERGQRYASLLQNEFAGNI SALADAENISRKIIITRCINTAKLP KSVVALFSPGELSARSGDALQ KAF*SASPD RADSSPG*EK RATT D/SRQFGGVDTAGNNLT*NIFRI SQRRNISSKFILQ*ACITLTTFIST CWAIIVTQSG/LMQPSAHPAR QPEHDIAFGKCSSSVSVHLA/LG SGEGATCFARGR*RPNGNSLN VSRMGTRSSYSCRRHSPAFHRS TPDAPTH*NCSS*L*CHSY*QR A*PGYRHD*CRMCC
7442	37810	B	7496	1	3597	
7443	37811	A	7497	1	666	
7444	37812	A	7498	1	738	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
7445	37813	A	7499	1	727	MKVLIVESEFLHQDTWVGNAV ERLADALSQNNVTVIKSTSFDD GFAILLSSNEAIDCLMFYSQMEH PDEHQNVRLQIGKLHERQLNVP VFLGDRKALAAAMDRDLLEL VDEFAWILEDADFYRRTAPVA RE*TRYPPGSCWPLF/TAPLMK YS/DIHEYSWAAPGHQGGVGF TKTPAGRFYHDYYGENLFRTD MGIERTSTAVSLDHSAGFGQS EKYAARVFGADRSWSVVVGT GSRNTI
7446	37814	A	7500	1	744	
7447	37815	A	7501	1	250	
7448	37816	A	7502	1	850	
7449	37817	A	7503	1	1085	GNLAAGKTIQAQDRDAVGILSS RTGESMENLQKNLLPKQRRRT RETFTMSGALDVLQKEEDVLK FLAAGTHLGGTNLDFQMEQYI YKRKSDGIYIINLKRTWEELLR QPRA/MVPIENPAD/VSVISSR/N TGQVCQGTVA/VLRLAATGAT PIGGIRFTPGFT/IN/QIQASLPGS PRAFLWVT*PPGAEPPLSRAS LC*PFLPLALVNP/SPLRRYV AIPCNNKGAHSVGLMWWM AREV/LRMRTISRHPW/EVM PDLYFYRDPREEIEKEEQAAAEK AVTKKEEFQGEWTAPAPEF/TLA TQPEVADWSEGVQGAFLVPIQ QFP/TEWWSAQPA/EDWS*A/P LAQATEWVGATTDWS
7450	37818	A	7504	1	1053	
7451	37819	A	7505	2	654	
7452	37820	A	7506	674	805	TLMQKSSIKYWQTESSSTSKSL STMIKWASSL*REIYSTKCPQEK AGKIQN*HPNITIKRTRARANT FKS*QKARNN*NQSRTEGNRDT KNPSKN**/MPGAGFLKGGTKLI DR*QD**RKKERRIK*/IAIKNDK GDITNPTIEIQTIREYKHLA NKLLENLEEMHKFLDTYTLPRLN QEEVESLNRPTGAIEIVE*SIAY QPKKVQDQMDSQANSTRGTRR NWWYHSF*TIPINKRGNP*TLM QKSSIKYWQTESSSTSKSLSTMI KWASSLGGKAGSIYANQ



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7453	37821	A	7507	1	1577	MGDFNTPLSTLDRSMRQKVNK DIQELNSALHQADLIDYRNLHP ESTEYTFFSAPHHTYSKIDHILG SKAPLSKYRSEIKINCLSDHSA IKLELRIKLLTQNRSTTWKLN LLNDYVWHNEMKAEIKMFFE TNENKDTTYQNLWDTLKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQE SKIRGELKEIETQKTLQKINESR GWFFEKINKIDRLARLIKRR EKNQIHAIKNDKGDMSNHTTE QTTIREYYKHLYANKLENLKEI DKFLETYSPLRLNQEEVESLNR PITGSEIEAIINSLPNKRSPGPDG FTAKFYQRYKEELLISNFSKVS GYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRMYLGIQPT RDMKDLFKENYKPLLNEIKEDT NKWKNIPCSWVGRIINIVKMAIL PKNWKKTTLKFIWNQKRARIA KSLSQTEQSWRHAT*LTQILQ GYNNNSMVLVSKQRYRSMEO NRALRNNTATYLPQSD
7454	37822	A	7508	58	330	FTENDDFQFHPCPYKGHLEIIFY GCIVFHGVVYPHFLNPVYHCW TFGLVPSLCYCE*CRNKHTCAC VFIAA*FIVIVVYTQ*WDGWVK WYF
7455	37823	A	7509	1246	1522	DCLGNAGSLFVPEYGLHYGHF HNIDSSYQ*AWMFFHLFVSFFI SLSSGL*FSLKRSFTSLVSWIPR YFILFEAIVNGSSLMIWLSVCLL
7456	37824	A	7510	140	577	YSMVYMHIFLIQSIIVGHLGW FQVFAIVNNVTINIRVHVS*QH DL*SFGYIPSNWMAAGSNGISSR SLRNRHTVFHNG*TSLSQSHQOC KSPVISPPLQHLFPDFLMIAIL TGVRYLIVVLICISLMADE HFFMCLAA
7457	37825	A	7511	399	677	NQREQRHNPESLGRIQSSV*RE IYSTKCPQEKAGKIQN*HPNITI KRTRKARANTFKS*QKARNN* NQSRTTEGNRDTKNPSKNQ*IQE LVF
7458	37826	A	7512	1446	1855	IYKLPWAVWPF*Y*FFLPMS/G GVFFHLFVSSFMSLSSGL*FSLK RSFTSLVSCIPRYFILSEAVNGS SLMIWLSVCLLVYKNACDFCT LILYPETLLKLSLRRFWAETM GFSRCTIMSSANRDLISSFRN

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7459	37827	A	7513	1	2982	
7460	37828	A	7514	5202	5430	
7461	37829	A	7515	2	454	
7462	37830	A	7516	2	744	
7463	37831	A	7517	1	2422	MCPILREHGRGSTEGRKRQKRLP LELTLKDEEVLAHRQIEIVAKA SPSKGNIIHFGYKGVEYHDQQ DVTSNFLGAMWLISITFLSIGYG DMVPNTYCGKGVCLLTGIMGA GCTALVVAVVARKLELTKA EK HVHNFMMDTQLTKRHCPWAA TIQPKLSFLISLPgcdYRGESAR ARPLSHIPPLQLGLGKDARYLRI CDRSLLCVCAAAGNAGLRPRD SPHTLLHWRSPYFFSPKPVPP QLLGGQPAHRRDDLGEAGV GRGGCCFAALRGVQSEKWSGF HTVPEPAPGQGDVMPIVLVRPT NRTRRLDSTGAGMGPSHHQQQ ESPLPTITHCAGCTTAWSPCSFN SPDMETPLQFQRGFFPEQPPPPP RSSHLHCQQQQSQDKPCPPFA PLPHPHHHPHLAHQQPASGGSS PCLRCNSCASSGAPAAAGADNL SLLLRITSSPGGAFRTTSSPLSG SSCCCCCSSRRGSQLNVSELTP SSHASALRQQYAQQSAQQAAS ASQYHQCHSLQPAASPTGSLGS LGSGPPLSHHHHHHPAHHQH HQPQARRESNPFEIAMSSCRY NGGVMRPLSNLSASRRNLHEM DSEAQPLQPPASVGGGGGASSP SAAAAAAAAVSSSAPEIVVSKP EHNNNSNNLALYGTGGGGSTGG GGGGGSGHGGSSSGTKSSKKK NQNIQYKLGHRRALFEKRRKLS
7464	37832	A	7518	1	579	

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7465	37833	A	7519	1	1184	MSSANRSILEVPHLDILLQELPG VSKVVTVEVRGNWQRWLKVR DLTKGVTFYFRVQARTITYGPE LQANITAGPAEGSPGSPRDVLV TKSASELTQWTEGHSQDTPIT GYVIEARPSVFGNGSFQVSKEE NQYFSEGLTSIEVPSQQVQOEG AVAMALMVPDEGLWDMFVKD IPRSATSYTLSDKLRQGVTYEF RVVAVNEAGYGEPSPSTAVS AQVEAPFYEEWWFLVMALSS LIVILLVVFALVLHGQNKKYK NCSTRQISTMEESVTLNNGGF AALELSSRHLNVKSTFSKKNGT RSPRPSPGGLHYSEDEDICNKY NGAVLTESVSLKEKSADASESE VSVGAYFRAVTISPYFCKDAGF AVRTIALGLAETAGSKADARK
7466	37834	A	7520	1	1347	
7467	37835	A	7521	512	1051	MAYCKSTPAVGLRVTV*SLSRL SLICYTFCIGAPSHLSVGSLLIAT SFIVSNRPCRAPYVDITYRLPSP LRLAGHRTLPLKPSFPRRSPPLL YYPSRPPAHYPLSPSSEPNRRY TMALTAVPPYPTSPLQAFPFLLH SRIPQLQLFLTNSFTSRTPVEP VQVLEILSQWKATTKWHYG
7468	37836	A	7522	352	546	
7469	37837	A	7523	1	360	
7470	37838	A	7524	3	349	
7471	37839	A	7525	1077	2142	SAVRYSVAITTADRRTAAGAIS YPTK*S*SEPIQEGQPEEQ/RAN YPNGTYPTSLRHLERLWLSAL SVKARF/YHQQYSLKKYRYKHI ADNVQQWLDEVFLRPKEMSDI HKLTFFIEKRERLKNVSFKSLHD VRTVEDPSGTQLEVVSNNPWD PKRQLLKWDGKTWGTWDIPD YSAAPPEAVPSLNNPQTFSEQK LDEALYHGAVLRVRPKAMTVA VIIAGLLPILWGTGAGSEVMSRI AAPMIGGMITAPLLSLFIIPAAY KLMWLHRRHLWKCKSARRPQ YQSGYTDHRHSRVKASPTAG LPSLTHEQQQKAVRIQELMAQ GMSSGQAIALVAEELRANHSGE RVARFDEDE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
7472	37840	A	7526	116	191	RLKFTETNLTYNIYVGSIIHLN LEIIHMSLH**MDRTNINIRVQIC FCEFKSLVLLDKPGRQELIDDL NKRTDNFLTDSGISVSDWIDAA TWEVFSSLRELELLGIKINRLAS QDLHGVLSSSETVAEDIWCRILD TVTRKGEHSRRIHSAADKSYLR PDLEWFQQRVEDDQSRSGRKI YVKRDLPHILTPFRAPMASVCA KRKGQVLHQYSLKKYRYKHI ADNVQWLVDEVFLRPKEMSDI HKLTFIEKRERLKNVFKSLHD VSEFLGRVLLHATDPAAPRPPA YSLHAIRGKSRGRKNS
7473	37841	A	7527	1	177	
7474	37842	A	7528	1	399	
7475	37843	A	7529	3	209	
7476	37844	A	7530	1	288	
7477	37845	A	7531	2	256	
7478	37846	A	7532	414	1188	TSFLTGGKKGSKKKVVDPPFS KKD/WL*YVKHPAMFNIRNIGK DVGSPTQTGTIASIDGLKGRV FEVSLADLQHDVAFRKFKLIT VEDVQGNCLTNFHGMDLTTRD KIMCSMVKKWQTMIEAHVD VKTTDGYLLRLFCVGFATKKR NNQIGKPF*AQHHRVRQIGKK MMEIMTREVQTNDLKEVVNKL IPDSIGKDIEKACQSIYPLHDVF VRKVKMLKKPKFELGKLMELH GEGSSSGKATGDETGAKVERA
7479	37847	A	7533	1	1140	
7480	37848	A	7534	131	410	
7481	37849	A	7535	1	861	
7482	37850	A	7536	1	406	MWEILELPRDLLNGFAQNADS NMDNKVQAEVALDNGNELVG YYSKASAGDTQANRVWSGPPA NSNRPAEGERNTININKKIDIN TKTPSVGHRHRQRPVKDTTKT R/KTRAELKILKTRVPLIFQRT AALRQR
7483	37851	A	7537	1366	1629	TQSPVQTKPTPITTRGGGFLPTQ PFPVILQRQFCPE*LVAFMGS*E DVP*GSFVSAESSIL*RAP*GA QSTCKPVNRNEKISKRIHV
7484	37852	A	7538	502	648	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/546,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *Stop codon, /-possible nucleotide deletion, vpossible nucleotide insertion)
7485	37853	A	7539	I	1169	PPLLIPRQTGSGVDLQQTPTDLQ LRVLTVRRKTNKQKGPHQNSI CTSPSSKTKDFKPTKIKRDKEG HYIMVKGSIQEEELTILNIYTPN TGAPRFIKQVLRDLQRDLDSHT IIVGDFNTPLSTLDSKRQK VDK DIQELNSALYQADLTDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCNRTEIITNCLSDHS AIRLELRIKKLTENRSTTWKLN NLLKDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDTGKAAC RGFIATNAHKRNQKRKMDTL TSQLEKEKQEQRHKSASRRNL QEEVESLNKPRTGSEIEAIINSLP TKKSPGADGFTAIFYQRYKEE/ PGTIPSETIPINRKRGNTP*LIL*G QHHPDTKA
7486	37854	A	7540	I	404	MDEFNLNTYTLPRNLQEEVESLN RPITGSEIVAINSLPRKKSPPGD GFTAIFYQRYKEELVPFLKLF QSIEKEGILPNSFYEAISILIPKPG RDTTIKENFRPISLNMIDAKILN KIILANRIQQHIKKLIHHDQVGF PGMQGWFNIRKSINVIQHINRT KDKNHMIISTDAEKAADKIQQP FMLKTLKFGIDGTYLKIRIKYL GIQLTRDVKDLFKENYKPLLNE IKEDTKWKNIPCSWVGRINIM KMAILPKVIYRFNAIPKLPMTF LTELEKTTLKFIWNQKRARIK SILSQKNKAGGITLPDFKLYYK ATVTKTAWYWKQRDIHQWN TTEPSEITPHIYNHIFDKPEKNK QWGDLSLFNKWCWENWLAIW RKLLKDPFLTPYTKINSRWIKD LNVRPKTIKLEENLGITIQDIG MGKDFMSKTPKAMATKAKIDK WDLIKLSFCTAKETTIRVNRQ PTKWEKIFTTSSDKGLISRIYN ELKQIYKKKSDNPIKKVVKDM NRHFSKEDIYAAKKHMKKCS SLAIREMQIKTTMRVHLTPPSLL IPRQTGSGVDLQQTPTDLQKLV LTVRRKTNKQKVHPPHNPICST PSSKTEKEKQEQTSHKASRRQ EITKIRAEKKEITQKNLQKINES RSWFLEKVNKIDRLRLARLIK REKQIDAIAKNDKGDITTDPT QATIREHYKHLVANKLENLEE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
7487	37855	A	7541	3	1284	SAADTQANRVWSVPPTNSNRP AAEGPDC*KEN*QKGHPHQNP CQSPSSK\PKVDKTTKMGKKQN RKTGNSKNQSTSPPPQEHSSPA MEQRITNAEKYLKDLMLKTT AQELHDECTSLSSPFDQLEERV SVMEDQMNMKREKFKREKRI KRNEQSLKEIWDYVKRPNPLPI GVPESDRENGNKLENTLQDIIQ ENFPNLRHANIQIQEIQRMPQ RYSSKRA\TPRYIIVRFTKVEMK EKMLRAARDKSLVTHKGKLIJR LTAGKFIALIAHKGNQERSKIDT LTSQKLEKQEQTHSKPSRRQ EITKIRAEKKEITQTTLQKINES RSWFFEKINKIDRLARLIKKKR EKNQIDAINKDKGDITDPTIEI TTIREYYKHHYANKLENLKEM NKFLDYTLPLRKQEEVELSNR PIKALKLRQ
7488	37856	A	7542	1	1082	MLSSVGLLTHRRKKKSTDTIN DESLNKERDMTGNPHIFPYQE IWQVFVSSGNNYITATGPTAV PPLLIPRQTGSGVDLQQTPTDLQ LRL\TVGRKTNKQKGHPHQNP CTSPSSKTKEIRTTIREYYKHL YANKLENLEEMDKF/H*HIHPPKT KPGRS*ISA*TNNRL*N*GNN** LTNQKKSRTRWIHSRILPEVQ GADKQRAKHE*TPHNCFKENK IPRNPTYKEHEGPLQGELQTTS QGNKRGYKQM/DRTFHAHG*E ESIS*KWPYCPR*FIDSPSSSYQ *LSSQNGKNYFKVHMEPKKSP YCQVNPKPKEQSWRHHA\*LQ TILQGSYNSQNSMVLVPKQRYRP MEQSPQK
7489	37857	A	7543	1	2012	MNLSRHLNEVKGELLWSLEWR DPDGGSSIRMEVGLGGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFGLQKQKMDLKGVFKSCFKI YCSSKHLLKTGFISEAVLCYGE GGEGDVT\TMKERWPHECIVLI QC�KGR\TPHTARYSSETKLPE ERSGSSICGSPISAVLQPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQPKMSPS SKTKDFKPTKIKRDKEGHYIMV KGSIQQEELTILNIY

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
7490	37858	A	7544	402	675	QGYPGTELSAPSGPNRHLQNF PPOINRIYILLSTTSHLFQN*PHS WK*STPQQM*KRRNRYKNQIL ELRIKKQTQNRSTTWKLNLL NDY
7491	37859	A	7545	21	428	DKTSRGTRIQHLLFTNIRCSAA SAADTQANRVWSGPPANSRDP AAEGPDC*KEN*QTERSTSPKS HLYVTIHKDQRNKIPKNPTYKG CEGPLQGELOTTAQQNKRRYK QMGEHMLMGRKNQYHENGH TAQGNL
7492	37860	B	7546	1	1650	
7493	37861	A	7547	1	946	MAMPPLIPRQTGSGVDHQQTP TDPQLRLTVRRKTNTQKGIPIH QNPNCSTPSSKTKELKEEVGTQ RKEVKNLEKRLDEWLTRIANA EKSLKDLMLQKTMAQELQLDK TTLNFIWNQKACIATILSKK NKAGGIRLPDFKLYYKATVTKT AWYWHQNRVIDQWNRTEASEI MPHIYNHLIFDKPDKKKQWGN DSL/K*MVLGKLASHMQKTEI GPLPYNFYKN*LKMD*RLKGG T*NHRNHRKPKQYHSGHRHG QRLHD*NTKSNNGKQGN*QMG SN*TKELL/RQKKLPSE*TRNL QNGRKFVQSIYLTGG
7494	37862	A	7548	189	380	QTERSTQNPICSTPSSKTKGR* NHKDGEKTEQKNWKL*KAERL SSSKGMQLLSNGTKLDGE
7495	37863	C	7549	1	2805	
7496	37864	A	7550	535	696	
7497	37865	A	7551	214	363	LLEGKLTNRKE*HQHQKQGH HQNPICTSPSSKTKVT*NHKDG EKT*QKS
7498	37866	A	7552	787	1056	GQKKKLMIGINSRHHGPQ*P ALQKMPAS*VTEIMNNHFLFCF RKKGRIKLVNSRVEHQAGSW GPWFQSLVAGQYFWTCSPDGP SPLP

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7499	37867	A	7553	1	4560	MKHTLIPRIKNAQLQMSSLAVP VNSLVCLGKILEYLDKWLVL D GILPFLQIQPSKESAVLMGILGIY KCTFTHKLGITKEQLTGKVLPH LIPLSIENNLNQFNSFISIKEML NRLESEHKTKLEQLHIMQEQQK SLDIGNQMNVSEE:TKVTNIGNQ QIDKVFSHIGADLLTGSDSENK EDGALNVPPAGAKPTQQRPTD MSALNNLFGPQPKVSMNQLS QOKPNQWLNQFVPPQVSPATG SSVMGTQMNMIQG
7500	37868	C	7554	1	1359	
7501	37869	A	7555	272	915	YPGKQGLEWTSKKLQQTCC*GS *LLEGKRTNRKDINTKNPSVRH HHQRPKMGKEKTEQKNRKLKIR APLLLRNTAPH/HAMEQSWM ENDFDELREEGFRRSNYSELKE EVRTNAKEVKNFEEKLDEWIT RITNAEKSLKDLMEKTTA:EN YVTNAQAPVANATN*KKGYQR WKT*K*MK*SEKRSLEKKE*KEK KQSLQEIWDYVKRPNCLIGVP
7502	37870	A	7556	196	494	HTDGVSVVWMSFLFVSFSPNSQD PQLQVCWSLLEVHSRPLPGYQ QQRIRLEPFKINV/T*ADHEAYR KTAVRRCSQTTQQAWEQSAHQ QHIRH*SCRYPG
7503	37871	B	7557	28	303	
7504	37872	A	7558	1216	1863	HPDITIKRTREARANTFKS*OKA RNN*DERRTEGNRDTKNPSKKS VN/RRSWFFEFKNKIDRRLARLI KKKREKNQIDA:KNDKRDITTD PTEIQTIREHYKHLKYANKLEN LEEMDKFLDITYLPRLNQEEVE SLNRPITGSEIAHINSPLTKKSP GPDGLTAKFYQRYKEE/PGTIPS ETIPINRKRGNPP*LIL*GLHHPD TKAWQRHYKKREF
7505	37873	A	7559	166	785	FRATSAADTQANRVWSGPPAN SNRSAEDPDC*KEN*PTKGGHP HQNPICTSPSSKTKARQANIQIQ EIQRMPQRYSSRRATPRCIIVRF TKVEMKEKMLRAAREKGGVTV HKGNPIRLTADLLVKTLQARRE WGPINILKEKNFQPRISYPAKL SFISEGEIKSFTDKQMLRDFGTT RPALKELLKEALNMERNNQYQ PLQKHVRL
7506	37874	A	7560	1	1164	



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7507	37875	A	7561	770	2670	RRARCSCAPSSSTTLGRTGPSLA RRRACPSSAGRSRW*ARTTPR GGRPSESGTPTTFEPASSPPGRSR RDFQEGQSWVRGWQL/WTSTV GCSPHIFWCVDCECTDCEGYLK GHYVAGLRRSFRLLGCRERLGG QEGKMSSGAESPPELLTYEEVAR YQHOPGERPRLVVLIGSLGARL HELKQKVVAENPQHFGVAVPR APWDVKLQWAEDPGSECDKE DEEEENEGARFLEHGEYKENLY GTSLEAIQAVMAKNKVCVLDV EPEALKQLRTSEFKPYIIFVKPAI QEKRRTPPMSPACEDTAAPFDE QQQEMAASAAFIIDRHYGHLVD AVLVKEDLQGAYSQKVVLEK LSKDTHTWPLVIPRQTGSGVDL QQTPTDLQLRVLTVRRKTKKQ KGHPHQNTCTSPSSKTKVGER VSVIEDQMKEMKREKKFREKR VKRNEQSLQEIWDYVVRPNLR LIGVPESDGENGTKLENTLQDI MRENFPNRRARQANIQIEIQRM PQRYSSRRATPRHIIIRFTKVEM KEKMLRAAREKGWVTHKGKPI RLTADLLAETLQARREWEPIFNI LKGNFQPRISYPAKLNFISEGE IKSFTDKQMLRDFVITRPAQL LKEALNLERNNWYQPLQKHAK
7508	37876	A	7562	181	690	OHAIVTGDVGMDDIPQEARQ YRHNQAYAYSIGDGAEDDDE RIVRFHTRCLNGRVLL*DK/IF RNDQAATFAAHQYPLFCSLHC* YPGTQGLEWTSSKHQQTCS*GS *LLWPGDERLWPSWEEQKLS LPTDPDTWL*GSPQAAQGPRCV PPGAQPLSSVTASLCHCA

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7509	37877	A	7563	2	2233	SSENILTVHEQANVESLKETKQ NCKDLDEDANGITDEGKEINEK SSQLKNLSELQDTSIQHDEEE STVISVSEDMNSEGNVDFECDT KLYTFLSSDESQQSENSENEED TLCFVENSQGRESLSGDTGSL CDNALFVIDTTPGMSADKNFY EEEDKASEVAIEEEKEEEDEKS EEDSSDHEDENEDEFSDEEDFLN STKAKLGRLLTPHMAGYSSETKL PEERPGSNICCSPISAVLQPLLI PRQTGSGVDLQQTPTDLQLRVL TVIKKTNKQKGHPHONPICTSP SSKTKDRSTRQKVNKDQIELNS ALHQADLIDYRTLHPKSTEYTF FAAPHCTYSKIDHIVGSKALLS KCKRTEHTNCLLDHSAIKLELRI KKFTQNCSTTWKLNLLNDY WAHNEIKAIEKMFETNENKDT TYQNFWDTFKAVCRGKFIALN AHKRKQERSKIDTLTSQLEKE KQEQTHSKASRRQEITKITAEL KEIETQKTLQKINESRSWFFEKI NKIETASKTNKKREKNPIDAIK NDKGDITTNPTIEIQTITREYYKH LYANKLENLEEMNKFLDTNTIP RLNQEEVESLNRPIITGSEIAIIN SLPTKKSPGPHGFTARFYQEQYK EE/PGTIPSETIPINRKRGNPP*LI L*GQHHPDTKAWQRHNKKREF *TNIPDDHQCCKNPQ*NTGKPNP AAHQEAYPP*SSGLHPWDARL
7510	37878	A	7564	3	377	DHNCATVLQPG*QSEIL*KEERE REREKKERKKERKKERKKERK KEGKQ*RGGRKKERKEKEIK KERRKGKKEKKEEKRRKERK KERERKKRRKEGRKKEYTRKA KRIHRPFEGNGSPLPAP
7511	37879	B	7565	1	834	
7512	37880	B	7566	1	915	
7513	37881	B	7567	1	666	
7514	37882	A	7568	330	793	SCWLCPGPCCPAQPQNTAPFIPE A*TPAMAERGPATAAGQLEFT GGALQTLFAWVSAAAAAEQWI LVNRKCCCLIVPLEVLSQRSTW PCIGLVMPVLPGLLRDIVHSDSI ASHYGVLLALYALMQFLCAPV LGALSDRFGRRLPGLLASLLGAT

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7515	37883	A	7569	991	1842	IQCHPHQATKNFLHRIGKNYFK VHMEPKKGPHCQVNPKEQS WRYVKQSKKIAVYAERSRCS GTEFAGTLILDFFSSRTAPSSRG R/P/GRLTRPGTPLRQSFQNDQ AATFAVQQYSLFCSLCC*YPGK QGLEWTSSKLQ/QYQLRERSS SPATEQSWMENDFDELREGFR RSNYSKLKEEVQTHCKEAKNL EKRLDEWITRITNVEKSLNDLM ELKNMAKELRDERTSFSSEFNQ LEERSVNIENQMNMKREEKFR EKRVKRNEQSLQEIWDYVKRP
7516	37884	B	7570	1	2448	
7517	37885	B	7571	2379	4476	
7518	37886	A	7572	1	570	
7519	37887	A	7573	1	1404	
7520	37888	A	7574	1	474	
7521	37889	A	7575	746	1215	PNINRFLKHYREPVPKKRERNY STLWPLCPSTLNKIYTIMSYLSP ATKEYPPFLLLLFQEC*AE*LLA LAVSQPLLSTTNCLKN*MVTW NGSLIPWSPCKINLTP*/PAVVL QNRRALDLLTAESGGTFLFLEE KCCCYVNQSGIITEKVKIEQGRI
7522	37890	A	7576	1	1178	MPESPTLLGRDILAKAGAIHL NIGEGTPVCCPLLKEGINPEVW ATEGQYGRAKNAHPVQVKLK DSASFYQRYPLRPEAQQLGQ KIVKDLKVQGLVKTCSNCPDTP ILGVQKPNGQWRLVQDLRIIDE AIVPLYPVNPYTLSSQIPEEA ELFTVLCLKDAFFCIPVHPESQF LFAFEDPSIPMSQLTWTVLPGQ FRDSPHLFHHTLAQDLSQFSYL DTLVLCPLRNQEQECHQATQV LLNVLATCGYKVSQKQAQLCS QQVKYLGVKLSKGTRAL/QQ*R TDRT*LSTSNCSNLHRSRGPSRG SLD*SQQLVY*WKFFCRKRTS KRGVCSGQ**WNT*KKSPHSRN *CSAGGTNSPPSGTRIIRRRKKGL IRIYMLPLILSAPYDHLH
7523	37891	A	7577	1	1338	
7524	37892	C	7578	109	231	
7525	37893	A	7579	279	346	LLRLALLQ*QKEEWVLFCCGA
7526	37894	A	7580	260	393	VEVVILMPVVPNLPSIPARITKG RMGTLLRLRLGTT*LYKSCSV

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7527	37895	A	7581	3	2677	TKETCFIRGPKTPVPVTDWEGS LPLVFNHCRDTSVIIHPRFKGVR PRRDACLGPSPLAASPAFLGKG QAE LGPNSSSSASAPPPYNLFIA PPHTWSGLQFRSVTSPPPAQQF TLKKVAGAKGIVKRLKTDAR SPWKTPRPSRTSPFRKAERTKG LLKIHLLTKLSHQLKKDWITLLP LSLLRIQACPRNATRLATGQLG YPFISQSYVLVNGFQTVEDLCE AADLRVSVADLRVSVTALKVA RLELFVPPGGLVVSASAVKLQ TFAVLQLIAKRWWDWGTLEQG AALIGEARDQAQTEGVGGSG MAGCRSRDLPRGKAARREI ERSAGLTIKKERCIRNGYSKEK MKLIVVSHGLHVNDLQHKLT FTKETYYTLARDSEKQKQGYL AGLEGAHANRVNQISDNLVV KTGALPPPYRTKGEKLYFYMSR QNCLFSVSGQLLQGFPPNGGQA APNPYALLSQIPEEAEWFTVLD LKDDDFCIPVHPDSQFFAFEDP SNPTSQLTWTVLPQGFRHILFG QALAQDLSQFSYLDLTVLCGVL KSPIIIVWELNQIDTIKNDKGDIT TDPTEIQTITIREYYKHLTYNKL NLEEMDKFLNTYTLPRLNQEEV ESLNRPTGAIEAIIINSLPTKKS PGPDGFTAEFYQRVADVRLREE KDENMILLVPLSDLLYQVHAIP QLPEVLAANSPTCHLDPTTITES
7528	37896	A	7582	1	459	MAVRYTDENVLRKGTREAGT MMRLRGTTTECCADFAAWDVT HDALRATGGELPGAQVMLTTT ECGRHVD FCDRAVWVLPWMWG YPLALPGEMRKLYTVRMAGRD ILAKAGAIHNLNIGEGTPVRCP L/EGINPEVWKTEGGYRQAKNA RPVQVKL

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7529	37897	A	7583	3	910	YFSQPLSYDWGALFFSHAFILM LESPTTLLGRDILAKAGAIHLNI GEGTPVCCPLLEEGINPEVWAT EGQYGRAKINARPVQVKLKDS ASFPYQRQYPLRPEA/LTKGFQ KIVKDLKAQGLVKPCNSPCSTPI LGVQKPNGQWRLVQDLRIIDE AIVPLYPAPNPYTLLSQIPEEA ELFTVLDLKDAFFCIPVHPESQF LFAFEDPSIPMSQLTWTVLPGQ FRDSPHLFHHTLAQDLSQFSYL DTLVLCPLRNRQQECHQATQV LLNVLATCGYKVSQKQAQLCS QQVKYLGVKLSKGTRAL
7530	37898	A	7584	158	1272	NPAARTPFFVIKKGKGRGRDIL AKAGAIHLNIG/GTPVCCPLLE EGINLEDWATEGQYGRAKNAR PVQVKLKDSASFPHQRQYPLRP EAQQGLQKIKDLKAQGLVKAC NSPYNNPTLGVQKPSGQWRLV QDLRIINEVTPLYLAVPNPYIL LSQIPEEAWEFTDLDLKDAFFCI PVHPDSQFLFAFEDPSNPMSQL TWTVSPQGRDSPHLFGQALA QDLSRFSYLGTLVLWPCIS/LCT *TMEQLQHRNKHHFRFSRTSCF QSGNNPYLKPHLCKI*QYCRHN QLPMHQCPHDHLH*TRFI/PIML YLSPTTKEYSFFLLSEQEC*VD *VLALAVPOPLLSSTTNYLKNS MVTWNGLPPTWSPCKINLTS

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7531	37899	A	7585	1	2083	MPLLLQMIATPLQQSLISTEDEM DELTEVGFERWVITNFTTEEPSA LGFTPEHKGNGVHAGKGPLESS SPDPFLCGQEKQEKAGLLHRQ YPLRLAEAKQGLKIVKDLKAQ GLVTPCSSPCNTPTLA VQKPNG QWRLVQDLRIINEAVVPLYPAV PNPYILLSQIPEEAEWFTVLDLK DAFFCIPVHPDSQFLFAFEDPSN PMSQLTWTVLPQGFRLSLHLFG QALAQDLSQFSYLDTLVLQYM DLLLLVTHSETLCHQATQALFN FLATCGYMYSKPKAQLCSQQ/R YLGKLKSGTRALSEEHIQPIIA YPHPKTLKQLRGFLGVIGFCRK WIPRYGEIARSLNTLIKETQKAN THLVRWTTVEVAFQALTQAP VLSLPTGQDFCSYVTEKTGIAL GVLTQIRGMSLQPV AHLTK EID VVAKG*PHCLRVVVAVAVLVS EAVKIIQGRDLTVWTS HDVNGI I.TAKGDLWLSNDCLLKCAQLL LEGPVLRLLCTCATLNPATFLPD NEEKIKHNCQQVISQTYATRGD LLEVPLTDPDLNLYTDGSSFVE KGLRKVG YAVVSDNGILESNPL TPGTS AQLAELIALTWALELGE EK RANIY TDSKYAYLV LHAHA AIWKEREFLTSE RTPIKHQEAIR KLLLA VQKPREVAVLHCRGHH K GKEREIQENCQAYIEAKRAAR
7532	37900	A	7586	80	678	LCCNMPPAAQHRERASNESRHG GCCPP/PWLLSS/APPHDAFTTPQ EAVLSAPSALPSSAATSLLSLT PQQMFCSKTAGPKPFSSNPIPR LKAPTSSC/PL*PQAAPSGNAHC Y*GHRRGRTVPEDPGCLSPRAR PHRTSGTSSPPLQPSRTIPPASS APKQGDAGSPPYQAVPEKNKP GATPRTCAESPKRLPRPGPKSFL

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7533	37901	A	7587	3	804	GLLQATALQPAQI*IFL*KKEE EEEEGGGEGEEKKKKKKTEEE EEEEERKK/EEEEGEEEEEEEE EEEEKEERTGAGDSSEDEGFDEI PSPGDSRQKTEGNAANIISGCD QRYEESMDLGRGIVSGHRYI FTRVSPLEAIGELLFPFSVAPA QGGGLGRRVDQLALPMGAQSL ERPFCVDGGSRRPLNYAVSSVE DLLNGNNFKCPTTLRTIEITVGN LIISPRQKQLNANIGKNFNAAEN HENAKTTTTSSTVGDATHLTA
7534	37902	A	7588	3	191	SSHPVFSRWWLSPHQSQCYT* GSGAQNLTAASPPFCVCRGDRGN HLRKDTKVEVKRKTCLW
7535	37903	A	7589	1	1899	HVGASDPDAGPGWGLTSRPR LVTPRSAPRGAFOGATVGLAP VEGMCRAESSGGVSTDHSELPI GAAATMAHEIGHSLGSHDPD GCCVEAAAESGGCVMAAAT/G VRGWGVGAAAGRLVLGTSSA AFLWSSLFLCKMGIMIIVSAS GWFMRLLKGGKLRQSGFTV*R LFSE*PGEVTPTPGGAPSGRST LGPGLLTIGASSSPVPLVV*LCA GYFPSLGSARLAAVAKPRGGD QRSAGVGGSLSHAQCPPRAGR HPFPRVFSACSRRLRAFFRKG GGACLSNAPDGPLVPVPPALCGN GFVEAGEECYCVSGQECRDLC CFAHNCSLRPGAQCAHGDCCV RCLLKPGALCRQAMGDCDLP EFTGTSSHCPDVPVLLDGSPC ARGSGYCWGACPTLEQQCQ LWGPESHAPAEAFQVVSAG DAHNGCGQDSEGHFLPCAGRD ALCGKLQCQGGKPSLLAPHMV PVDSTVHLDGQEVTCRGLAL PSAQLDLLGLLVEPGTQCQPR MVCNSNHNCHCAPGWAPPFCD KPGFGSGMDSGPVQAENHDTF LLAMLLSVLLPLLPAGLAWC CYRLPGAHLQRCSWGCRQGPC VQWPQRWPTQGPVPPGRRSPHG VGPHSHWTALAPGP
7536	37904	A	7590	2	280	
7537	37905	A	7591	1	1266	

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7538	37906	A	7592	1	458	LQSQSIFEIHSQKTIKKCLDLFLFLAEKENYKNFFFAFSKNLAKLGIHEDSTNRRRLSELLRYHTSQSGDEMTSLSEYVSRMKETQKSIYYITGSPCWCLVFFSLSCPCVEGSKLRVSSPISLLLTAGLDVVYCGLFYFLHFVCLKLYAK
7539	37907	A	7593	1	862	
7540	37908	A	7594	3	437	IPEF/LNF/IRGVVTLGLPLNISREMLQSKILKVIKKNIV*EC/LFELLSLEAEDKENYKFFYEAFSKNLKLGIHEDSTNRRRLSELLRYHTSQSGDEMTSLSEYVSRMKETQKSIYYITGESKEQVANSFAFVERVPLSHLAPPAGV
7541	37909	B	7595	106	1966	
7542	37910	A	7596	453	719	ARGSKHTGLIAQWAHEQSGHGRAGGYAWAQHGLPLTKADLPAMATAECPIQQRPTLSPRYGTIPW/WAWDAPGGRGCWRLQKAGE
7543	37911	A	7597	3	837	PECVIGIDILSSWQNPHTGLTRVRAIMVGGAKWKPLELPLPRKIVNQKQYHILGGTVEISATIKDLKDTEAVTPTTSPFNSPIWPVQKTDGSRWMTVDYCKLNQVVTPIAAAVPDV/VSLLEQINTSPGTWFEWSPK/KALQQVQAAVQAA LPFGPYDPADPMVLEVSVA DRDAIWSLWNAIGESQRRPLGFWSKALLSSADNYSFPERQLLAS YWALVETERLTVGHQVTLRPE LPIMNWVLSDPSSHKVSQAQQRSIIKLKWIHDWVRAGPEGT
7544	37912	A	7598	1	399	
7545	37913	A	7599	126	392	ARGSKHTGLIAQWAHEQSGHGRAGGYAWAQHGLPLTKADLPAMATAECPIQQRPTLSPRYGTIPW/WAWDAPGGRGCWRLQKAGE
7546	37914	A	7600	1	1677	
7547	37915	C	7601	37	465	
7548	37916	B	7602	1805	2542	



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7549	37917	A	7603	3	865	VIPTTISQNFPIWPVQKTDGSGWRMTVDYCKLNQEENFNNQVDRMTHSVDTTQPLSPA THVITQWAHEQSGHGGRRDGGYTRVQQHGLPLTKADLATAGKVFQKAV*ALN*HSIYGTLSLARIHRSRNQGV EVEVAPLTISPDPAPAKFLLPVPPTLRSGALEFLVPEEGMLPSGDTTVPLNWKRLRPPGHFGLLFPLHQQANKGRLSPHSRERGTSVFASNSNQPVLTALNNEPAGPNKRDI GKAKGLKFHHGPHRQERDMLE/SML*PWGYPVGKQWNHLIKKQGRH
7550	37918	A	7604	3	857	VTASLSPVVATSPQPMPLPSDFPLSEINPMLPEATVIASPKIARQDNVDSQEPPTTPQFSSRPITRLKSQWAPRGPECVIGIDILSSWQNPHTIGSLTGRVREGYMVGKAKWKPLELPLPRKIVNQKQYCIPGEIAEISTTIRDLKDTGVVIPTTSPFNSSIWPVQKTDGSGWRMTVDYCKLDQVVTPIAAVPMVSLVKQINTSPGTWQHITHLDVLLWRIYQVTQKAASFEGWGEQEKALQQVQAQVQALCHLGHMTQQIQWCLRRNGEMCDYILYGL
7551	37919	A	7605	1	608	MAPGMVPIPPPGKYHSPGKLIYSTPPKPGTYGISDSLSQYPTSAKAEPVPPTHKNPRRESPIPHSSPSSFDG/PSNPSFGDARPHQNKTSGRGRPAPRQVRPTTTTTPAPPARSPNSAHSPAFRDLPFRAEKGTAARVPREPHSPAPKNGSLQPPAGELLQRGARTTLPRILGTAPGPHLPGCSAPPAP*RPAAPIGL
7552	37920	A	7606	179	544	HTRLHSHPQLRGFPWSLHFSVIRSPASGHLEFPFARSSGSGSTSPLSFGAMITTEKQALGGRAAFPPKYK*AQGRAACFVLTSQQQPSWQ*GVTVTATGSPMHRGTFWH SCTGTPGSGDR
7553	37921	A	7607	90	653	VPGERPRGSGSPQVLPYGPTWCSSNTPEPQSLRAPQ*LQVPPVLQSRGQR*QPQMP/VRSPKAP*VQMPPTPSSAKGPHLDGVRVPAANPE*PTAGPTRAAILRATPAPSLPMPTGNRPSRGNLSQDSAPASDAGWPPTEAVTCTP/PWSRENPPQRNL*AHPRQGRPVPGTERRNGRGAGCRL

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7554	37922	A	7608	1	804	
7555	37923	A	7609	28	682	TTCEMSDLEDDDETQLSAHG/T LAALQEFYAEQKQIEPGEDDK YNIGIIEENWQLSQFWYSQETA LQLAQEAIAAVGEGGRIACVGS P*CLPET/HESCAEKTFSIYFEY DKRFAME*KEILIFYDYNPLD LPERIAAHSFDIVIAADFPFYL ECLRKTSSETVQVLTGRKILL/CT GAHHGRTGSRTPLE*RCARLFP RHRTRNFGKWSFRLVYVNL
7556	37924	A	7610	1	611	MAPKAKMEAPAPPEAEAKVKA LKAKKVVVLKGVHSH/KKKKKKI RTSPTR*/PLRLRRQPKYPWES VPRRTSTQISSGERPLENKQPRY PRESSPPPGEQAPKYVPEERSPG ETRLDHLCLSIKFP/LTH*VLP MKIEDNNTLVPLVNVKANKH QIKQAVKKLYDI/DVAKVNTLUI RPDGEKNGICSDLAPDYDALG CLPTKFGII
7557	37925	A	7611	1	1035	DKDSLDCSCKTSCSYNCSKPRS SWQDQDISSGTGLHSRLTANT GKESKTVQASLDQQLGRLLSVS LRLGVEPSLQSSGNLLVSLLSR FITYKVTIVEWVKTYALGLDLK KSERPGFESELHSHNSCECAVS HLKPVHLRVSPMGHSEYYLV TADYSEANGSQSAGDEFFQTQS FPSRQQALFRPKIQTIREYYKH LYANKLENLEEMDKFLNTCTL QRLNQEEVESLNRPIGTSEIEAI NSLPTKKRPGDGTAKFNQRY KEELVIYKKFQIPCIPELNSTIS ANSTNADTCTPKYVTFNSKGT AQNADSDSAGLE/CEPDVLIH** SLRLGVEPSLQSSGNLLVSLLS RFITYKVTIVEWVKTYALGLDL KKSERPGFESELHSHNSCECAV SHLKPVHLRVSPMGHSEYYLV TTADYSEANGSQSAGDEFFQTQ SFPSRQQALFRPKIQTIREYYK HLYANKLENLEEMDKFLNTCT LQRLNQEEVESLNRPIGTSEIEAI INSLPTKKRPGDGTAKFNQRY YKEELVIYKKFQIPCIPELNSTI SANSTNADTCTPKYVTFNSKGT AQNADSDSAGLEWSLMFCISD KVSDDDDADA VDS

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7558	37926	A	7612	3	573	KEETFSAWYVDGRVLVVIVTF GIILPLCLLKNLGYLGVTSGFSL SCMVFLIVVIYKKFQIPCIPEL NSTISANSTNADTCTPKYVTFN SKTVYALPTIAFAFVCHPSVLPI YSELKDPSSQKKMQMVSNISFF AMFVMYFLTAFGYLTFYDNV QSDLLHKYQSKDDILITVRLA VIVAVILTVPLV
7559	37927	A	7613	1	831	MSELEDRLFENTQSEESKGKRI KKNEVCLQDLKYSCLKRANLRD TGLKEEVIYKKFQIPCIPELNS TISANSTNADTCTPKYVTFNSK KKMQMVSNISFFAMFVMYFLT AIFGYLTFYDNVQSDLLHKYQS KDDILITVRLAVIVAVILTVPV LFFTVRSSLFELGLRKQRFNLW PSIPVVTICILLVVINLVGDLHTP P*RIFFGVVGSYILLNMLFILP/S IFFILKITDQDGDKGTQRIWAAL FLGLGVLFSLVSIPLVIYDWACS SSSDEGH
7560	37928	A	7614	1	1118	FNCEIFYSF/SYGDEEISKTFALN ERRGEIKIRKLD FEKIVSYQVDI KASDGAAGLSGKCTVIIQVVDIN DNAPELTMASFTSPIRENSPETV AALFSIQDRDS/FALRSLDYEAL QEFEFRVGASDPGF/PALSSEAL VRVLVLDANDSSLFVLPPLQN GSAPECTEL/IPGRAAEPGYLVTK QLLKATEPGLFGVVAHNGEVR TARLLSERDATKHRLVVLVKD NGEPPRSATATLHVLLVDGFSQ PYLPLPEAAPAQAEADLLTV YLVVALASVSSLFLLSVLLFVA VRLCRRSRAASVGRCSVPEGP PGHLVDVSDTRTLQRYKYEVF LTRGSGTNEFKFLKSVIP/QASG RCE*WEEKSNFVNGFGFN
7561	37929	A	7615	1	764	TRPGAHGASLTDLANLSEGVSL AERGSFGAMDDPFKNKALLFS NNTQELHPDPFQTEDPFKSDPF KGADPFKGDPPFQNDPFAEQQT STDPPGGDPFKESDPFRGSATD DFFKKQTKNDPFTSDPFTKNPS LPSKLPFESSDPFSSSSVSSKGS DPFGTLDPPFGSGSFNSAEGFAD FSQMS/KGKSTPVSQLGSADFPE APDPFQPLGADSGDPFQSKKGF GDPFSGKDPFVPSSAAKPSKAS ASGFADFTSVS

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7562	37930	A	7616	1	817	MGFCHVQASLKLLASDPFGTLDPFSGSGFNSAEGFADFQMSKTDPPQRSELKVGTAARLVTRLDPVSGPHVTR*PELTVALVPSCRASPDAGSVVGAHL*GLGTTGAADGGTPNSNRSFVLGVIIIVVWSMCQLYLVP PPPSGPFTSSLGAGFSDDPFKSKQDTPALPPKKPAPPRPKPPS/GHRLPVPDGGGPGPPCSP/DPE*QQMPWDVPVWGA RGSPPSPCPGPRKCRMCVVP RV IQHP SLLLPSLVGRRSQQIWRSHMPAAAPS
7563	37931	A	7617	3	1039	GSLMFQVQPMVEIDGMKLVQTRAILNYIASKYNLYGKDIKERALYAMTHDDEAELRTPAACCKL*SECQFRTRVDAVRTMMIP/AFTQVLKSHRQDYL VGNKLSWADIHLVELFYVVEELDSSLISFP LLKVKLLASSVKPVLP SALTWP AHAVAQNI VTSWLTGGRFIELKT VQILDRLELEKPCIDAEDECFT EWSTFTLLKAWDEY LKAWFALHLL EAMFQPSDSGKSFIFNMS VGYNLEGQPLNPKNYSQGVPRVLKSHRQDYL VGNKLSWADIHLVELFYVVEELDSSLISFP LLKPHTHVDNTKKGSHPHMCAITDYVNNPNDRMPQREITFVS
7564	37932	A	7618	2	698	NQKTVTMAGKPKLHYFNGRGRMEPIRWLLAAAGVEFEKFIGS AEDLGKLRNDGSLMFQQVPMVEIDGMKLVQTRAILNYIASKYNLYGKDIKERALIDMYTEGMADLNEMILLPLCPAEKDKAKIALI KEKIKSRYFPAFEKVLQSHGQDYL VGNKLSRADISLVELLYVVEELDSSLISNFP LLKALKTQNPATLPHG*RSFLQPGSPRKP PADAKALEEARKIFRF
7565	37933	A	7619	102	825	RNLQETA IMAEKP KKLHYFNARGRMEPPRWLLAAAGVEFEKFIKSAEDL DKLRNDGYLMFQQVPMVEIDGMKLVQTKAILNLHLP ANYNLLMGKDIKGREP*FDYVF*EGFSQILGLN*SSFLPVC/PPELEKDAQALPLIQEKTKNRYFAFEKVLKSHGQDYL VGPTSLSRGWTFIWWELLYYVEGA WTPRLISSP LLKALKTRISNLPTVKKFLQPGSPRKPMPDEKSLEEARKIFRF

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7566	37934	A	7620	2	1256	CHCGPP/VKVEAYGSQVLKGVLAQVQLTVGVPVGRTHPVVIFPV PECIIGIDMLSSRQNPHTGSLTG RVWTIMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFNPIWPVQK TDGSWRMTVGYCKLNQVVTP AAAVPDVVSLLLEQINTPPGTWY AAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFVLPQGRWEI NMTKIQQPSTSVKFLGVQWCG ACQDIPSKVKDKLLHLVPPTTK K/EAQCLSGFRREHPIHLPIYRV SRKAANFEWSPEQEALQVQV AAVQAAWPLGPYDPADPMVLE VSVADRDAWSCWQASI/GHK VGHAQQHSIIKWKWYIRDWAR ADPEGTTKGQGRWWQLAE RQDSRDREAAIGERQETA VGKT ARDGEAVCD
7567	37935	A	7621	1	518	MTVDYCKLNQVVIPIAAAVSD VVSLLLEQINTSPGTWYAAIDLA NAFFSIPVHKAQQKQFAFSWQG QQYTFTVLPQWYINSALCHNL IRRDLDCFSPLDITLVHYIDDI MLIGSTIKWVHSS/DSIIKWKW YVHDWARAGPEGTTNGLAG*S GTCKKHEWKTGDKGIRGRG
7568	37936	A	7622	1	696	
7569	37937	B	7623	1	1014	
7570	37938	B	7624	1	837	

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7571	37939	A	7625	1	2592	MVRKAKWKPLQLPLPRKIVNQ KQHRIPGGTVEISAITKDLKDA GVVIPTTSPFNSPIWSVQKTDGC WRMTVDYCKLTQVMTPIAAV VPDVSLLKQINTYPGTCKIFLG VQWCGACRDI/PSKVKDCLLHL APPTTKKEAQLVGLFGFWRE IIIPHGLVLLQPMYQVTRKAASF EWGLEQEALQQVQAAVQAA LPFGPYDSADPTVLEMSVADRV AVWSLWQAPIGESQWRPLGLW SKALPFSADNYS PFERRLLACY WALMETEGLTMGHQVTMQPE LPIMNWVLS DPSRHKVGHAQQ HSIIKLKWIYICQARAVPEGTC\
7572	37940	A	7626	20	238	*LNKEVAQMP/MGTTTRKWTAA ALQSLSGISLKDSGEGKSSQWT ELQAVHLVVHFAWKEKWPGT WKKHDWKTGDNEIWGRGIWM DCSEWSKTVKIFVSHAHEPSGH GGRDGGYAWAQEHELSTKAD LATGIVEPCICQQRPRLSPRYG TIPQGGTFILTGINTYSIYGFAYP AHNASAKITIRGLTECLIHHGI PHS/IVSD*GTHFTAKDVETRIH RPRNQGVVEVAPLITITRSDTL AKFLLPVPTTFRSANLEVLLE GGTLPPGDPTTIPLNWKRLRPR GHFGLPLPLSQQAKKGVSULA GVTDLDYQDEFSLLLHNRVTA AFPSLLHSSFAYLDNMIEKANK CHVEGDVHVS DPAQRRECDRH
7573	37941	A	7627	3	229	
7574	37942	A	7628	1086	1369	ETGMLPLRLLPFLSDFAGPLH TSIMPTRRFCSKSPT*HTLATAL SQGLS*GT*NEASLTKEKVGKN RCRYSYSPPSGIREGKAQLCFY THWK

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7575	37943	A	7629	1	1805	MSGRSRGRKSSRAKNRGKGRA KARVVRPAPDDAPRDPDPSPQVS LGEDTQAAQVQAGAGWGGLE AAASAQLLRLGEEAACRLPLDC GLALRARAAGDHGQAAARP GP GKAASLSERLAADS VFVGTAG TVGRPKNAPRVGNRRGPAGKK APETCSTAGRGPQVIAGGRQKK GAAGENTSVSAGEEKKERDA GSGPPATEGSMDTLENVQLKLE NMNAQADRAYRLRSRKFGQLR LQHLERRNHLIQNIPGFSGQAF *NHVLLASFLNSQEKVEVLSYLN SLEVEELGLARLGYYKIFYFDR NPYFQNKVLIKEYGCGPSGQVV SRSTPIQWLPGHDLQSLSGQGNP ENNRSFFGWFSNHSSIESDKIVE IINEELWPNPLQFYLLSEGARVE KGKEKEGRQGPQPMETTQP GPLSFVWVAVSPSWLPGQQGP QELPVDRLPLVHETHYTPPQL SRNPTGCQTDGRAGLPVTPCDK KALPCAQCFVSHLLYCMGLQP RQKEKINPEVSSITNVAPKDME KVHAGALDKPMCGRQGKESQ GATHHATPSAISPAPSHPLGSSE TLIDGLAHFLEHSQINPSSLRS VLIQRQHLRHVAVTNG
7576	37944	C	7630	66	206	

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7577	37945	A	7631	3	1643	VQASQAEADQQQCTCLKQLQ/S\ QLSRL*KQAIELREAVEQHKVK NNDLREKNWKAMEALATAEQ \ACKEKLHSWTQAKEES/ERNQ LCLIEAQTMALLALLP\ELSVL AQQNYTEWLQDLKEKGPTL/L KHPPAPAEPSFGTWAFQV*GEA E\ETQSTICRAEF\DQYRSILGGD GRALLRDLQKSVEEEEQ\W/R AKVGAAEEELQKSRVTVKHLE EIVEKLKGELES\SD\QVREHTL HLEAELEKHMAAASAEQNYA LLEVAG\LRQLLE\SQSRLRPP KNRNPQKTEPMSFALGQASS*V KLKSHVED\GDIAGAPA\SSPEA APQPSRDPRSA*RTQLELDQKPI PWRMRQTTSRQKLHGSPFEAE SDLRACSVYKEGFWEKLPHSA APPRSFFRNRRRAFTA*RRDLEK RGRSLTSD\LGARPRRLQELSE RRTQEQLGKGRRTRVKKLQEI/Q L\EKAEDGSS\SKEGTSVL.SFLFG KKKLLFQLYQNALTHSFTIKPT NLHSVYPGPNFV\LREKAHEET SLFRRPQEVRTFPGGPILLNGTC
7578	37946	A	7632	3	247	
7579	37947	A	7633	3	389	GQEFSPKVY/FVNQTMGN/SCG PIGLFNAVANNQDKLGFY\GP LLNQFLF*NR*KCPPKDRAKCF ER\NEAIRAAH\DAVDKEG\QCR VDDQGEFFFLFCLQNVDPSPM NLDG\RMPPFRGPMAPSFRTP



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7580	37948	A	7634	1506	3135	RGLGGGLAEQELQPWSPERSPV HNN/RM/QEKS LKDL MEL KTM AQELRDECTSLSSRFQLEEKV SVMEDEFINEMKQEEKVREKRIK RNEQSLQEIWVYVVRPNLHLIG VPESDRENGTKLENTLQDIQEN FPNLRQANIQIEIQRMFPQRY SRRA TP RHIVRFTKVEMKEKM LRAAREKEIQTTIREYYKHLYT NKLLENLEEMDKFLDTYSLPRLN QEEVESLKRPTGSEIGAINSLP TKKSPGPDGFTAIFYQRYKKEL VPFL LKFQSTEKERILPNSFYE ASIIIPKPGRDITTKENFRPISL MNINAKILNKILANQIQQHIEKL IHHDQVGFIPGMQGWFNIRKSI NVIQHINRTNEKNHMIISIDAEK AFDKIQQPFMLKTLNKLGDGT YLVIVRAIYDKLTANIILNGQKL EAFPLKTGTROGCPLSPLLFNIV LEV LARAIRQEIKGIQLGKEQ VKLSLFADDMIVYLENPIVSAQ NLLKLISNFSKVSGYKINVQKS QAFLYTNNRQTESQIMSELPFTI
7581	37949	B	7635	1	594	
7582	37950	A	7636	434	744	TLACLARLGKFSWHISCRVFSNL VPFSPSLSGTPIRRRFGLENRVT ATRILRFSDRLKRRRTTRLYP GSEGPPTESR*LLAQQSEIKLQ GGSEAGGGAPA
7583	37951	A	7637	1	1077	
7584	37952	A	7638	1	348	
7585	37953	A	7639	1	831	
7586	37954	A	7640	275	457	LIAYQPK*AQDYMDSQLNSTRG TKKSC*GRL*GSGVHIGSMVPV TRTAGLPFFAGPCR
7587	37955	A	7641	341	504	ILRFSDRLKRRRTTRLYP GPTPRESR*LLAQQSEIKLQGGN EAGGGAPA
7588	37956	B	7642	1	627	
7589	37957	A	7643	121	375	DGQQLIALHRLALRELQQA VHAGLPQQA KILFDGGSEIGIKH*L RCAHCPLSSRETCRASCINESAT RGERPFAYWAPGWFFHHQ
7590	37958	A	7644	3	479	
7591	37959	A	7645	382	642	
7592	37960	A	7646	273	1464	

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7593	37961	A	7647	76	1763	IFGITRFLPFIYQKIHIFSKEQLPD LHSHFSDLNLEAHMYASQWFL TLFTAQKFLCMVFHIIIDLLCEG LNIIHFVALALLKTSKEDLLQA DFEGALKFFRVQLPKRYRAEEN ARRLMEQACNIKVGYYTGTEL Q*DFSLDSLVSWSWDSGCCGK ASWQDDGRNLHYGSL*RPCFQ PAAR*RLPH*SGGHQQAQVYG TNKKLKKYEKEYQTMRESQL QQEDPMDRYKFVYL*VTPAVA FILGIFIRS*EKERGKRKWLSTF KNETKRKNGKVLF*LCMSYPQ RLLAGELFQD*HKDVSNLPLSV ENVKNTNSLGRKNKNHK\REN RRLQEASMRLEQENDDLAHEL VTSKIALRNDLQAEDKADVL NKELLTKQRLVETEEERKQGE EETAQLKEVFRKQLEKAEYEIK KTTAIIAEYKQICSQSLSTRLEKQ QAASKEELEVVKGKMMACKH CSDIFSKEGALKLAATGREDQG IETDDEKDSLKKQLREMELELA QTKLQLVEAKCKIQELEHQRG ALMNEIQAAKNSWFSKTLNSIK TATGTQPLQAPVTPQPPKEST
7594	37962	B	7648	1	618	

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7595	37963	A	7649	1	2375	MAGAPPPASLPCCSLISDCCAIN QRDSVGVVRPSKPGAGYNLVVR RFLSLLEKRSIPVGVTRFSRCRP SPLSLTRKGNSLTPCASRIINMH FQAFWLCLGLLFISINAEFMDD DVETEDFEENSEEIDVNESELSS EIKYKTPQPIGEVYFAETFDSSGR LAGWVLSKAKKDDMDEEISY DGRWEIEELKENQVPGDRGLV LKSRKHHHAISAVLAKPFIFAD KPLIVQYEVNFQDGDCCGAYI KLLADTDLLLENFYDKTSYIIM FGPDCKGEDYKLHFIHRKHHPK TGVFEKHAKPPVDLKKFFTD RKTHLYTLVMNPDDTFEVLVD QTVVNGSLLDVPPIKPPKEI EDPNKKPEEWDERAKIPDPSA VKPEDCALGLELWSMTSDIYFD NFIICSEKEVADHWAADGWRW KIMIANANKKKHKDTEYKKTDI CIPQTKGVLEQEEKEEKALEK PMDLEEEKKQNDGEMLEKEEE SEPEEKSEEEIEIIEGQESNQSN KSGSEDEALAEQPREPGVPGP IPPKRPSRSPPEPRAAKRLPTQE LRGESYTMASGTARGSPKER LGLTTKTGEKVAQGFCREPGL RRPPNAQARDRSSRAPATHRKE LKPEREHISCSRSHIRYQEWVSL RDTVHRNLVLDTRKHPALILVE YKERTSSPATEQSCMENDFDEL REEGFRRSVITNFSEKEDVQT
7596	37964	A	7650	914	2786	
7597	37965	B	7651	1	2369	
7598	37966	A	7652	333	752	MSYVSRVYCGGRKNVATVSKG WAGSLA WPGGFPKVKGGGS WRPSGGV/DVAAPVRAALALL SGPIASESPLTTNPHSHSARRPR TYI/GHAPALRVTN/PESFSYWG TRGPSATMACDGLTRTGHSPTS RARSPLLCARSL
7599	37967	A	7653	1	177	RPLPSRPHAAPPGHHTISSGPCG HRKFSPKAGDSNTPRTSRPRV SCALPPDVRGSWLS*KWNQIW YHTLPQPQENTPKSQENKPKSK PQPTQR*TRGPW/PSSRCRVRSG /THRRPGLFSL*KQ/PSESIHRSR ALSAFTPAEMISTLPPPTTSKSPL AARAAPPNG*SPKAGDSNTPR TRSRPRVSCALPPDVRGSWLS

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7600	37968	A	7654	1	1430	MQDTCSEIISPADFTPTFSSSLKIR FSTDSPSQIFKKKHCIQKIVLILLP KNSYTRRLVSNQMYLESFEH QCRKTHILCKRTAGSGPFCSCPT GQPRHNSSASKCPASERGLCLK/ PKSKREKREPGVAPAPLHAAP SSPGLGAPQLR*PGRTRSGFRD HVGSGPPRAGPRLFAPRPVLS RCSANPSGSPHTQSPKQSSGTQI SGRADQVCGCWIRKRGVPGAA RGSPGCARTCHSRGHPHAAPFP QCNSLAPSAAGLWRTQNAGP SG/HAQPSCPPPVPL*PPHPH*G LSFSSCSRSWVPNTTP/EPREGE GQVPGRRASAPGASFSAPGT/P RAPQLPHFPVAQSPPAVAA SSECKREARRSPGASALHLP KSARPRQAPCPTLTDGGHIFPAS AARP*HKGHQTAEGKNPGRAD TSTSPFATFFISGGEKSRSPVL PERTRQREEAGPPSSPLRGLW LTFWVFL
7601	37969	A	7655	1	609	
7602	37970	A	7656	3	649	AKD/ELHIVEQGHDIRGRSIKIT/ LATLKMS/VQPTFS/LGGFEIQPT VV*GLKCVSGPCHISGQHLVA/ VEEDAEESEDEEEENVKLLSISER RSAPGVVSMVPQKKVK/LAAD EDDDDDDEDDDDDDDDDDFD DEEAEEKAPVKKSIRDTPAKNA QKSNQNGK\DSNPYSHPRSQG/ QDPFRKQKTPKTPKGPSSVE DIKAKMQASIGKKRIEVLGTy
7603	37971	A	7657	1	1013	PWCDSVLRGCSLEQRFSFISVRL SYLSACRHPMEDSMMDMSPL RPQNYLFGCELKADKDYHFKV DNDENEHQLSLRTVSLGAGAK DELHIVEAEAMNYEGSPIKVT\A ATLKMSVQPTVSLGG/FEITPPV V/LRLKCGSGPVHISGQHLVA/ EEDAEESEDEEEDVK\LLSISGK RSAPGGG\SKVPQKKSKTCML MKDDDD\DEED\DDDD\DDD DF\DEE\AEKAPSERNL\YRDT PS/AKNAQKSNQNGK\DSKPS TPRSKGTIPSKKQKTPKTPK\ GPSSVEDIKAKMQASIEK\GGSL PKVETKFINYVK\NCSRM\TDQE A\AQDLWQW\RKSL

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7604	37972	A	7658	9	271	GRVCKALWHSDDWHTARVLCIN STTTITASCNP/RHTARRSI.TTPT *MCRLENWTKNLLFNGPVPVVL VMSSLFIASVFMHLHWGKYTRS
7605	37973	C	7659	189	500	
7606	37974	A	7660	5	291	ATPSPSPPG/VPT*RPPELLGP ERLLGPEGS/PGGGALPGVPPSR FVRTASSTLFLPPSRPAFPSSIP LVPSPPRHCARSRETWPRTLRI SAP
7607	37975	A	7661	1	431	LALQFSFLQNRQGLNLLIAEKG RLCIFLNEECFCYLNQSGLVYD NIKKLKDRVQKLANQANNYAE PPWALSINWMSWVLPILSPLIPV FLLLLFGPCVFCLVSQFIQNRQ AIANNI*QMLLLTTPQYQPLPQ NLSSVESLPL
7608	37976	B	7662	41	1547	
7609	37977	B	7663	74	298	
7610	37978	A	7664	3	647	ELWTRGPRKRQNGSSKPLWLL YGESGAQKSVVEVTKPRLLWP QWQHRRARRPCLQQAPCSSRPH APASLPSSSPTARDTKHRAQV KTTDSGARRRDGRVLGVLEVS RSIADGQYKRCGVTSVPD/IRR C/QLTPQ*PGSILLACDGLFKVF TPEEAVNFIL/SCLEDEKIQTR REG KSAADVRYEAA/CNMLANKA VAAGARPDNVTV/MVVRUGH
7611	37979	B	7665	1	1302	
7612	37980	A	7666	3	1268	SCARVAAWGGKLRRLGLAVSRQ AVRSPGPLAAAVAGAAAGAG AAWHHSRVSAARDGSFTVSA QKNVEHGIIYIGKPSLRKQRF QFSSLEHEGEYYMTPRD/FLFSV MFEQMERKUQSRS*QKRFI EDT LSGIPTAGCGSFFQRPWAIKGL ISYNRVIFFALQSSLNPIPGFH VAFKMLDTDGNEMIEKK/ENFL SCRRS*VNKMT*LTVKTNETW SGSNK*KNLKL/DTLQMRFFG KRGPRKLHYKEFRF/WENLQT EIQGN/VEFLQFSKGLSFMKR RR TLQSGYFFSTNTENKDIYWK NV REKLSAGESISLDEVKAFCHCT RQIGTLCY/SAMQMFTLAHRPV RLAEFKRAVKVATGQELSN NIL DTVFKIFDLGDDECLSHEEFL G VLKNRMHRGLVGTSTTSEYTR IL EVCEERKH

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7613	37981	A	7667	2	342	QNRGPGRT*DFLPNS/VGEKILS FCNCSLGSIGALGPACCRVLSEL SEEQVFHVNYLDVEELSLRLC QCLVELSFQLATAYHGSATTRE AARGEAAACRAHLMFWCLCIWQ FCRL
7614	37982	A	7668	1	1166	VGCVLGRVEAAVTAPAGTEE GMSEEEQSGSTTTGCGLPSIEQ MLAANPGKTPISLLQEYGTIRG KTPVYDLLKAEGQAHQPNFTF RVTVGDTSCGTGQGPSKKAACH KAAEVALKHLKGGSMLEPALE DSSSFPLDSSLPE DIPVFTAAA AATPVPSVVLTRSPAMELQPPV SPQQSECNVPVQALQELVVQKG WRLPEYTVTQESGPAHRKEFT MTCRVERFIEIGSGTSKKLAKR NAAAKMLLRVHTVPLDARDG NEVEPDDHFSIGVGFRL/DVL QNRGPGCTWDSLNRNSVGEKILS LRSCSLGSLGALGPACCRVLSE LSEEQAFHVSYLDIEELSLGLC QCLVELSTQPATVCHGSATTRE AARGEAAARRALQYLKIMAGSK
7615	37983	A	7669	2	328	
7616	37984	A	7670	181	1271	LEASLDQH*ASVHSFRSHIHVIS RTHRKISQRPSELDAEHAQKV LEMEHTQQMKLKERQKFFEEA FQQDMEQQYLSTGYLQIAERR GEWGLGLLVWGLTGACGCHD SSWGLVRWYKCYSKFVDEPC LQFERNCKPIGSMSSMEVNV MLEQMDLMDISDQEALDVFLN SGGEENTVLSPALGRVDKLALA EPGQYRCHSPPKLQQWCGSVM NSSQRFDMLHSGNFEIHLSELL VVKDWRLQGGADSPAGLTGNS SLFVRQAFRGVPAMGKAMGSS QVLQAPGESSTCQNEITLQVP NPSELRAKPPSSSSTCTDSATRD ISEGGESPVVQSDEEEVQVDTA LATSHTDREATPDGGEDSDS

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7617	37985	A	7671	60	965	QRGVGGVGRGRQRQQPEA* GEETAAAAMLETLRRLRLSVQ QDFTSGLKTLSDKSREAKVKSK PRTVPFLPKYSAGLELLSRYED TWAALHRRRAKDCASAGELVDS EVMMLSAHWEKKKTSLSVELQE QLQQLPALIADLESMTANLTHL EASFEEVENNLLHLEDLCGQCE LKRCKHMQSQLENYKKNKR KELETFKAELEDAEHAQKVLEM EHTQQMKLKERQKFFEEAFQQ DMEQYLSTGYLQIAERREPIGS MSSMEVNVDMLEQMDLMDIS DQEALDGLPELWRRREHCAVP
7618	37986	A	7672	1	124	
7619	37987	A	7673	3416	3920	CCLIKNDIKEKLHYSDCRLNVG QPCILPRNAFEFDLLIFYLGNLH FYISEIGLLGYCTFFFFFEMESC SLTQAGVQ*CNLGPLQLPPL E*F/SCLSLPSSWDYRHHVPPHWL IFVFLVEMGFCYVQGAGLEFLT SGDPPTSASQARITGVSHHAQ PGYCILILGFC
7620	37988	A	7674	1	387	

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7621	37989	A	7675	1	1827	MKKVGGRVFWAKERASAEAL RHELAGLLKCKKGSAADADQG GLGQGCRRRHRSRWEGFTRGAS RAARLGNEEQDAASAGPGPNG CGHLGAEEPSAAASGMDQCVT VERELEKVLHKFSGYGQLCER GLEELIDYTGGLKHEILQSHETC LSVLLSLPMVMAGSGLNKVL QLCRFLHMKTTGEMNYGFHLA HHMALGTSIFGEEGRYSLSTS NSSIAALLCALYPHFGFTALD NRYHLQVALR/HLVVLAAEPRA FLVPVCGGTQTRPCYALLGSLP YKGTQWYEQTKEDLMAPTLL PELHLLKQIKVKGPRYWELLID LSKGTQHLKSILSKDGVLYVK LRAGQLSYKEDPMGWQSLLAQ TVANRNSEARAFKPTISAFSTSD PALLSFAEYFCKPTVNMGQKQ EVLDFSSVLVECVYPRETPAE MLPAYIAMDQLIRRLGEREMS ETSELWQIKLVLEFFSSRSHQE RLQNPPPLKRGALLMELGNSPPF CKCTNNNTLDTWLQVRGDIC VNAYLTGQPLAEESSQDMLACF LVFHFVPSSTALPTL*D*KGSTS FAVELLFKFKASLKMPSAELCLR LAPLPSLEIPQNGDVTVSGGEP
7622	37990	B	7676	374	515	
7623	37991	A	7677	102	1237	HSRAACPDNTNRLVPGASR*HY LHRCRSRHSS/NIGKNI/HSRA GAVNNQSRPQSHSSGEFSLHD HEAWSSSGSSPIQYLKRQTRSSP VLQHKISETLESRRHKIKTGSPP SEVVTLQQFLEESNKLTSVQIKS SSQENLLDEVMSKLSVSSDFLG KDKPVSCGLARSVSGKTPGDFY DRRTTKPEFLRPGPRKTEDTYFI SSAGKPTPGTGKIKLVKESSL RQSKDSNPYATLPRASSVISTAE GTTRRTSIHDFLTKDSRLPISVD SPAAADSNNTAASSEYHLHQ WSSHLDIPHTHTIGSCAQNDLAI DMPEPLYAQARNSTRGRSHFL NQTFATIRMPSDAFGLAKDK HRTIYCGPFISAILPEYRIS



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7624	37992	A	7678	1256	1971	HNCALHADSTMRGKAPLFRPT YKLMQELLLRIFRWISQKQCNV EVTSLICWF/CTCTYSGWVEAYP TRTEKPYKKGKNDPSTKGQC NPLELVITNPLNPHWKKGERVT LGIDRARLDPRVNILVRGGEVY ERSPEPVFQTFYDELNVVPPEIP GKTRNLFQLAECEVAQPLNVTS CYVCGGTVTGYQWPWKAREL VPVDPVPDEFQAQKNYPDNFW VLKPSITGQYCIAREGKKFTHP
7625	37993	A	7679	1	1710	
7626	37994	A	7680	1	561	
7627	37995	B	7681	1	642	
7628	37996	A	7682	2	611	
7629	37997	A	7683	1	1718	MLSIQSTHAEKELENNFFQNTD WYFHTSHHLSLRFFSARESN SMKLYEEAYMERYRDFLPATM WSAHEVDVPGQATWIKQSE KDPVHLQKGNPSTKGQC PLELVITNPLDPCWCKEERVTL GIDGAGLDQVHILVRGEVYKH SPEPVFQTFCEDELNVVPPEIPGK TRNLFQLAWHVAQCLNVTS YVCGRTIIGDQWPQEAQELVPT DPVPDEFQAQKNHPDNFWVLK A/IIHQYCIAREGKEFTHPIG*L SCRRQKLYNGTTKTIT/WRGSS NHTERNPFSKFPKLQTVWTHLG VPRAWEQPPLGFLGYVRAW LLTGLLDHWAGSCCLLGT/KPS FFPTAP*KQGKLLGFPVYASRE KRHAIENWKDDWPPERIIQY YGPVTWAQDGLWGYQTPYVVL NRHRLQAALHITDKISRALTIL AWQETQMRNAISQNRALDYL LAAEGGVYGKFNLTNCLHVD DQGGVVEDIVRDRTKLAHVPV QVWHEFDPGAMFGKWFPA GFKTLIIGVLIIGTCLLPCLLP VLLQMIKSFIALTVHQNASAQV
7630	37998	A	7684	3	406	TLISFIYPAQNPELLNKLQRKT TVLAMDQVPRVTIAQGYDALS SMANIG/YLIVGGGVAGLASA GAAKSMGAIVRGFDTRAALAE QFKSLGAEPLEVDLKESGEGQG GYAKEMSKFIEAEMKLAFAQQ CKEVDI
7631	37999	A	7685	1	236	
7632	38000	A	7686	1	978	
7633	38001	C	7687	415	453	

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7634	38002	A	7688	3	408	
7635	38003	B	7689	1	2137	
7636	38004	A	7690	112	3688	GNWGARKLGTHINMANLLKTV ATGCSCPLI.NNLGSCKGLRVK KDFLRTFYTHQELWCKAPVKP GIPYKQLTVGVPKEIFQNEKRV ALSPAGVQNLVKQGFNVVVES GAGEASKFSDDHYRVAGAQIQ GAKEVLASDLVVKVRAPMVNP TLGVHEADLLKTSGTLISFIYPA QNPELLNKLSQLKTTVLAMDQ VPRVTIAQGYDALSSMANIAGY KAVVLAANHFGRFTGQITAA GKVPAPAKILIVGGGVAGLAS
7637	38005	A	7691	2	288	EFPATIQSNRARGAKPGRRVDR GPQARCFDVGCGPRSPAPSNGLR NSEPSP*GR/CGRSPVSPALSSSR DVNL.PCMLSSGTDGACSEVLV GTLYRPL
7638	38006	A	7692	54	522	RFHMSSLSASPPRRLWTQMNT QCLVFSASHLPRCQEMLFQGT *EKPHSPRCFSPAKKPRPAGAPA ASHKCR/CT*PGPPSEPTV/PSD KAPLVGNAESQSVASPSGPPAP CSPVAGWPGTYKAIPASGTVAP TPLSAGTTDMTRLCLPSLELL ND
7639	38007	A	7693	3	57	RAGAGRSERAVAEES*GGLSGS CGRHNPGQSRQRRPSQDVELE DCCRGC*SGSLWRLRLPKRPA PFGGFSVPASSAASIPTGSAVVQ PGPLPGPTGKSPPVFAGSGPSSN PQPAFS\NMRTDGSKPGSA/SF APLTPPLEPAGLRAPSSGVSP LPATIQSNRARARSPGDA*AAP PRPGVLTSAVPLPRRV/CLRNS RAFAPAVRTNAVTP*PGGVSGP SQRRAEAA
7640	38008	A	7694	3	237	
7641	38009	A	7695	114	186	

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7642	38010	A	7696	73	904	FGGFLANLSYQEALSDTQVAIV NILSSTSGFLTLLAAVFPSSNSGD RFTLS*ELLAVILSIGGVGLVNL AGSEKPAGRDVTGSIWSLAGA MLYAVYIVMIKRKVDREDKLD IPMFVGFAGLFNLLLLWPGFFL LHYTGFEDEFEPNKNVVLMIHIN GLIGTLVLSLFWLWGCFLTSSL IGTLALSLTIPLSIADMCQMOKV QFSWLVFFAGAI PVFFSFFIVTLL CHYNNWDPVVMVGIRIFAFICR KHRIQRVPEDSEQCESLIMHSV SQEDGAS
7643	38011	A	7697	1	308	
7644	38012	A	7698	3	397	
7645	38013	B	7699	1	963	
7646	38014	A	7700	3	1433	KIRVTSKALELGKAQGGTGTG GSGRGWGRPNSSGKKEGHFYNN ISE*VGGGASRSAGAPRRWRRG PRMLQITNASLGLRFRRLLYW FL*GPSTLRGVESGSGGLEVLW GSRDPAGRMKVSNNVSCQASVS RMHAAFGGTFK*APAPTAHPF RAPQLICLAQVWAATGRRVAR VGMLSL*EGPGELVAGESGCA AVMQHLRAGPFRALLFTSNLD MDFRVSCLGWCMTSDFLTRPL SLLSLQEERMMVYVAFSEFFD SAMESYFRAGALQLLLVGDV CHGLFVGWAREGL*QSSLPHC AGGGRDRATCTPVRPRRGAIAK PSGTTISVTASVTIALVPPDQPE VQLSMTMVRVPEWGLLAGG QGKMGCGLLSR*AGALPCTSVI GGQSHLSTGMGWAGFVRS*PS PSPRKA/RGVMEERIGVNW GPD*ATNHAVSGGRMGKEGGP SPLSIAPQCHRPADVRASATPTP
7647	38015	A	7701	2	391	MALRGKALRTTSDLRFRRIYSN HSATWKSAL/L*IPLQAPLK/IM LPELG*MPQCSNERTWRGVQ DPHYPEGIKLCAMKVVTNPGGI PSPIGA*SPTFAKGLREVIEKNR PADVRAS/ATPTPSHSSCLSP
7648	38016	A	7702	1	189	
7649	38017	A	7703	202	455	KCDILPTALDSIHH/SSHRVHLA HSPHSLQ**HPHPLAQPSQQRDP SVPL**MSLADPESHSSESHF HL*PACRV*AYDLLPL
7650	38018	A	7704	313	378	

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7651	38019	A	7705	126	1246	PNGLRPPCPSPASETPGNAPVCD PGSSSQGAQGLKNAWWAPGM A/ASRSLHSLHIPVR/RACALPAQ SLLGPLRSFRCHLSDPVFRTGAP PGQGSWQYKVLVHAQERELTQ LREKLREGRDASRLNEHLQAL LTPDEPKSQGQDLQEQLAEGC RLAQHLVQKLSPENDNDDED VQVELAEKVQKSSAPREMOKA EEKEVPEDSQEECAITYSNSHGP YDSNQPHRKTKITFEEDKVDST LIGSSSHVWEDAV/HHYSRK* K***GRGRKRASVSQKPEETPS\ PRPEPPPRGSGEAERSVGSWDA SSRSLRRLHPLREPVTPLPSRFR GRCGASAAIFGSCVPHGGSTRA GMMGSKEVGKGGDPGEETSPV ALFS
7652	38020	A	7706	3	5665	LLEKLQRRIHDKAVALERAIDE KFSALEEKEKELRQLRLAVRER DHDLERLRDVLSSNEATMQSM ESLLRAKGLEVEQLSTTCQNLQ WLKEEMETKFSRWQKEQESIQQ QLQTSLHDRNKEVEDLSATLLC KLGPQGSIEAELCQRLQRKER MLQDLLSDRNKQVLEHEMEIQ GLLQSVSTREQESQAAAEKLVQ ALMERNSELQALRQYLGGRDS LMSQAPISNQAEVPTGRLGK QTDQGSQMIPSRDDST
7653	38021	B	7707	1	1098	
7654	38022	A	7708	193	5850	HCQRNTTGEHCEKCLDGYMIK S*DSLFGDVWN*LPIFASNFSFA EL*K*GFVRDYHK*TFVCS/CLL NP*GPEFVGKKIKRKKNHDAK YLNV*YS/CFRCAPGYGYNPLLI GSTCKKCDCSGNSDPNLFEDC DEVTGQCRNCLRNTPGKYCHIL SIKKCISRLFLFPTVCNCGGGP CELH*EQNFWFKNYFNRSRHPLP QTDVSWCSAKTACL*HAFDL*F *RNVSPPGCDKCVWDLTDALR LAALSIEEGKSG

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7655	38023	A	7709	1	713	TPCFESPN/ETGTYFSTKAGYVL LN/ESSN/GIEFEIAFKVPRSSS GTLVHGHSVNGEYLVNVMKN GQVIVKVNNGIRDISTSVTPKQ SLCDGRWHRITVIRDSNVVQL DVDSEVNVHVVGPLGIQKPIDH REFVLVGGVPRILY*HPRFCPP QNPFTG/CIR/HFVIDGPPQWSFQ VKAAPGQAGARKASNSLSQQP GHGQKHSCKYKVPRLALEKE HKASPGGTVTLSPFVGSFSSS
7656	38024	A	7710	3	322	DGVSHCRPGWSAVA*SQLTAT STSWVQMIACFTLPSSWDYRCT PPCLTNFCVCFISDRDVMWMLA GW/LKNS*PQAIRPPQPPKVLGI TGHEPRAPGQKILTFHILT
7657	38025	A	7711	2	480	YSPPECPCFCGKIEEHSDEMETH VKTKHANLLDIPLEDCCQPLDYD CPMCGLICITNYHILQEHVDLHL EENVTFSKAWIESSVLVIYNWLT SFSKKKTERGD/PEESRQIEIEF QKLQRQYGLDNSGGYKQQQLR NMEIEVNRGRMPSEFHRKKA DMMESLA
7658	38026	A	7712	187	468	
7659	38027	A	7713	1	1110	MHCIETGVERRILGLLLFRGSLA SVIRPGEVLDAAHALVCQRGPK GKPSGAQCQSCWPLGRPKALT QLVPASFVCLACAFGAERLGDS ALRSSDLTHLLVNTMLSCNIC GETVTSEPMKAHLIVHMESEII CPFCKLSGVNYDEMCFHIETAH FEQNTLERNFERINTVQYGTS NKKDNTLQCGMEVNSSILSGC ASNHPKNSAQNLTKDSTLKHE GFYSENLTESRKFLKREKQSSSL TEIKGSVYETTYSPPECPCFCGKI EEHSEDMETHVKTCHANLLDIP LEGMDRVQCSGDLQLAHQLQ EEDRKRSEESRQIEIEFQKLQR QYGLDNSGGYKQNNYEIWR* K*IGEECLHLNFGEKLI
7660	38028	A	7714	2	303	
7661	38029	A	7715	97	233	RTVTCYHRNSRACHPQQITSCP *HRALPCLPLWSPKCPSRWPF G
7662	38030	A	7716	229	359	MKVVVYCSVTGMGKGQHRMP SKG*GWVQRYNRDGPSPRVLE LF

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7663	38031	A	7717	1	1185	MSTIDDPRLQGRMCLMLRGT PEQKALVIGGEACMWGEYVDN TNLVPRLWLCPPSTQDLANEI REMTILHRHIPDRGKGVMRSCS FRTPRPFTLACGPEKSLMDPQS QSNSEGASSSLVVKLADTDRE ALRRMQQMAGHLGAFHPAPLP LGACGAYTTAILQHQAALLAA AQGPGLGPVAAVAAQMQHVA AFSLVAAPLLPAANAANSPPGSG PGTLPGLPAPGVNFGPLTFQT NGQPAPTRSTITGSPLI/SGWSQ SRPILRIMKYAEQRIPTLNEYCV VCDEQHVFNQNGSMLKIQPTII QVWREDIPVNYMKELELVTKA GFRALLSAPWYLNRSYGPDW KDFYIVEPLSFEPTPEQKALVIG GEACMWGEYVDNTNLVPRLW AHRQL
7664	38032	B	7718	1	1196	
7665	38033	B	7719	184	1689	
7666	38034	A	7720	228	407	
7667	38035	A	7721	1	725	MQRGALSPVLMLSAAPEPPRP PPGLSPPGSGPGSGSRHGSARPG PTPEPSGSLGAALDSSLRAAVA FKAEGQRCYREKKFREAGKY HRALLQLKAA/LGGPP*RPARP RPPGPTSSPGPARLSEEQRRIVE STEVECYDSSPA/CLLQSELVNY ERVREYCLKVLEKQGNFRFP YRAGIAFYPLGDYARALRFLQ EAPSRPPDNTNVLRYIQLTLK MNRCSLQREDSGAGSQTRDVI
7668	38036	A	7722	1	262	NGKEPGRYTFEDAQEHYKLM KSDSYPRFIRTSAYQELLQAKK KGRNIPFPCHKNCTPTLRASTN LL*KEGKSLTSKRLTSLAQS
7669	38037	A	7723	1	1392	

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7670	38038	A	7724	1	1544	MAQGNNGYQTSNGVADESPN MLVYRKMEDVIARMQDEKNGI PIRTVKSFLSKIPSVFSGSDIVQ WLIKNTIEDPVEALHLGTLMA AHGYFFPISDHVLTLDKDDGTFF RFQTPYFWPNCWEPENTDYA VYLCKRTMQNKVARLLEADYE AESWA/RGLQRAFAFKWIEFIF MQAGAAQAKVDKKRDKIERKIL DSQERAFWDVHRPVPVCVNTT EVDIKSSRMNRPHKTRKSVY GLQNDIRSHSPHTHTPTETKPPT EDELQQQIKYWQIQDLRHLK MSKVADSLLSYTEQYLEYDPFL LPPDPSNPWALSDDTTFWLEVA SKEPSQQRVVRWGWFAWDEGI GKTQLGRRNSFLKIF*EFRISGS GNFKVLGWASGRTLKKRPFKE VPSRVQEIWQFLAPGAPSAINL DSKSYDKTTQNVKEPGRYTFE DAQEHYKLMKSDSYPRFIRSS AYQELLQAKKKGKSLTSKRLTS LAQSYLNGSSCSMNADWSHCT HFVAQCDCLEQRTLEQDVA
7671	38039	C	7725	81	439	
7672	38040	A	7726	531	686	GWQWLHRPPGATQHCNGNLP AEESLPARATN*ARPAATHRGG RGQDLPPGG
7673	38041	A	7727	93	428	LHCQVHLSLIDLPLINSFLLLF *D*VSLLLPRLECSGAISSHCSL H/LGPGSRDSPASAS*VAGITGT CHHVQLIFVFLLETGFHRVSQD GLDLI/NLVLRLPPPKVLGLQA
7674	38042	B	7728	99	425	
7675	38043	A	7729	35	861	
7676	38044	B	7730	141	586	
7677	38045	A	7731	116	926	AEIVAEQVSEEGGKSRKGPQFG KSQYQELIRRSECGLNREGESI KANMQQVIYIPITLAEVVLRP HSYPSKKTGLTLAAASIAIYISR *EWLYFETGTWVYPVFAKLSLL GLAAFFLSLYVFIASIVLLGEKL NHWKWVSVRNSTLILYIRMAK SHITQSPSLAHMPCSIKIEMAE VPSSAQSMNWCEKLLVFPPR*C CFLRPRDSVSPVFAWFLMHF NTRLFQEAFFGQPOILQRWRLE SVGICFQWPDWKSPAKHQLVK

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7678	38046	A	7732	32	394	GKAVLPIMRETLDGFHYQHCC PDLPGTDLGHPGSPDLGEVKFL SQT*EVTSLVQSGKVWR*WTAI CTHTSQLSISLLAFCLRSASATS LTLSHCVNVVKGLLDFKRRRG HSIGGAPEQR
7679	38047	A	7733	1	765	
7680	38048	A	7734	3	1295	QARVSQELKKAARKRTVSISEGP DTLGDGMRRERRETLALAPEPEP LEKEACEKWKRFPSASATSLT LSHCVDVVKAILDFKRRRHSI GGAPEQRYQIIPVCVAARLPTR AQDVLDAHLSEVQCCSFIPNS SLLATGGADRLIHLWNVVGSR LEANQTLEGAGGSITSVDPDF G/SNQVLAATYNQAAQLWKVG EAQSKETLSGHKDKVTAAKFK LTRHQAVTGSRDRTVKEWDL GRAYFSRTIQCSFSYCNVDVCG DHIISGHNDQKIRFWDNRGPHC TQVIPVQGRVTSLSLSDQLHL LSCSRDNTLKVIDLRSNITARG FRADGFKCSDWTKAVFSPDR SYALATLPVMGPF*IWECGTPG KNWKKQELGTPIALPVQTPW PWCLLPSPHGETWTQGRKGC AFGSAHDLPALGWRLLEA
7681	38049	A	7735	123	463	DVEVGLISQLQDCELGCGIPLK VFPAVFRPLPLSLHTFLPLPLSRT LASGGDGA TSACCRCPGAVSI S*L*QTVASP*VLVHVSRKEVT GKTARAI RDMCLEKDTLGLFLR
7682	38050	A	7736	1	489	
7683	38051	A	7737	1	423	
7684	38052	B	7738	1	900	
7685	38053	A	7739	1	1824	
7686	38054	B	7740	400	969	
7687	38055	A	7741	3	4781	EISATQII VCTPEKWDIITRKGG RTYTQLVRLIILDEIHLHDDR PVLEALVARARNIEMTQEDVR LIGLSATLPNYEDVATFLRVDP AKVLFYFDNSFRPVPLEQTYVG ITEKKAIKRFQIMNEIYVEKIME HAGKINQVLVVFVHSRKETGKT ARAI RDMCLEKDTLGLFLREGS ASTFVLRTEAEQCKNL*LKDLL PYGFAIHHAGMTRVDRTLVED LFAIDKHIQVLVSTATLAWGVN LP*HTALFK
7688	38056	A	7742	2	518	



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7689	38057	A	7743	18	1108	CSGIPRFRDSQSTRAACFFPAWT RMRAPSMDDRAAVARVGAVAS ASVCALVAGVVLAQYIFTLKR KTGRKTKIIEMMPEFQKSSVRIK NPTRVEEIIICGLIKGGAALKQIIT DFDMTLSRFSYKGRCPCTCHNI IDNCKRLQMNVEKSYCQLKEK YYAIEVDPVLTVEEKYPYPMVE WYTKSHGLLVQALPKAKLKE IVAESDVMLKEGYENFFDKLQ QHSIPVFIISAGIGDVL EEVIRQA GVYHPNVKVVSNFMDDETGV LKGFKGELIHVFNKHGALRN TEYFQSN*KTNSNIILLGDSQG DLRMADGVANVEHILKIGYLN DRSGMSF*EKYMDSYDIVLVQ DESLEVANSILQKIL
7690	38058	A	7744	105	548	PQTPRLKQSYHVSLPSSWWHDHP VAGKRA*HAH*FYIMAQLFLPA ASPGPTPASQQLVWTQCLPISW RPWSAHSFLKSSSPGPGPTPASQ QGLWTQLPRSFQRPWPKSSSSR PGNGPGRAASRPRAQLRLPGG LSRFNDGHGNFLAQ
7691	38059	A	7745	186	650	RCPGCPTTASARESREAESRGR GSSGASWGAVQWEEPQPRLL RGTDDCMIFWAPHGSSTWRRR CVHSRSTAADPVLTPSPA/STPS SNCSGSGTSLAALPLPLPQTLGP *QPGWKGTPOCLNTWGVSITS TGRWATPKIPGLTVPPENMDS MWG
7692	38060	C	7746	212	556	
7693	38061	A	7747	2	312	PDLK*STCLGLPKCDYRW/RA TMPGWENIFSSMNHITLNLTG AVTSTRDNS*LHRVSCISSPWCC CLSPCPCRVSA GTGRVPSC LCH SGAWNRLDQDINRNSC
7694	38062	A	7748	2	366	FLHTKYLFCGKIAHPHYFIRSH FFFLLRQS/LYSIAQGGVQWGN LGSLQPPSPGFKQLSCLSLPSSW NYRCAPPCPANFVFLVEMGFH WIKPG*SRN*PRDPPASASQAG ITGVSHHAQP
7695	38063	A	7749	1	446	MPILFTTVSSALSGAQHADAQ CDRKGHRTTIQGSRVNLVQPSV GPKVEETQCWGPGRGMGPAPE APRERRVRSGRS GDPGVA/PR AASGVGGRYAITRGRASAAVP CRSGGARRGGAGQAADCGPG H*KESESRGPEGPAEGSQPL

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7696	38064	A	7750	1	744	GGLIPRAQRESKRRSRGRARAA SGV/VWALCYHPRQSECCGTL* KWRSSPRRCWRTSGDCGPGH* KESESRGPEGPAEGISASLKM* WFASGTCLSRCLTLRQRK*LKK IKIWIWK/SEK/PAEAT*SEGQPP F*GPRQTGAEGF*LEPPQPGMSL KLFKVILKG*DSRTKMGDQQPP RVHGRTHGPLQLTPVKQGQS CPVKGPSPSGIWP*KPLL*CLAT L*WQEGTFLSGLLGPGTPGAS VGHKIY
7697	38065	A	7751	316	650	SYNTHGTFHVPTANVLVVDL MCHLEKLAKYDDIKKMKVQKA LEGPL/KGILDYTEQQVSSNFT SDTHSFTFDAGAGTAFNNHFFK LIF*YDNEFGYSNRVVELMFHP ASKG
7698	38066	A	7752	2	775	QARRARSRNSRGLSQSAAARPLA AKTAWRTVAPQPWAAAPR*R SSCPHSSCSATSPGARACQSSA HSPSPRLQAPPPPTSSSGSVPE AATAPLAASARRGTPRPTGRP SWAGTRQGSWAGTORPWVWA PAPAGPPRAAAAAAR*GRDKS QLTCPPRHSTPPGSAAGASRHR RRGLAGPAPSPGCRAARPPWP SAAAAALGLGGRGPDVLVHCEI HWPLEFQSLCCCLLTSRGGEAS CHPEFHLFMHDFLPGSF
7699	38067	A	7753	1	552	MQTLFTLLQPSSQTGPQPVIC CVYAESGARDSGQP/PSKVPVPS FCTPAATQRG*REPGCSHPAGD CSAPQQCS*PGQ/RIS/RGDKVL ASNTYLPGPGLPGGQGPPGTW MKVETITQ/TNTGTENRVFSL LYMTISKQYLSEEGSHWLSCL INALQAFFSNAAIWLVTWFELS RVLGGAEND
7700	38068	A	7754	2	538	LGKYYITGDKVLASNTYLPGP LPGGQGPSPGPKGSPGFPRY A/GLLGQPGSRGSGTHGTIS*/ G/LPTKQGRRGVPGPPGPPERD GSKGERGAPGRGSPGPPGSD FLLMLADIRNDITELQEKVFG HRTHSSAEFPLPQEFPSYPETM DLGSGDDHPRRTETRDLRAPRD
7701	38069	A	7755	146	373	

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7702	38070	A	7756	678	1582	CQGNLSLGSVWPSGDWEDKHS Q*CPVVCSPQNLSQTSRHINDR DYRLPRAETHSSSYAQYSTPSN LVVHPTATPSTVPSSPFTLQSD/ YQPKKSFDDANGASTLSKLPPT SSVPAQKTERKESTSGDKPVSH SCTTPSTSSASATE/S/TTSAPPTS ASAGPCFSCSTARQYLPYFRDP NLLRTIAVLLKATVAALINS*C GTYLKIK*SSYSSCDTSLTAVYN S*VSYCWITCFQHNVSDFFSSCSA /PTQAQPSNQSPMSLTSDASSPR IICFSKE*GTPQTNTVPIQTFGFS TPPVSSQAKG
7703	38071	A	7757	1	1365	MHLIPATNCDTLVECLPGKL TRDLVCTAFTFGTSSYPQENS HNHSAHSSNSHSSNPSNPSK TSDANILSQTSRHNDRDYRLPR AETHSSSTPVQHPPIKPVVHPTAT PSTVPSSPFTLQSDHQPCKSFDA NGASTLSKLPPTTSSVPAQKTE RKVLQQLSKHNRKVMIRALIT SHLDLLYIEKDLRYQKNIESTSG DKPVSHSCTTPSTSSASGLNPTS APPTSASAVPVSPVQSP/PSLT SGPKSS*TIA/PALQATLQLNNS NVDISKINEAQPSNQSPMSLTSD ASSPRSYVSPRJSTPQNTVPIKP LISTPPCFITAKG*LLQ*LSQGTS VHSQPHTAACNC*/PSSK/SHEP VSPRSLQRSSQSPSPGSGFILL NSSNGIQMATVVPQEFFLARFH VFHLTPGTRRPPQWKISLKHV SRDGPADSWQEGRASRFTAE GRRH

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7704	38072	A	7758	2	1256	CHCGPPV/KVEAYGSQVLKGVL AQVQLTVGVPVGPRTHPVVIFPV PECIIGIDMLSSRQNPHTGSLTG RVWTIMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFNSPIWVPVQK TDGSRWMTVGVCCKLNQVVTP AAAVPDVVSLLQEINTPPGTWY AAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFVLPQGRWEI NMTKIQGPSTSVKFLGVQWCG ACQDIPSKVKDKLLHLVPPTTK K/EAQCLSGFRREHIPHLPIYRV SRKAAANFEWSPEQEKALQVQV AAVQAAWPLGPDYDPADPMVLE VSVADRDADWSCWQAS/GHK VGHAQQHSIIKWYIRDWAR ADPEGTTKGQQRWWQLAE RQDSRDREAAGIGRQETA VGKT ARDGEAVCD
7705	38073	B	7759	56	3476	
7706	38074	A	7760	3	591	DPADPMVLEVSEADRDVPI ESQQRPLGFWSKALPSSANNYS FFKRQLLACYWVVLVEIEHLM GHQVTMRPELPIINCVLSDPCSH KVGHAQQHSIIKWYIHDWA EGTSKLHEEVAQIPMVSTPSLP QPAPMASWEVPYDQLTEEEKT RAWFTDGSARHAGATQKWTA VALQPLSGTSLQDSSEKSSQW
7707	38075	A	7761	1	558	
7708	38076	B	7762	1	1189	
7709	38077	A	7763	604	1760	NSWCRWFNFRY*YPTFYWES* NT*IPLEWFG*NHDASCP*TLD SKSFSFETRTGSPCSSLQTAYC GTLWIVQGV
7710	38078	B	7764	1	474	
7711	38079	C	7765	1	3384	
7712	38080	C	7766	1	333	
7713	38081	A	7767	1	390	
7714	38082	A	7768	3	728	
7715	38083	C	7769	184	529	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, V=possible nucleotide insertion)
7716	38084	A	7770	2	837	CHCGPP/VKVEAYGSQVILKGVL AQVQLTVGVPVGRTHPVVIFPV PECIHGIDMLSSRQNPHTGSLTG RVWVTIMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFNSPIWPVQK TDGSRWMTVGVCCKLNQVVTPI AAAVPDVVSLLGEINTPPGTWY AAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFVTLPGQRWEI NMTKIQGPSTSVKFLGVQWCG ACQDIPSKVKDKLLHLVPPTTK K/EAQCLSGFRREHIPHL
7717	38085	A	7771	2	469	
7718	38086	A	7772	3	587	YPASAGLMLQNFVGVLGRYHF AIHSPAAGGLDGLHAVAAIQG ITKIETTPNHQRAPAHWLLTQ QAHLQPSPLHFNPLTLCLMHC PTAIPHCFADARTVWNIPTSSLI GHKKENLKEFISGLIVHEILEE VLQAEQDFQPFTRVTVHWGKG NDQTFRGLLDTGSELTLIPGDP KHHYGPPVKVGYAGQALL
7719	38087	A	7773	1	633	MTVDYRKFNQVVTPTMAA/AVP DAVSLLGEINTFPGTWYAAIDL ANAFFSIPVHEAHQKQFAPLPQ GYINFALCHNLIRRELDFLLLL QDITLVHYIDDILLGSSEQEVV NTLDLLIHKRSKEAEHTAASRIR VSCLPEQKSHEQTLPWEQVPSS GDIKEYFPNAFVLLTTASLQGG DNTSQLQLTWKAPEDIKMSKT DADADEIEIALRG
7720	38088	B	7774	1	1431	
7721	38089	B	7775	75	947	
7722	38090	A	7776	6107	6706	MVVVFLHKCLHYFHSTQLVISR YNSPTSEYFQALDLTWALGT VGSAPPILPDLGGTNRQPPFIL SHSGLHRNVLPETDSQSEDRL PVTWLAVSACCCQQMVGGNP TRSKL*RTGSHYHLPG/WEP*RP HFPHAGSLAQWLLCSSLEHSF GA*ELPCNPCKGWCLCPCHFI YIFFNSFLSNCPQLCNSHSSYFI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
7723	38091	A	7777	1	3179	MAEGKEEQVLSYTDGSRQREN EEDAKAETPDKTIRSHETYS.LPR EWYEGNRPHDSITTSQWVPPTTR GNYGSTIQDEIWVGDSGYVVRP VPVPRSLNSDISYFGVGGKQAV FFVQGSARMISKPADSQDVHEL VLSKEDFEKKEKNKEAIYSGYI RNRKDDYDNHTGIDLVTGIIATII KGSNEEDTDPLFIGKVRTLEFP FVNGSAEIMLMPSNQQHKTDE KGRANLGVFSVFAPRGEHTLQ VKAIYNKSIIEGP
7724	38092	A	7778	281	1531	VRVLSPEVKELKLWKNTHKLL SYPTVGAAVTQLQNLAMGVI GSHGARQQVVALNRQRQGD LPFTRVTVHWGKG/NMQIFGGL LDTGSELTLIPGDPKHHCAPPV KVGAYGGQVINGVLAQVQITV GPQTHPVVISPVPECIIGIDILSS WQNPHIGSLTGRVRAIMVGKA KWKPLELPLPRKIVNQKYCIP GGTEEISATIKELKDAGEVPIPT TFPLNSPIWPVRKTDGCWRMT VDYCELNQVVTPTAATVPD VSLLEQINTSPGTWYADIDLANA VFSIPVHKAHQKQFAFSWQGG QYTFVTLPQEYINSLGLCHNLI WRDLDGFLLLQNITLLVHYVD DIMLIGSSEQEVANALDLLVSM ASSRVPYDQLTEEEKARFTDGS ARYAGTTRKWTAAALQPLSRIS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, /possible nucleotide insertion)
7725	38093	A	7779	332	2159	RGYVFCSWKKTGDS/WRMTVD YCKLNQVVIPIAAAVSDVVSLL EQINTSPGTWYAAIDLNAFFSI PVHKAQKQKQAFSWQGGQYTF TVLPQWYINSPALCHNLIRRD DCFSLPLDITLVHYIDIMLIGP RQLLACYWALVETECLTLGHQ VTI*PELPIMNWVLSDPSSHKVG HEQQHSIIKWKWYVHDWARA GPEGTTTTVISQWPHEQCCHGG RDGGYAWAQQCRLPLTKADL NTATAKRPIQQQRPTLSPQYG TIPQGDQPATWWVVDYMGSL PSWKGQRFVLTGIDTYSYGFGA YPACNASAKTAICGLTECLIHH HDIPHISIASDQGTFFMAKEVVRQ WAHDHGIHWSYHVSHHPEAA GLIEWWNGLLKSQLCQCGDN TWQGWGKVLQKVYVYALNQIIP IYGTVSPIAKIHRSRNQGLEVP LTITPRDPLAKFLPPFATLQSA GLEVLVPEEGLPPGDTMIPLN WKLRLPPRHFGLLPLNQAK KGVTVLAGVTDLDYKDEITLLL HNGGKEEYAWNTGDPLGLLLI LPCPMIKVNGKLQKPEALVP KGVVFPFGDTMLSLSWKRLP SGHVGLLMPLSQQVQKGVTVL
7726	38094	A	7780	84	202	
7727	38095	A	7781	1	551	RWGSHTVAQAGVQCDHGSL QPRSPGVK*SSHLSLLGSWNHR HATITPG*FCFFSRIRSHCAQA GL*LLTSHNPPALASQT.VGITG VSHWTWPNTGFSVLATNKNL KFFHYAISKCLVRKLSRLKI EERNKALSAPVVSIFDRVLR LLGYSASDWQPEFVETAVSNFV IYGFIRGQ
7728	38096	A	7782	1	678	MPACRLGLLATALIISLLFGFTI VSGTGAETGVCPELQADQNC TQECVSDSECADNLKCCSAGC ATFCSLPNGQLAE*FESEESSL DTVSPFVVFSISSTLRIE*ARA GDSSQDKEGSCPPGVTI*LPFSS GLCRDQVPGGTAQCPGQIMK CCRINGCGKVSCVTAQFLSSSH HQAQVRRDSFLPGPASGFQAIH LPSPFFGTLYSLFGLTTSFSLSQP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7729	38097	A	7783	1	1972	MAVNGCLEGPSSNFLSCLFIVA LVGSESTHPLCLEQPATQETRY QLQLRPAQRASWIGYAIAYHL LEDYEMAAKILEEFRTQQTSP DKVDYEYSELLYQNQVLR GLYREALEHLCTYEKQICDKLA VEETKGELLQLCLRLDAADV YRGLQERNPENWAYYKGLEKA LKPANMLERLKIYEEAWTKYP RGLVPRRLPLNFLSGEKFKECL DKFLRMNFSKGCPPVNTLRSL YQDKEKCAIIEKL VVGYESLTK SCRLFNPNDDGKEEPPPTLLWV QYYLAQHYDKIGQPSIALEYIN TAIESTPTLIELFLVKAIYKHA GNIKEAARWMDEAQAALDTAD RFINSQCAKYMLKANLIKEAD MSSKFTRGGTSAVENLNEIQCM WFHTECAQAYKAMNKFGEAL QKCHEIERHFIEITDDQDFHTY CMRKITLRSYVDLLKLEDVLRQ HPFYFK/EQARIAIEIYLKAS*QP PYR*GIGKTRRLDTAKLSDEL KKLRNKORRAQKKAQIEEEK NAEKEKQQRNKKKKDDDE EIGGPKEELIPEKLAKVETPLEE AIKFLTPLKNLVKNIETHLFAF EIYFRKAAMVYYLDPSSQKR AIELATTLDESLTNRNLQTCME VLEALYDGLDCKEAAEIYRA
7730	38098	A	7784	264	429	HRAAPATSDTQE*HRSNAFGEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEETLFSN
7731	38099	A	7785	1	681	
7732	38100	A	7786	415	692	
7733	38101	B	7787	1	2204	
7734	38102	A	7788	1	615	MPVDHPPIKAFSEKRTSQSVNM LAKTHPYNPLWAQLEWFKLEI SPKSPINTDKFLLKRLSVPGSDS CRVRMENVLASQVLHPGQLM M*EGSGWAEART/V/CS*AANP *KWHPASLPLPW*CRVRMENV LASQVLHPGHADVDVGGKWLG RSKDHRAPEQQTRESGIRLPSLF PGSAEQPWRGNAQWHLWSKA LRGVFGMIPDLSLYEFHQSAKK SSHFKPPQPLLYWTLVNFLLPFS LHSSWFMWSSNQGMCKEEV



SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, V=possible nucleotide insertion)
7735	38103	A	7789	3129	3197	TQNRACSPDTEQLARQSGTYP VSLGQATVLEDSKAALPGLGPT LMAVTVVTTEAAVAIGCEAAH SSREDFTNHQLWRRITVEGKKG EGKNKFMGGVNTTVPLKTS RKGSPPSPHLREKPSLEKVTFOI GSFASPESEFESRMKKMEERVK ACGPSLEASEAADVAQDPQVS RSPFKPGFQENVCCPQNRLSEG DEGESDKGFAEDRGSNDMAA DIAGQLSHAADLTGASHDDVT YAIKPTCWPGLDIIPCL
7736	38104	A	7790	1	1069	MAEKEAGMSYMAEVLGFVA VIIIEAELKRIFENFTVAEERS TDETFSLAETCSSNPAMVRRK KIAISIIIFSLCEKEEAQRNFQDF FSHFPLFESHMNRKSAIEKAMI SCRKIAESSLRVQFYVSRLEMA LGEFRGTIWNLYSVPRIAEPVW LTMMSGTLEKNQLCQRFLKEF TLLIEQINKNQFAALLTAVLTY HLAWVPTVMVDPHPIKAFSEK RTSQSVNMLAKTHPYNPLWAQ LGDLYGAIGSPVRLTRTVVVGK QKDLVQRILYVLTIFYLRCELQ E/IPADLEWQSW*R*PAMVRRK KIAISIIIFSLCEKEEAQRNFQDF FSHFPLFESHMNRKSAIEKAMI SCRKIAESSLRVQFYVSRLEMA LGEFRGTIWNLYSVPRIAEPVW LTMMSGTLEKNQLCQRFLKEF TLLIEQINKNQFAALLTAVLTY HLAWVPTVMVDPHPIKAFSEK RTSQSVNMLAKTHPYNPLWAQ LGDLYGAIGSPVRLTRTVVVGK QKDLVQRILYVLTIFYLRCELQ ENQLTWSGNHGEQDQVLNGSK IITALEKGEVESEYVITVRNE PALVPPHPTTNSRETQPLADR
7737	38105	A	7791	118	273	FSLSNLVQFFRVCDNHLTKLH FCFLQAEVKASNFCYDSLGH LGSHTTVECIATDEHTLHLTSP MG*SQGQKFLHRLFSWACPGIP PHS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7738	38106	A	7792	1	551	MQPELPIMNWVLSEPSHHKVG HGQQHSIIKWRWYICDWAVVG RESTTNGLA\GWS\GTWKKHD WKJNDNEIWGK\SMWDLSEW SKTVKIFVSHESAHHIT*KSSAE EDFNNQWDGMTCSVDTTTHPLS LTTSVIAKWAHEQSDHGGRYG GYAGAQQHGLPLTKADLAMTT AECPICQQRPPLSP
7739	38107	A	7793	1	782	MTKIQEPSTSVKFLGVQWSGA YQDIPSKVKDKLLHLAPPTTTK EAYLGL\FGFWRQHPIH\LGTEQ EKTQHVVQAAVQVAFLEPYD PADPMVLEVSVAADRDAIWSLW QAPISESQWRPQGFWSKALPSS AANYSPFERQLLAYWALVET EHLTMGHQVTKQPELPIMNWV LSDPSSHKVGCAQQHSIIKWKW YICDRARAGPEGTTTPVITQWA HEQSGHGGRDGGYTWAQQQG LPLTKADLATATAECPICQQQR PTLSP
7740	38108	A	7794	65	230	
7741	38109	B	7795	1	2115	
7742	38110	A	7796	1	246	
7743	38111	A	7797	1	1293	MAAAACLDASGEARPLRPPW SQQGRKQAGALPPTKLAGLLA QLQPAEAPDLGIPVLSATREDPL SPQARKCLLPLPGLSPCSQHLL WCRASCGRWGWPSRPSRVCTG LDTAVTPAPCRLSPLWTSADK RGREASRGEGSSKWACRHPSA QTAWAVEGDRHFLSRKQGIT GKTPPSSQGQPEAWGLSCSPH TLHTSFFLDTGPLNGGTEKAVT QTGPKHAPCSPGCQQGGKGC GPSGTPDLGALRARA\TVGLCS SWHLQASGHHCIPQYLQKLL VVHLVQPQCTKPPVPPSFRLL MTIENMNHKLFIPHKDYTANRL VSGLLQLPSNTSLVIDETL\EQ GQLDTPGVHNVTALSNLITWQ KVDYDFSYHQMEFFCN\KVFIT SEGRSLLPADVPDSLTA\ANST KHGGST*TAFSQRCLLPC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *Stop codon, /-possible nucleotide deletion, V=possible nucleotide insertion)
7744	38112	A	7798	1	2555	MPShLNQHqIIHTKEKSYKCEE CGKSfKRSSNCTTHKRiHTGEK PYRCEEgGKAfRWpSNLTrHK RiHTGEKPYTCeeGQAfRRSS TLtNHKRiHTGERPYKCEEgGK AFsVSSTLNDHKRiHTGEKPYT CEECGRAfNCSSTLKtHKRiHT GEKPYKCEECDKAfKRHSSLA KHKiHTGEKPYKtGSiCILLQR YCWSTT*tiHfKK*S*EN/pGSC DLNtLRLKKDYQRvGNCKGQK SSyNGiHQCLSAtrSKtCQYNK CGKAfGLCSiFtEHKKiFSREK YKCEEgGKDCRLSDFTiQKRiH TADRSYKCEEgGKAckKfSNL TEHNrVHTGKKPYKCEEgGKT FTCSSALtKHKRnHTGDRPYK EECHKAfRWCSDLtKHKRiHT GEKPYKCKECHKAfRCCSDLT KHKRiHTGEKPYKCNecGKAf MWISALSQHNRIHTGEKPYICE ECGKAFTYSSTLiSHKRiHMeLR PYKCEEgGKtKfWfSDLTnHK RiHTGEKPYKCEEgGKSfTCS NLIKHKRiHMEVRPYKCEEgGK tFKWfPDLtNHKRiHTGEKPYK CEEgGKTfTCSsSLiKHKRSHtG DR/PYKCKEEGKAfRWfSALL NISKHKRiHTGEKPYICEEGKA FIRSSTLTSHKRiHMEERPYKCE ECGKtCiIHIGEKPYKCNecGK GfMWISALRKHKRiHTGETPYI
7745	38113	A	7799	212	461	TEHLySPHWKGCGRKvKRLf QVRGRGwIQTRQPGSMVKEP PLSEAGAEshVSC/RQGDcSRPP SfPLSPERVTPWLpDSiITW

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
7746	38114	A	7800	1	1398	AAARELELLRASLEHQGVSE LLRGRLRELEEAREAAEEAAAG ARAQLREVAITQTPWSCAEKAA QTESPAE/GPP*LRARPDWTE TRAVAPAGILKSIMKKRDGTP GAQPSSGPKSLQFVGVNLGEYE SSSEEDT/NDSDGDSENGGAEP GSSSGSGDDSGGGSDSGTPGPP SGGDIRDPEPEAEAEPPQVAQG RCELSPLREACVALQRQLSRP RGVADGGAVRLVAQEWFRVS SQRRSQAEFVARMLEGVRLRG PELLAHVVNLADGNGNTALHY SVSHGNLAIASLLDGTGACEVN RQNRAGYSALMLAALTSVRQE EEDMAVVQRLFCMGDVNAKA SQTGQTALMLAISHGRQDMVA TLLACGADVNAQDADGATAL MCASEYGRLDTVRLLLTQPG/C DPSILDNEGTSALVALE/AETG MKVAALLHAHLSSGHPDTQSG VTPLAPQTANTW
7747	38115	A	7801	3	408	
7748	38116	C	7802	141	251	
7749	38117	A	7803	1	1173	
7750	38118	A	7804	451	853	LQMHRLCGHSLSGCGWHTAR GQELVGCFL*GGGQLLGLOH PL/AENPTFQEYSLITSEAGLLEG RKKKNKTSRGPSPATCPLGLP RTSPGATRPGPVS/HA/IASQRD SSRTRFSSSLDAIARPYTTPSA
7751	38119	A	7805	1	2950	MAASRLELNLVRLLSRCEAMA AEKRPDDEWRLEKVGVTYSVA SGRVLFQDFTEQFQVLLPKDAQ PCREVISTLLEKMKIDKRNQIG KTKVEPGV/EA/WPLRRVRRQPD QRQGLGAHRAGEAPGTRGDAR PVHRGPLQVGGCCQPHSGAPAG AADRPSSQAGELPHPRHHRGA EAVAAGAAARAPHDLRTVRRLP PSRRAAGEAGAAGCH/RMPSW STFQKPTTTTPWRDSSSTLSSNHP LTASGCAGWPCSRMST
7752	38120	C	7806	398	415	
7753	38121	C	7807	13	81	
7754	38122	B	7808	1	972	
7755	38123	B	7809	1	1803	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
7756	38124	A	7810	1	929	IAAAPELLERSGSPGGGGGAEE EAGGGPGGSPDGPARGPSREL AVVARPRAAPTGPSSAAAMAR PLVPSSHKALLLEKGLQEPPV EGFRVTLVDEGDLYNWEVAIF GPPNTYYEGGYFKARLKFPIDY PYSPPAFRFLATKMWHPNITYETG YVCISILHPPV/DTDPQSGELPSE RWNPVTQNVDRHSS*V*SSLLE RRPNTFLRPANVGRLPWMLQG SWEREQGGRIRELHRTSFRKQV LGTKVDAERDGVKVPITLPEY CVKDQGRAPDEGSDLFYDDY YEADARVEEADSCFGDEDDDS
7757	38125	A	7811	2	296	LSLSFFFVKAHFVVKSMHSHKD ASGISGMDFFYVQ*FSWQTAY AGEVGRWLSPALTERGSGQTL* TWCWRVFCVCLIGHMWVTEA YVTVKH*NYSKVK
7758	38126	A	7812	397	410	SPGEI*G*VPPLG*GVLLYQPP LFKIWEAPLLPDLLQQ*KLYSL WLNKALGK
7759	38127	A	7813	2	739	ELCALVFGVNTFFATIVKTIITHI VSDVRGLGLPVRKQDSVVVFL DCPSIW*LRVIDLLILRVHLQIH LWGLRGRRAEFKHI/RSAAEKK LTRIPSVNGE*TGKSPAPANS/PP RGARDMWRTGRAPAPRPLVGG PSPSDRGPASTTSPELAVGAVN GGPSSANISRGFVQQSFHGNMC WFAECPGVAGVPFTANIAGTPEP GGLGQGRQCSLATQCHKPELK LQAKPAFFSFLSLFFFLKHIL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
7760	38128	A	7814	594	2868	CWTSRNRRLPIPGSCHPMELPRPF RGKAKVQNHQLVHVNKALIN RGSLSFWLDDGAIAQAWHCPVK TYYQYTPVSSKAMY/DAFWNG/ KFRDC/AFHSWLNEDPFVCEYQ GQSSDLQPVPVNAAGGSGGGS GGGSEGGGSEGGGSEGGGSE GGSEGGGSGGSGSGDFDYK MANANKGAMTENADENALQS DAKGKLDVATDYGAIDGFIG DVSGLANGNGATGDFAGSNSQ MAQVGDGDNPLMNNFRQYLP SLPQSVCECRPYVLSAGSEIGAA CASRSGYDNKGVRDIGYTDCK RSEDLDPLRHQILGGKKA/QFTL QGFPTLPEGAPAGNSGSLAVHK TAQSSYRHHALLITPMSGTRF PPIPGPVVNIIRVFPAPSECRIC YSWSWVPGSPVHCQSDGVSPI SYAPLASQYSSSLFRRNRQPYA PYDLSVMTSPRTLREQIRIRYA PSAPRLPPPEVYCSNNTIVYVRN NPSGPTPGFAGGTLLEGRSGGP FRFYAKRAKGDVLPFSLNLPL QTLIRFMVDIACGMEYLSRNFI HRDLAARKCMYEFWRTRGWE TAAAYYGGGTTFFRKESQKLQ QSAKKRDAELANGALGIIELNN DYTLKKVMKPLITSNTVTDEIE RANVFKMNGKWYLFDTDSRGSK MTIDGINSNDIYMLGYVNSLT GPYKPLNKTLGLVLQMGDPND
7761	38129	A	7815	2	474	RRFVSADNCRSLRWKSLYTPLD ADASVLSTGIDATQTNHGRQH LDETQVRVFGQHLMQGSYTTQ DGRSDVAISCCKLEMAQQSY DQLLAASTENWRQWWQKRRIT VNGG/GSSPASDADQTPAPGFR RDVGDRDWFAWRQCLLKALT RRRPVAYIVISSAMSGLPKQS D
7762	38130	A	7816	302	409	
7763	38131	A	7817	199	359	ARRQQVSVKSYRWEEDQHCG ELQGSSE*VSDGLFKPP*S*HGW VEEEROKEQN
7764	38132	A	7818	1853	2032	VKQSTALLPHAVAC*PKVISSG ARGLSILVLIRIVMMVMMLP QLALSGWGRFRVLPG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, V=possible nucleotide insertion)
7765	38133	A	7819	118	445	AAGGEPGDAPWVPGVWEPPE VCRGPPPSSTFHPVLSTFGASG PENSRDCSWLSPQH*AA*VASG NNGPQAAQGSLSGIPDAA TLSG I*RASILHVSVVETIISSPGFR
7766	38134	A	7820	1	770	MRVLGIETSCDETGAIVDDEK GLLANQLYSQVKLHADYGGVV PELASRDHVRKTVPLIQAALKE SGLTAKDIDAVAYTAGPGLVG ALLVGATVGRSLAFALGRFGDP CTPYWRASVSARCKIPAPNFR CALLGSAA YAVNHGTGLSKKP TTLGSDHSKTPAQLAKRAGEA RRNGWQGALFPWESARSGE TP/VICRH*HSHRAAKSGLGA GGTSSGGRYRLGGYSILADHGG *KFHCA*RHGATSGDGKVL
7767	38135	A	7821	3	834	VGRVEIADQYQDLAILWNCLG SDHASSRQRRPFRGKAKVQNH QLVHLQSSHQPWLPHPFLAG* WGDSGLGGGSIEGGSEGGGSE GGGSEGGSGGGSGSGDFDYE KMANANKGAMTENADENALQ SDAKGKLDVATDYGAAIDGFI GDVSGLANGATGDFAGSNS QMAQVGDGDN SPLMNNFRQY LPSPQSVVECRPYVFGAVRHDV RRIRVTGVTRVTPPEEVDTSVH SRGAHRIRSGFAPKRSVRVTTD TCIKRNSCTGVKSLSLWDGGGF
7768	38136	A	7822	1	1044	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
7769	38137	A	7823	3	1472	GVVGERAGMARPGRPREGGGS G/GYSRPVPPAGGPGP*RGRTRI/ SGLANGAGPVVFQFLTELTRLF QKCRITSGSVYITLKKCKQREGS RAMLPGFYPYTPVSSKAMYDAY WNGKFRDCAFHSGFNEDPFVC EYQGQSSDLPQPPVNAAGGSGS GGSGGGSEGGGSEGGGSEGGG SEGDSSEGGGSGGSGSGDFF YEKMANANKGAMTENADENA LQSDAKGKGLDSVATDYGAID GFIGDVSGLANGGATGDFAG SNSQMAQVGDGDNPLMNNFR QYLPSPQSVCECRPYVFGAGKP YEFSDCDKIKILRGVFAFLLYV ATFMLPVIANIAPQKRPFMQQT RCEVQCREDIEVQKLKSYDKLL ASINKKPGVNGWQKRRTVNA GEAHDQALDYALYHLRIMTP AHDERSIAAKGLTGEGYKGH VFWDETEVFLPFHLFSDPTVAR SLRLRYRWHNLPGRARRKRDN GWAGGAPISVGKARAAAKK
7770	38138	A	7824	601	853	
7771	38139	A	7825	2	644	MAQQQ/RKFAHKPAKSKTAA/ A/ASEKNRGPGRGVRVAPKKA RVVQQQKLKKVSLCCSGWS*T PGLKASSRLCLPKCWDYRRDTL WLFLSATFICRWNLKRSSEGGK IEHDVVMKA/SSSLPRLKALLK APSPRRNGAAAA/TSSTPPLRT AGPQLQGQHPTPLPSIWGPLQV NSHRLSLFRMRTLSPSDWASPR HSSGGPKGAENPGNDQGRYSH
7772	38140	A	7826	1	2616	
7773	38141	A	7827	1	504	



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7774	38142	A	7828	1	1068	MAEIQHKTRIFLLEGRDLLAAV KTGSGKTLAVLPAJELVVKLK MPRNGTGVLLSPTRQLAMQTF GVLEKELMTHHVHTYGLIIGSN RSAAEQKLANGINIIIVVTPGRLL DHTQNTPGFMYKNLQVEDLAR ISPKKEPLVYGVDEDKANATVD GLEQGHFVCPSEKRYLLFTFL KKNQKKKLMVFFSACMSVKYYP YGLLKYYDL/PVLAIHGKQKQN KHTTTFF*YCNADSGTLFQLE KLIEKNYFLHKSQAQETYKSYIR AYDSYSLKQIFNINNLNLPHIAL SFGFKLPFVDLNMNSNEGKQK KQGGFGYQTKKVEKSIIFKHIS KKSSAAGSSLTQEMPVILNNF
7775	38143	A	7829	3	1851	
7776	38144	A	7830	1	905	MVFDAYLTGWRFEDTVVQSN MKHQPFIIVNKHNVQVEYKGE TKSFYPEEVFMVLKMKELAET YLGKTVTNAVVTVPAYFNDSQ HQATKDAGTIVSLNVLRIISKPT AAATAYRQKGIDFNTSIFHALF EELNAVLFHGTLDSEKALGN AKLDSQIHDIVL/GPFEQGRH* MYGPGS*EIQS*R*EAEGQDVIQ EFS*KLCIRYESSC*R*ETSRQD* R*GQTEDS**GY*NYQLAG*ES DSEEGRISTSKSGESLQPHNYQP VPEYRRHTRRNAWGIP*WWSS LCWSFPRAPIEAD
7777	38145	A	7831	2	886	ARGACSSWVFCGLRYWSQAY TPATMSKGPVAGIDLTTTYSKV GVFQHGKVEIIANDQGNRTTPS YVAFDTDERLIGDAKNQVAM NPNTNVFDDAKRLIGR/RFDDAV VQSDMKHWPFMVVNDAGRPK VQVEYKGETKSFYDDEVSSMV LTKMKEIAEAYLGKTVTNA/V VTVPSYFNDSQRQATKDAGTI AGLNVLRINEPTAAAIAYGLD KKVGAERNVLIFDLGGGTFDVS ILTIEDGIFEVKSTAGDTHLGGE DFDNRMVNHFIAEFKRKHKKDI SENKRAVRRLRTTK
7778	38146	A	7832	2	375	ASIEIDSLYEGIDFYTSITRARFE ELNADLFRGTLDPVEKALRDA KLDKSQIHDIVLVGGSTRIPKIQ KLLQDFYEAVAYGAAVQAAIL SGDKSIENVQDLLSLDVT/PPF LGIEATAGVMTVPH

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7779	38147	A	7833	1	218	
7780	38148	A	7834	508	883	YYHSYQADT/IILGGEDFDNRM VNHFAIEYKRKKHKKDISENKRA VRRIR.TACERAKSTVSSSTHAS TEIDSLSEGDIYTSSTCASFEEL NADLFLSLDLPVEKALRDAKLD KSQIHDIASINPDEAVAYGAA VQAAILSGDKSENVQDLLLDV TPLSLGIETAGRVITDLIKHNTTI PTKQTQTFTTYSDNQPGVLIQL YEGEHTMTKDDNLLDKFELTGI PPAPRGVPQIEVTFDTNSNGILN VSAVDKSTRKKNKITITNDKGGH LSKEDIEYMVQEAKEYKAEDQ KQR/D/KVSSKNSL
7781	38149	A	7835	1	194	
7782	38150	A	7836	1	1482	MVFDKRLIAHRFDDAVVQSE MKHWPFMVVNDAGRPKVQVE YKGESKSFYPEKVSSMVLTNM KEIAEAYLGKTVTHAVVAVPA YFNDSQRQATKDAGTIIVGLNV LRIINEPTAAAYGLDKRHRSSL ILTASLGGAGSL*STQA/SIEIDC LYEGINFCTSITHARFEELNADL FRGTLDPVEKALRDAKFDKSQI HDIVLAGGSTRIPIKQLLQDFF NGKELNKGINAEAVAYGIAV QAAILSGDKSENVQDLLLDVDT PLSLGIETAGGTQILITTSYDSQP GVLIIQAYEGKHAMTKDNNLLG KFELMGIPAPRGVPQTEVTFD SDANGILNVSAVDKSTGKENKI TITNDKGCLSKEDIERMVQEA KYKAEDEKQRDKVSSKNSLES YAFNMKATVEDEKLQGGKINDE DKEKILDKCNEIIWLNENETAK KEEFEHQQKELEKVCNPIITKLY QSAGGMPGRMPGGFPGGGAPP SGGASSGPTIEEVD

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7783	38151	A	7837	2	2221	PRVPRVRSAPALGFFVASFVIG ARPTQQPWSKGA V GIDLGTT YSCVGVFQHGKVEIIAN\DQGN RTTPSYVAFTD\TERLIGDAAKN \QVAMNPTNTVDFCQTV*LDGR FDDAVVQSDMKHWPFMVVND AGRPKVQVEYKGETKSL\YPEE\ VSSMVLTKMK\EICRSLTLGKT VTNA\VTVP\SYFND\SRQAT KDAGTIAGLNVLR\INE\PTAAA IALQKFRQKRFGAERNVLIIDL GGGTDFVSILTIEDGIFEVKSTA GDTHLGGEDFDNRMVNHFAIE FKRKHKKDISE\NKRAVRRLRT ACERAKRTLSSSTQG\SIKIDSL* EGIDFYTSITRARFEELNADLFR G\TLDPGEKAL\DAKLDKSKIS *YLSWVGGSYSYPRLQKSCCQ DFFQWEKELELRSINPGWKAV/ AFIGAAVPGQPFLSGRQVLENV/ QDLLLLADVTP\SPWVLKTAGG VHDCPPSKRNTIPTKTQTFTT YFWTTQPGCGLFRFYEGRALP WTKDNQPALASFELTGIPPAAPR GV\PQ\EVTFDIDANGYTPWSL AVDKKYGKKRTKITITN*QGPF *AREDIGTYGSEAEVTKLEG GGRQEGTRVSSNDF*GPMPPN MKSTLLKDEKL\QGRINDEGQ NRRFLDQV*KLKSNWL**ESRL LEKEEFEHQ\KELE*VCNP\IIT QAGTQSARRHCQGGNPWGAFL
7784	38152	A	7838	3	757	PPFGGRVVR\HPVILASTVDSY ERRNKGAARVIGITLLGTVNKH SVEVTSCFSVSHNESDEVAVDM EFAKNMYEL/H*KVSPNELILG WHDITEHSLVLIHEYYSREAPNP IHLTVDTSLQNGHMSIKAYYST LMGVPGRIVGVFTPLTVKYAFY DTECIRVDLIMKTCFSPNRVVG LSSDLQQVGGASARIQD\TSLIVL QYAEIDLSGKVSADNTIRKVGH FLMSLVNQVPKIVPDDFETMLH SNINDLLMVT
7785	38153	A	7839	1	1821	
7786	38154	B	7840	16	1305	
7787	38155	A	7841	1	359	

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7788	38156	A	7842	2	1085	GVAPWGRGRAAPRCASATVGG SGIGRLR/GITSSGLKMDNKKR LAYAIIQFLHDQLRHGGLSSDA QESLAEVAIQCLETAFGVTVEDS DLALPQTLPEFEAAATGK/EMP QDLRSPARTPPSEEDSAEAERL KTEGKPKQMKIVENF/EAAVHF LTEKPFELNPSQRPSPYFCNRAA AYSKLGNAGAVQDCERAICID PAYSKAYGRMGLALSSLQQHLA EAVAYYKKALELDPDNETYKS NLKIAELK/LREAPSTGGVGSF DIAGLNNPGVMSMASNLMNN PQIQQLMSG/MISGNNPLETP GTSPPSQNDLASLIQAGQQFAQ QMQSVGIPRVV**SAQESSIRSR TPSASNDQOE
7789	38157	A	7843	225	398	FIIDYTNSCFIHQNICLICSNRNF RQSNVVMICHY*TLQEIKTFC* MNSSLWSIIIF
7790	38158	C	7844	162	269	
7791	38159	A	7845	273	501	HKDQPIQTENDHPSTNFSVLK LHDPLLNEMDLIVWVSF*Q*SC FYLVHPNCCSPLV*HP*SENPKF SNEYFLRVS
7792	38160	A	7846	1	867	
7793	38161	A	7847	185	1325	EEQQTNLASKKKSCIMLEKTEN KIRLVIVSEEEKKVLKRP**K MTVRAHHGSRTPHSWVESNY YWDICDQWMS/EPVGYMPCQH CQVAKNTVIVAPKQHLQGGKI PWSLVTVDLMGAFSYKPKQS/N VYAIIMTDLFTKWIVILPLCDVS ASEVSKAIINIFFLYGPPQKJMD QRDEFIQQINIELYRLFQIKQIVI SHTSGTVNPTSTNTIKAFLSK HCADHPNNWDDHLSAVSFAN VTHLEPTKNTPYFQMFKVEKNP LYYLPETSDSLHEVDGDNTSMF AKILDIAIKEADKIMENKTTSLG QMENNLDLDELNKSIIIVKKKPK QLNPFHLKVGHGSEFKTEKLV GRMVVFQSWNGVGPLCHRLY YRKWMCCP
7794	38162	A	7848	2	455	MADRLTQLQDAVNSLADQFC NAIGVLQQCVPASPENNIQTAI NKDQPANPTEEYAQLFAA/LIA/ RTAKDIDVLIDSLPSEESTAALQ AASLYKL/EEENH/EAATCLGG MLFIEGDMLLGGRYKGA/LDI/ AQSQLEGGSGYP*ASLFPDS

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7795	38163	A	7849	229	560	
7796	38164	A	7850	1	1077	
7797	38165	A	7851	25	690	WPSDEAEGYSEIHFEVFKDVR KRFPQHTIMAGNVVTGEMVEE LILSGADIHKVIGIPGSVCTTRK KTGVGYPQLSAVMECANAAH GLKGHIISDGGCSCPGDVAKAF GAGADFVMLGGMLAGHSESG GELIERDGKKYKLFYGMSSSEM AMEEVLGGVAEYRTS\EGKT/ VEVPF*REMLEHTIPRHP*GGIR STCTYVGA\AKLRRR*ARTNYL HPEVHPAR
7798	38166	A	7852	768	1857	EGGHHFGGQGDASAPFGSASI LPIKLDVHPHDGRRRAEKSXPG GNPQRQLYCQPPAGCLPGAVY RPRRSRGARMYSRYSPAERRNP DQRAGYCAQPDRLRFSRADD RSRWRHVHFGTSRHCAGDRAV RPPPHSAAEALPVLPVFQ*PTA DQVLFPSLIAACYNHNQNKIL EQEMSCVLLATFIQTRAQQRKY KRRNNRGIPRESTAREQARHNA NKAQQPRKHARNGASPAQQRK NRAAADKDEKPAQQKDKAR QSAPEKKNRAIRGTNSREQAAK AERNRRQRGGQKGAQGGQHR EEAGEPTYVDEKAQAATSPPPQ TPHPAPDHDDAEDHRTDTRNR NAHQPKVYTHKDTPTNESR
7799	38167	A	7853	1403	2028	RRIQTNGRTFHAHGGPSRGLPE ELGKDHRKETSSRTL*QFQPN AKSPGQNLRESMNPVC/MTQQ ARRLQRLAKDLLKQVQVQDSG SWANNKVSALDRTLGEITRILE KERSRRGKGPSKEDLEGAAN/G VRRTM/WMSGNLVKESQPHPT HRPNILT*YPSIFP*RTLLTLWL KVQLQQLK*KMEKSGKKIKKK PKR*KPG*TSGLTNL
7800	38168	A	7854	1	675	

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7801	38169	A	7855	2	1110	AQEEAAKVNIEAFINTLEAQNKRHDVLSKLLKEYEQLNELQEERQRRQEEKQARDEAVQERKRALFAERQARVEELLMKRKEQEARIEQQRQEKEKAREGAARERARDREERLAALTAQPRSYGRVTEKNSAQA**KYSKAH/RNRLNKEKKKLLS*AVGDMQILIMPPN*PLYERKKQCSLCNVLISSEVYLFSHVKGRKHQQAVRENTSIQGRELSDEEVEHLSKKYIIDIVVESTAPAEALKDGEERQKNKKKAKKIKARMNFRakeYESLMETKNSGSDSPYKAKLQRLAKDLLKQVQVQDSGSWANNKVSALDRTLGEITRILEKENVADQIAFQAAGGLTALEHILQAVVPATNVNTVLRN
7802	38170	C	7856	65	425	
7803	38171	A	7857	1	1131	
7804	38172	A	7858	953	1311	FLFFIFNFYFFFGGRKCPLLVAPRLEVQMAVILGSLQPSPPGFK*FSLPQSPSSWDYRHAPTHAQNFFVFLVETGFHHIGQAGLELQTSGDPPTSASQTAGITGVSHRAWPGTILFLK
7805	38173	A	7859	2	857	FVDIFQRWKECRGKSPAQAELS YLNKAKWLEMYGVDMMHVVRGRDGCESLGLTPTGILIFEGANKIGLFFWPKITKMDFKKSKLLTVVVEDDDQGREQHTFVFRLLDSARTCKHLWKCAVEHHAFFRLRTPGNSKSNRSDFIRLGSRFKFSGRTEYQATHGSRLRRTSTFERKP**TSLSIPETFNVSQSKQPSDSSPALLKQIQKSNNYQPPISILISIPSPAPGGILTTPQMSGHPFQDDRSHWKASASGDDSHFELCPTTQNPEGTLGGMKPYDVSEINVM TAL

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7806	38174	A	7860	1	936	MELTHLQHPHEQEDVHAVGLL LGLREQHHMVSEGPQQSWQE ERTELAASVRLLFNMYPLLIHK NHASPGIPNLLHPRGLRAITIA VFGKQNTYIRLEPFKINVLEQIT KHIEKLQCGEHNFPQEIQEGK SHQNQHEAHFVVELCKYFLCQ EYLPSTITILTTYTQGLFCLRLK MPAKTFAGVRVHVVDKYQGE ENDIILLSLISNRICVALSRAKKG MYCIGNMQMLAKVSLWSKIIH TLRENNQIGPMLRLCCQNH PET HTLVSKASDFQKVTEEGC/MLP CEFRLCGCHVCTRAWHPYDSS
7807	38175	A	7861	218	580	
7808	38176	A	7862	3	1636	
7809	38177	A	7864	24	386	
7810	38178	A	7865	2	999	GRVGGFFAGNPGSDSFGGLLLG LTPVLRWVADGGTIPKRHEL KGPKEKVEVDKTELVAQWN YCTLSQEKLRRIVAL/CNFAD FYNKIEPVIEFLDKSAEKGSG RQASHIKTH*RIVDRAESFPDNP CPGKGIKGN/D*KVDKHDDIQA GASSSSVPVGGPGRWNGRHRFL PSGGCGLCCFS*AEPWKEIKAG VCHTCGAGLSRRMMIIVLNGT KEDVDLLKTMMEERRL*SEAG KENKENPRQSLFQNDVSERS PRAIKS*DRGSLKKPAFDSREK KTNLAPKSTAMNESSGKAGK PPCGATKRSIADSESEAYKSLF ITHSSAKR
7811	38179	A	7866	1	559	MGCDGGTIPKRHELKVGPKKV EKVDKDAELVAQWNYCTLSQE ILRRPIVACELGRLYNKDAVIEF LLDKSAEKALGKAASHIKSN VTELKLSERALKIEKAEVCHTC GAAFQEDDVIMLNGTKEDVDV LKTRWRREG*ERRGKKTKKP KAAEVCFQNPVDSGRKPQGPS KVKTREALKKPS
7812	38180	A	7867	188	368	YVACMPAWPNVTVANQLFNV YFPARDMTVPSSPG/QPVVDQL STQGQARRDALEVVGYES
7813	38181	A	7868	179	554	LRPADPRSLVPGWALGLGPGAI LGPGRVTFPGGRPPPTHPPLSF PPGGRQPLWVPALPAEEGRE/R LGREREGRGKAGAGMA*AGL VL*CLQLQVQGGPLGGSWLST RLRSPRCHPWLLRRHLP

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7814	38182	A	7869	2	131	YKSELEEQLTSVAEEMRARLSK ELQA*KDRLGENMEKVRGRVL KYRGEVQAMLGESIEELRVRLA LYLRKRLCTGLRDADHL* RPA GREYGESKRTL
7815	38183	B	7870	1	3639	
7816	38184	A	7871	279	1077	IQHPRLSADDFRNCETEPAM/* HAVENDIHLGCELETEIQAF KEELL/FMKKNHEEEVKGLQAQ IASSGLTVVVDAPISQDFAKIMA DIWAQYDEVAQKNREELDNNR SQQIEESTTVTTQSTEVGA AK AMLTELTRTVQFLEINLDSMRN LKASLENSLREVARYALQME QLNGILLHLESELAQTWAEGQC QAQEQALLNIKVKLEAAIATY RRLEEDGKDFNLGDTLDCSNS MQTIQKTTTRQRMQDGKVLSET NDTKLRH
7817	38185	A	7872	712	855	
7818	38186	B	7873	50	788	
7819	38187	A	7874	201	372	ICQMILKRRVLS* TQKHQATHG WNSAYSLTAPFPVSCQDHL C* P L* AEAQISKEEP
7820	38188	A	7875	3	323	FFFETEFHSAVQTGVQWHD PSS PQPPPPRFK* LSRPSLPSSWDYR HVPSPHGPFLHFQ* KRGSTNQA GLELPTSGDLAAFA\SPSARITG VSHCARPNYQCFLFKY
7821	38189	A	7876	1	911	MLLTLAGGALFFPGLFALCTW ALRRSQPGWSRTDCVMISTR LV SSVHAVLATGSGIVIRSCDDVI TGRHWLAREYVWFLIPYMIYD SYAMYLCEWCRTRDQNRAPSL TLRNFLSRNRLMITHHAVILFVL VPVAQRLRGDLGDDFFVGCIFTA ELSTPFVSLGRVLIQACNM EMT ESLKQQTLLYKVNIGLTLGNF FPCRUILLFPFMVWSYGRKKGL SLVPSTLQHPILTATWANA FPR* APQIYWFCLLLQKAVRLF DTP QAKKDG* MLLGVRRLTPAAS STQHSMQIVPWWASDFGY
7822	38190	A	7877	2	283	SCHCTPAWILALSPRL ECSGAIL AHCNLHLWG*SDSPAS SRVA GTAGACHRAWLIFCVL VEMGF HRVA/PLVLNS*AQTIR LPRPP KVLGLQA



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7823	38191	A	7878	1	1042	PKVRSPIRKRLAPAPAFVRKQE LKKIVDPALL*KKSEFGLHLDRI QPQKRPPPLL*KWPRYIRV/QG RRAILYKURLKGPFCDDYPGFTQG PGTPQTS*SSLKLVAHKYRPRD KAQRSKQRLLA\RAEKAAAK GAVPQERAHVPVLRAGV\NPVSP PLVGEQEKLSLVVIA\HDRGSPS ELVVFLPALG/RVKMGVPYCIHK GKGKTGDGLVHQKALHPLSAF TQVNSIEDKGA/ALKLVGSYQ GPNYNDRYDEVGRSFTQNTVIH KFSQITGWLNL*EVLSDDLG TAKQN*RN**PKSQKTVSQAN CLFLSFQIRRHGGNVLGPCKSV ARIAKLEKAKAKELATKLG
7824	38192	A	7879	3	472	GRGVAYRGPSPRGTGPRGDE RLQHGGG/SREGPPAAPAAAA GYGQSCCLIEDGERCVRPAGNA SFSKRVRKSSISQKKLLDIDKSV DLFQLQVNTLRRYKRHYKLQT RPGFNKAQLAETVSRHFRNIPV NEKETLAYFIYIMVKSNSKSLDQ
7825	38193	A	7880	3	638	GRGVAYRGPSPRGTGPRVR*T ASARRRTAAKGPPPPQLPPRA TAKSCCLNIEDGERCVRPAGNA SFSKRVRKSSISQKKLLDIDKSV VRHLVNCDFHK\NFIQSVRNKR KKEDQVYDGRENS/SPSTDTDIP EVDLFPACQVNTLRLRYKRH* QVARPRPGFNKAPVSRQL*VDT FRNIPVD*KETLALLSSSMVKSN KSLDQKSGGWQA
7826	38194	A	7881	1926	2448	DFIAVITTRKQLKTKYNAHHSK QAITHFSPKISDLILCLKKIM NRHFSKEDIYAAKKHMKKCS SLAIREMQIKTTMRYHLTPVRM AIHKSGNNRCRRGCGEIGTLLH CWWDCKLVPQLCKSMWRFLR DL/DPAIPLLGYPKDYKSCCYK DTCTRMFIAALFTIAKTWNQP
7827	38195	B	7882	446	625	
7828	38196	A	7883	1	1875	

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7829	38197	A	7884	31	809	KPRLENYVKNAAEASGADAINW KKGY/LVMEDEMNMKREGKF REKRIKRNEQSLQEIWDYVYKRP TLHLIDVPETLNAHKRQERSK TDTLTSQI.KEL.EKQEQTSHSKAS RRQEITKIRAE.LKEIETEKTLQKI NESRSWFFERINKIDRPLARLIK KKREKNQIDAINKNDKGDISDP TEIQTITIREYYKHLIYANKLENL EEMDKFLDTYTLPLRLNQEEVES LNRPIITGSEIVAIINSLPTKKSPG PDGSTAEFYQRYKEEL
7830	38198	A	7885	1	2142	MIILIDAEKAFDKIQPFMLKTL NKLIGIDGTYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLAQAIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLSNVSKVSG YKINVQKSAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNACSWIGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGKRGGIALVDIPVNDKL MVLEVLAIRQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLSNFSKVSQYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWNIP CSRIGRINIMKMAILPKVIYRFN DIPKLPMTFFTELEKTTLKFIW NQKRACIAKTILSKKNIAGGITL PDFKLYYKATVTKAWYWYQ NRDIDQWNRTEASEVTSIYNH LIFYKPKDNKKWGNDSLFNKW CWENWLAICRKLKLDPLTPYT KIHSRWIKDLNVRPKTIKLTLEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVVIKLSFCTA KETTTIRVSRQPTIEWEKIFAIYPS DKGLISRIYKELKQIYRKKVTNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTTM

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7831	38199	A	7886	209	3816	QGRPTFRFRKYREHHKDTFREE QLQDT*SSDSPKPK*RKCC*GQ PERKVKLPTKGSPSD*KRISRQ/ KTLQARRQSWFFKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTETITIREYYKHLVANK LENLEEMDKFLDTYTLPRLNQE EVESVNRPTGSEIEAITNSLPTK KSPGPDGFTAIFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASII LIPKPGRDITTKGNFRPISLMNI DAKIL
7832	38200	B	7887	1	3570	
7833	38201	A	7888	2	1624	
7834	38202	B	7889	67	3156	
7835	38203	A	7890	1	1416	MIILIDAEKAFDKIQPFMLKTL SKLGTDTGYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTROGCPL SPLLFNIGLEDLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVSQY KINVQKSQAFLYTNNRQTESQI MSELPTTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPR DIDQW/NRTEPSEIMPHTYNYLI FDKPEKNKQWGKDSLFFHKWC WENWLAVCRKLKLDPLTPYT KINSRWIKDLNIRPKTIKLTLEN LGITIQDIGVGKDFMSKAPKAM ATKAKIDKWDLIKLSFCTAKE TTIRVNRQPTTWEKIFATYSSD KGLISGIYNELKQIYKKKTNNPI KKWAKDMNRHFSKEDIHAAK KHMKKCSSLAIREMDIKTTMR YHLTPVRMAIHKSGNNRCWR GCGEIGTL
7836	38204	A	7891	1	1932	

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7837	38205	A	7892	1	2347	MELKTKARELHDECTSLSSRFD QLEERVSVMEDEMNMNLP TK KSPGPDGFTAIFYQRYKEELVP FLCLKFSIEKEGILPNSFYEPSII LIAKPGRDTTKKENFRPISLMNI NAKILNKMLANQIQQHIIKLIIH HDQVGFIPGMQGWFNIRKSINV IQHINRTKDKNHMIIISDAEKAF DKIQQHFMLKTLNKLVLLEVA RAIRQEKEIKGIQKGEEVKVSL FADDMIVYLENPTVSAQNLLKL IGNFSKVSQYKINVSQAFLY TNNRQTERQIMSELPFTIAKRI KYLGIQLTRDVKDLFKENKPL LKEVKEDTNEWKNIPCSWVGRI NIVKMAILPKVIYRFNAIPIKLP MTFFTELEKTKLFIWNQKRAC IAKSIFSQKNKAGGITLPDFKLY YKATVTKTAWYWYQNRDIAQ WNRTEPSEIMLHIYNYLIFDKPE KNKQWGKDSL FKNWCWENWL AICRKVKLDPFLTPYTKMNSR WIKDLNVRPKTIKTEENLGITI QDIGVGKDFMSKTPKAMATKA KIDKWDLIKLSFCTAKETTIRV NRQPTTWKIFATYSSDKGLISR IYNELKQIYKKKTNNPIKKWAK DVNRHFSKEDIYAAKHKMKKC SSSLAIREMQIKTTMRYHLTPV RMAIIKKSGNNRKIQ/GGIWCD RIL*R*TTCTCRVAKEIQSL*RI/W KRLQRTLSIPVLDAV*PPMF*AS
7838	38206	B	7893	1	1710	
7839	38207	B	7894	1	2265	
7840	38208	B	7895	1	2142	
7841	38209	A	7896	1	1791	
7842	38210	A	7897	1	1878	
7843	38211	A	7898	1	2091	

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7844	38212	A	7899	1	1751	MIISIDA EKAFDKIQQPFMLKTL NKLGDGTYFKIIRANYDKPTA NIILNGQKLEALPLKNGTRQGC PLSPLLFNTVLEVLARAIRQEKE IKGIQLGNVEVKLSLFADDMIV YLENPIVSAQNLLKLISKFSKVS GYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPLLKEIKEDTN KWKNI PCSWYGRINIMKMAILP KVIYRFNAIPKLPMPFFTELEK TTLKFIWNQKRARIAKSILSQK NKAGGITPPDFKLYYKATVTKT AWCWYQNRDIDQWNRTEPSEI TPHIYNYLIFDKPEKDKQWGKD SLFNKRCWENWLAICRKLKLD PFLTPTYTKINSRWIKDLKVRPKT IKTLQENLGFTIQDIGMGKDFM SKTPTAMGTDKIDKWDLIKL KSFCTAKETTIRVNRQPTKWEK IFTTYSNDGLISRIYNELKQIYK KKTNNPIQWAKDMNRHFSIE DIYA AKKHKMKCSSSLAIREM QIKTTMRYHLTPVRMAIHKKSG NNRNHLDFKHIRILGICYL/D*KI YQP*LHLVSRNRKPEKLSPKQA

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7845	38213	A	7900	1	2540	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQPDLDIDYGLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITSYLSHSAI KLELRIONLTQNHSTTWKLNLL LLNDYWLHNEMKAEIKMFET NENKDTTYQNLWDFAKAVCR GKFIALNAHKRKQERSKTNTLT SINKIDRPLARLIKKKREKTQID AIKNDKGDITTDPTMQTTIRE YYKHLANKLENLEEMDKFLN TYTLPRLNQEEVESLNRPIGAE IVAIINSLPTKKSPGPDGFTAIFY /HEL/LKENKIPRNPTY/RGCEGP LQGELQTTAQ*NRGKQKQME HSMMLMDRKNQYRENGHTAQG NLQIQCHPHKATNDFLHRSGKN YFKVHMEPKKSPHRQVNPQPK EQSWRHAI*IQTLQGYSNQN SMVLVPKQRYRSMKKNRRLRN NAAYLQLSNL*QT*EKQAMGK GFLI**MVLGKLASHM*KAETG SLPYTLYKNQFKMD*RLKH*T* NHKNPRRKPRHYHSGHRHGGQ LHV*NTKSNNGKSN*QMGSN *TKELLHSKRNYHQSEQATYKL GENFCNLPI*PRANNQNLQ* TNLQEKKNQPHQKVGKGHEQT LLKRRHLCSQKTHEKMLSITGH QRNANQNHNHIPSHTS*NGNH* KVRK*QVLNGLDDVQLFR*NK QPCSHKACLVVSSYRRA*SLV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
7846	38214	A	7901	1	1593	MGKKQNRKTGNSKKQSTSPPP KERSSSPAMEQSWMENDFVEL REEGFRRSNYSLEQEDIQTKGK EVENFEKNLEECMTRITNTEKC LKELMELKTKARELHEECRSLR SRCDQLEERVSAAMEDEMNEMK REGKFREKRIRNEQSLQEIWD YVKRPNLHLMGVPESDGENGS KLENTLQDIQENFPNLRINKI DRPLARLIKKKREKNQIDTIKN DKGDITTNPTIEIQTITREYYKHL YANKLENLEEMDTFLDTYTLPR LNQEEVESLNRPTITGAIEIVAINS LPTKKSPGPDGSIAEFYQRYKE E/PADKQLQQSLSIQNQCTKITSI LIHQQTNRPNHE*TPHNCFK ENKIPRNPITYKGCEGLLPGLQ TTAQGNKRGYKQTEHSLML GRKNQYRENGHTAQGNF*IQ HPHQATNAFLHRIGKNYFKVH MEPKKSPHRQVNPKEQSWR HHTT*LQTLQGYSNQNSMVLV PKQGYRSMQNRALRNNAAYL QLSDL*QT*EKHAMGK/EFPI**
7847	38215	B	7902	1	2337	
7848	38216	B	7903	1	1677	

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7849	38217	A	7904	1	1722	MAGYPSEMKLPEELSGSNICCS AVFTVLQLLLIPRQTGSGVDL RQTPTDLQLRVLTVRRKNKQ KRTSTPKPHLYVTIHKDQSKKL TQNHSTTWKLNLLNDYVW NNEMKAEIKMFFETSENKGTIY QNLWDTFKA VCRGKFIALNAH KRKQERSKIDTLTSQLEKEKQ EQTHSKASRRQEITKIRAEQKEI ETQKTLQKINESRSCFFEKINKI DRLLARRIKKKREKNQIDAIGN DKGDITADPTEIQSTIREYYKHL YTNKLENLEEMDKFLDTYTLPR LNQEEDESLNRPITGSEIEAIINS LPAKKSPGPDRTAEFYQRYKE ELHINRTKDKNHMTISVDAENA FDKIQQPFMLKTLNKLVLVLA RAIRQEKEIKGQLGKQEVKLSL FADDVIVYLENPIVSAQNLLKLI SNFSKVSGYKINVOKSQAFLYS NNRQTESQIMNELSFTIASKRIK YLGQLTRDVKDLFKENYKPLL NEIKDDTNKWKNNIPCSWVGRIN IVKMGLPKVVYRFPNAIPKLP TFFTELEK\ITLKFIVNQKRARI AMTILS*KNKAGGITLP
7850	38218	A	7905	1	2310	
7851	38219	A	7906	195	791	GILSFAKDMNRHFSKEDIYAAK KHMKKCSSSLAIREMQIKTTMR YHLTPVRMAIIKSGNNRCWR GCGEIGTLLHCWLDCKLVQPL WKSVMWRFLRDLLEIPDPAIPL LGIPNEYKSCCYKDTCTRMFI AALFTIAKTWEPPKCSNMIDWI K/KMWH/IYTRDTMRPKNDEVQ SLVG/TWVNWETTFSTVIAVQK PTRLSH
7852	38220	A	7907	1	984	
7853	38221	A	7908	1	2076	
7854	38222	A	7909	1	1872	
7855	38223	B	7910	1	3309	
7856	38224	B	7911	133	3213	
7857	38225	A	7912	1	1364	
7858	38226	A	7913	1	3249	
7859	38227	A	7914	1	2757	



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7860	38228	A	7915	1	2268	MAGYPSETKPPEERSDSNICSSA IFTVLHPPLLIPRQTAFGMDLQQ MPTDLQLRLVLTVKRKTNKQKG HPHQNPRTSPSSKTEDFQPTKI KRDKEGHYIMVKGSIQQEELTI LNIYAPNTGAPRFKEVLKDLQ RDLDSTHIMGEFNTRLSTLDRS MRQKVNKDIQELNSALHQADL IDISRNLIHPKSTEYTFPSAPHRT YSKIDHIVGSKALLSKCKRTEII TKCLSDHSAIKLELRINKLTQNC STTWKLNLLNDYVWHNEM KAEIKMFFETSENKDTTYQNL WDTFKAVCRGKFIALNAHKRK QERSKTDLTSLKELEKQEQT HSKASRRQEITKIRAELEQIETQ RTLQKISESRSWFEKINKIDRS LARLIKKKREKNQIEAIKNDKG DITTNPTETQTTIKEYYKHLVK NKLLENLEMDKFLNTYTLPRLN QEEVESLNRPTGSEIVAIINSLP TKKSPGPDGFTAIFYQRCKEEL VTFLLKLFQSIEKEGILPNSFYE ASINLIPIKPGRDTTKKENFRPISL MNIDAKILNKILANRI/WGN*AE ERNKEYSIRKRGSIQVPCVCR*H DCVSRKPHHLSPOSP*ADKQLQ QSLRIQNQCTKITSILIHQ*QTNR EPNHE*TPIHNCFKENKIPRNP YKGCGLQGLQTTAQ*NRK GHKQMEEHSMMDRKNQHRE NRHTAQGNL*IQCHSHQATNDF
7861	38229	A	7916	1	4729	

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7862	38230	A	7917	1	2685	MGDFNTPLSTLDRSTRQKVNK DTQELNSAPHQADLIDYRTLH PKSTEYTFSSAPHHTYSKTDHIL GSKALLSECKRTEIHTNYLSDDS AIKLELRKLNLTQNRSTTWKLN NLLDDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDFAKAVC RGKFVALNAHKRQGRSKIDT LTSQLEKEKQEQTHSKASRRQ EITKIRAEKIEIETQKTVQKINES RSWFFERINKIDRLARLIKKKR EKNLIDAIKNDKGDITTDPEIQ TTIREYYKHL YANKLENLEEM DKFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLTTKKSPPDG FTAEFYQRAIRQEKIQLGQK EEVKLSLFADDMIVYLENPIVS AQKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNI PCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELKKTTLNFIWNQK \RAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMPRIYNYL IFDKPEKNKQWGDLSFNKWC WKNWLAICRKLKLDPFLTPYT KINSRWIKDLNIRPKTIKLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLSFCTAKE TTNRVNRQPTKWEKIFATYSSD
7863	38231	A	7918	1	1205	
7864	38232	A	7919	1	2274	
7865	38233	A	7920	1	2307	

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7866	38234	A	7921	569	3030	RKH*TWKRTSSTSHHKNNMPN* LEKQEQTTH/SKPSRRREITKIRA ELKEIETPKTAQKINESRSWFSE RINKIDRPLARLRKKKKREKNQI DTIKNDEGDITTHPTIEHTIIREY YKHLANKLENLEEMDKFLDT YTLPRPNQEEVESLNGPIAGSEI QAIINSLPTKKSPGPDGFYQRYK EELVPFRLKLFQSIEKIGLPNSF YEASIIIPKPRDRTTKKENFRPI SLLNINAKILNKILANRIQQHIK KLMHHDQVGFIPGMQGWFNIR KSINVIQHINRTKDKNHMIIISID AEKAFDKIQPFMLKTLNKLGI DGYHKIIRANYDKPTANIILNG QKLEAFPLKTGTROGCPPLSLL FNIVLEVLARAIQKETEIGIQL GKEEVKLSLFADDMIVYLENPI VSAQNLLKLISNFSKVSQYKIN VQKSQVFLYTDNRQTESQIISEL PFTIASKRIKYLGIQLTRYVKDL FKER/YNEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAI SIQLPMTFFTELEKTTLKFIWNQ KRAHIAKSILSKKNKAGGIMLP DFKLYYKATVTKTAWHWYQN RDIDQRNRTEPSEIMPHVYNHLI FGKPDKNKQWGNDSLFNKWC WENWLAICKKLLDPFLTPYT KINSRWIKDLNVRPKTIKTLLEN LGNNIQDIDGMGKDFTSKTPKA MATKDKIDKWDLMLKLSFCTA
7867	38235	B	7922	1	3171	
7868	38236	A	7923	1	2646	

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7869	38237	A	7924	321	2211	CCQFSMARRGHLPRSVQVSIPIG QSPVPRAAYQDSGRVYKEPTAD C/VGPRQT*CMAPHCHLGGWH MLALSLGKGAGAGGKESTWEP SPGIRMTKTYSTRREQSHPTI/ KGQIKQMNLRETCSWTFHKKF LKTVAQFISHPHKNTCLAMAVS ANRSMRQKFNKDTQELNSALH QVDLDIYRTLHPKSTEYTFESA PHHTYSKIDHILGSKALLSKCK RTEITNYLSDHSAIKLELRINKL TQNRSTTWKLNKLLNDYVW HNEMKAEIKMFFETNENKDTIY QNLWDAFKAVCRGKFIALNAH KRKQERSKIDTLTSQKLEKQ EQTHSKASRRQETIKIRAEKKEI ETQKTRQKINESSSWFFEGINKI DRPLARLIKKREKNQIDTIKN YKGDITTDPTIEQTTIREYYKHL YANKLENLEEMDKFLDYTLPL RLNQEEVECLNRPITGAEIVAI NTLPTTKSPGPDGFTAIFYQRC SRWIKDLNVRPKTIKLTLENLGI TIQDIGTGKDIMSKTPKAMATK DKIDKWDLIKLSFCTAKETTIR VNRQPTKWEKIFATYSSDKGLI SRIYNELKQIYKKKSNPIKKW AKDMNRHFSKEDIYAACKHMH KKRSSLAIREMQKTTMR
7870	38238	A	7925	1	3057	
7871	38239	A	7926	1	1830	
7872	38240	B	7927	1	3192	
7873	38241	A	7928	1	3484	MGTSVQNGEERAGTSGQGSV EQLSGSSVQLPPGLKLCFEPYFS SCASDCILHASPLSLMAASGSQ NPNLWASWLCKWVQCPEQ LGCHLTSSVIYGLRYYPQAKRS ELELRDCEGLCNQTSPLSLDG MGWKAEEESNSGIRNIWIPI AFATHKQYNVRQVISPSPPYWS HRGNGNNSLCVTRLSSGLKQP VAGTGRGLEGGSGTRDLMPPFL SAAPKEQPPILAPARRSWFFEKI NKIDRLRLARLIKKRE

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7874	38242	A	7929	I	1946	NLTQNRSTTWKLNLLNDYW VHNKMKAEIKMFFETNENKDT TYQNLWDTFKAVCRGKFIALN AHKRRQERSKIDTLTSQLELE KQEQTHSKASRRQEITKRAEL KEIETQKTFQKVNESSWFFERI NKIDRPLARLIKKEKNQIDAI KNDKGYITDPTIEHTTIREYYK HLYANKLENLEEMDKFVGTYT LPRLNQEEVESLNRPIITGSEIVAI INSLPTKKSPGPDGFAEFYQRY KEELAGRDTTKEENFRPISLMN IDAKILNKILANRIQQHIKKLIH HDQVGFIPGMQGWFNICKSINV IQHINRTKDKNHMISIDA EKAF DKIQPFMLKTLNKLVLVFLAR AISQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS NFSKVSQYKINVQKSAFLYTN NRQTESQIMSELPFTIASKRIKY LGIQLTRDVKDLFKENYKLLSK EIKEDTNKWNIPCSWVGRI VKMAILPKVIYRFNAIPIKLPM FFTELEKATLKFIWNQKRARIA KSILSQKNKAGGITLPDFELY KTTVTKTAWYSYQNRDIDQW NRTEPSEITPHIYNYLIFDKPEK NKQWGDLSFNKWCWENWLA ICRKLKLDPLTPYTKINSRWIK
7875	38243	A	7930	I	4801	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRAEITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYWVNNEMKAEIKMFF ETK\ENK\DTTYQNLWDFAKAV CRGKFIALNAHKRRQERSKIDT LTSQLELEKQEQTHSKASRRQ EITKRAELKEIETQKTLQKINES RSWFFERINKIDRPLARLIKKEK EKNQIDTIKN

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7876	38244	A	7931	1	3146	MGDFNTPLSTLDRSSRQKVNK DTQELNSTLHHADLIDYRTLHP KSTEYTFFSAPHHTYSKIDHVV GSKALLSKCKRTEIITNCLSDHS AIKPELRICKLTQNRSTTWKLN NLLNDYVWHNKMKAIEKMF ETNENKDDTTYQNLWDTFKAVS RGKFIALNAHKRQKRCRCKIDTL ASQLKEVEKQEQTHSKASRRQ EITKIRAEKIEITQKTLQKINES RSWFLERINKIDRPLARLIKCKR EKNQIDVIKNDK
7877	38245	A	7932	1	2669	MHNTDGNRFLSHWGYRQALSI SKPASASLHPSSKTKPLGTQSKT VVAKRNRHGGKERSSSPAME QSWMENDFDELREEGFRRSNY SELREDIQTGKEVENFEKNLE ECTRITNTEKCLKELMELKTK ARELREECRSLRSRCDQLEERR KQERSKIDTLTSQLEKEKQEQ THSKAGRRQKITKIRAEKIEIT QKTLQKINESRSWFFERINKIDR PLARLIKCKREKNQIDTIKNDK GNITTDPTIEQTIREHYKHLA NKLENLEGMDKFLDITYTLPLRL NQKEVESLNRPTGSEIVAINS PTKKSPGPDGFTAIFYQRYKEE LHINRAKDKNHMISDAEKAF DKIQQPFMLKTLNKLVLVFLAR AIRQEKEIKGQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLL SNFSKVSGYKINVQKSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGQLTRDVKHLFKENYKPLL KEIKEDTNKWKNPCSWVERIN IVKMAILPKVIYRFNAIPIKLPM TFFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGITLPDFKLYY KATVTKTAWYSYQNRDIDQW NRTEPSEILPRIYNYLIFDKPEKN KQWGKDSLNFNWCWENWLAI CRKLKLDPLKPYTKIKSGWIK DLNVRPKTIKTEENLGITIQDI GMGKDFMSKTPKAMATKAKID

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7878	38246	A	7933	1	2962	MNNSIKEKVKLSLTQWEMQTK PNNNTVDLKDQAEVNLSTDY RKQHVMLPTEINSDDSLKIGVI RLANWIKSQDPSVCCNQETHLT CRDTHRLKIKGWRKIYQANGK QKKAGVAILVSDKTDKPTKIK RDKEGHYIMVKGSIQEEELTIL NTYAPNTGAPRFIKQVLSDLQR DLDSYTLIMGDFNTPLSTLDRS TRQKVNKDTQELNSALHQVDL IDIYRTLHPKSTEYFFSAPHHT YSKIDHILGSKALLS
7879	38247	A	7934	1	4220	MGDFNTLLSALDRSTRQKVNK DIQELNSALHQADLIDYRTLHP KSTEYFFSAPHRTYSKIDHLV GSKALLRCKCRTEIITNCLSDHS AIKLELRKKLTQNHSTTWQLN NLLNDYVWHNEMKAEIKMFF ETNENKDTTYQNLWYVKDTRI SGMLWYVKAVCRGKFIALNAH KRKQERSKIDTLTSQLEKEKQ EQTHSKTSRRQETIKRAELKEI ETQKTLQKINECRSWFFEKINKI DRPLARLIKKKRE
7880	38248	A	7935	1	3229	MGKKQNRKTGNSKTQASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELREECRSLRSR CDQLEERVSADEMEMNEMKRE GKFKREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLRDIIQENFPNLARQANVQIQ EIQRTPQRYSSRRATPRHIIVRFT KVEMKEKMLRAAREKDRSTRQ KVNKDTQELNSA
7881	38249	A	7936	1	3227	MGDFNTPLSTLDRSTRQKANK DTQELNSALHQVDLIDYRTLH PKSTEYFFSAPHHTYSTTDDHIL GSKALLSKCRRTETITNYLSDHS AIKLELRKKNLTQNRSTTWKLN NLLNDYGVHNEKAEIKMFF ETNENKDTTYQNLWDAFKAV CRGKFIALNAHKKQERSKIDT LTSQLEKEKQEQTHSKASRRQ EITKIRAEKEIETQKSLQKINE SRSWFFERINKIDRPLARLIKKK REKNQIDTIKN
7882	38250	B	7937	1	2089	

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7883	38251	A	7938	1	3527	MELKTKARELREECRLSRSPCN QLEERVSAEMEDEMNMKREG KFRDKRIKRNEQSLQEIWDFVK RPNLRLIGVPESDGENGTKLEN TLQDIIQENFPNLRQANIQIQEI QRTPQRYSSRRATPRHIIVRFTK VEMKEKMLRAAREKAPHHTYS KIDHILGSKVLLSKCKRTEIITN YLSDHSAIKLELRJKNLTQNHST TWKLNLLNDYVWVHNEMKA EIKMFFETNENKDTTYQNLWD TFKAVCRGKFIALN
7884	38252	B	7939	1	5238	
7885	38253	A	7940	1	3587	MENDFDELREEGFRSSNYSEL WEDIQTKGKEVENFEKNLEECI TRITNTEKCLKELMELKTKARE LHEECRLSRSCDQLEERVSAM EDEMNEMKGEGKFREKRIKRN EQSLQEIWDYVKRPNLHLIGVP ESDGENGTKLENTLQDIIQENFP NLRQANVQIQEIQRMPQRYSS RRATPRHIIVRFTK VEMKEKILK AAREKDRSTRQKVNKDTQELN SALHQADLIDIDIYRTLHPKS TNEYFFSAPHHT
7886	38254	A	7941	1	6202	MVKGSIQEEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH LKSTEYFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSHDS AIKLELRJKNLTQNRSTTWKLN NLLNDYVWVHNEMKA EIKMFF ETNENKDTTYQNLWDAFKAV CRGKFIALYAHWRKQERSKM DTLTSQLEELEKLEQTHSKASR RHEIAKIRAELEIE
7887	38255	A	7942	2	3134	WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYIMVK GSIQEEELTILNIYAPNTGAPT QQVLSDLQRDLDSHTLIIGDFN TPLSTSDRSTRQKVNKDTQELN SALHQADLIDIYRTLHPKSTEY FFSAPHHTYSKIDHILGSKALLS KCKRTEIITNYLSHSAIKLELM IKNLTQNHSTTWKLNLLNDY VWVHNEMKA EIKMFFETNENK DTTYQNLWDTFKAVCRGKFIAK NAHKRKQERS



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7888	38256	A	7943	1	4455	MELKTKARELREECRLSRRRN QLEERSVAMEDEMNMKREG KFREKRIKRNQSLQEIWDYVK RPNLRLIGVPESDAENGTKLEN TLQDIHQEDFPNLAQANVQIQE IQRTQRYSSRRATPRHIIVRFT KVEMKQKMLRAAREKDFKPT KIKRDKEGHYIMVKGSIQEEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHPKIS
7889	38257	A	7944	1	6108	MTGSNSHITILTININGLNSAIK RHRLASWIKSQDPSVVCIQETH LTCRDTHRLEIKGWRNIYQANG KQKKAGVAILVSDKTDKPTKI KRDKEGHYIMAKGSIQEEELTI LNIYAPNTGAPRFIKQVLSDLQ RDLDSHTLIMGDFNTPLSTLDR STRQKVNKDTQELNSALHQA DLIDIYRTLHPKSTEYTFSSAPHH TYSKIDHIVGSKALLSKCKRTEI ITNYLSDHSAIKLELRIKKLTQN RSTTWKLN
7890	38258	A	7945	2	788	CGLAIYNCTIVDLHFPLALYKK LLKKKPSLDDKELMPDVGRS MQQLLDYPEDDIEETFCLNFTIT VENFGATEVKELVLNGADTAV NKQNRQEFVDAVVDYIFNTSV ASLFRCSFSGFGKVCGGKGLAR LFQPNELQAMVIGNTHF*WKG TGKDYRNTKGNIAEHPITIKIF WEVFHLEPLEKKK/RFLFLTG SDRIPILGMSK/LVQSTGGG EEYLPVSHTCFNLADLPKYTK KETLRS*T*SQAIHNEGFSLI
7891	38259	A	7946	1	1647	
7892	38260	B	7947	363	550	
7893	38261	B	7948	1	1123	
7894	38262	A	7949	1	3136	MVTHQQPAARKPNMTSKPKP MGPKAHGIFSGTRKNNLEIYMD QTRTGIAKTKLSKNNKSGGMT LPDFKLYYKAIKACGGSY NSDTEDEETEPSSSQQIENSI TMNKMMLLKAKMKNMNLSSK HITQVSEDEEDDDGCDLFADSE KEEKDIEDIEENTRPKRSRPTSF ADELAARIKGDVAVRVDDEPTT VSYEDDRRGKNQDAYTEGGLS TIKTVNCSSSLTLRRSKTSEDITQ EKKERRTPSDEED

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7895	38263	B	7950	303	1010	
7896	38264	A	7951	3	280	
7897	38265	A	7952	3	514	FYLKELDPAEHSYVLIRKIDPAL VWGLTGDDGTPKTRLLMITLD SIFMQASCVPPEEVVWEVLRLVE AHVSSKKHFVFGESMKLITKAS VQGEYLVHK*VSHSNPTLYVFL WGLSKETRQMEVPEFVAKVND THPSSFSVGSK*GI*EKEGGRYP VPMEGSCRLVTVTASV
7898	38266	A	7953	2	351	
7899	38267	A	7954	2	529	EKGERPHWSNKPNSNLRKTHEL DIDENPASDFDDSGSLGFKYG SGQKYGGIPYFSHRQVR**EKN VKLKAKYLNMRGQIKMKNKIH FFTKETEPFFKKSKILSKVEKF LTWVYNKPMDEEASQESSHDN GHDASTCDSEEQDMSVKKGD DLLETNNPEPEKQCSVSSAGEL
7900	38268	A	7955	1	1370	MPVGTSNFLLGLLENPNLPLT RPSFPFSQREASWGQKATTGP GEGECTRLGFSLLLDVFCALHG PREKCVIELRSGHLLAISPGGVR EALISDETYNIVWGHRRGFAQV AIDAKVVEKFLTWNKPMDEE ASQESSHDNVHDASTSSDSEE QDMSVKKGDDLETNNPEPEK CQSVSSAGELETENYERDSSLA TVPDEQDCVTQEVPSRQAETE AEVKKKKKKKKKKVNGLPPE IAAVPELAKYWAQRYRLFSRFD DGIKLDREGWFSVTPEKIAEHIA GRVSQSFKCDVVDAFCGVGG NTIQFALTGMRVIAIDIPVKIA LARNNAEVYGIADKIEFICGDFL LLASF*KADVFLSPPWGGPDY ATAETFDIRTMMSPDGFELFRLS KKITKNIVYFLPRNADIDQVAS LAGPGGQVEIQNFLNNKLTI TAYFGDLIRRPASET
7901	38269	A	7956	3	560	RIHTGEKPYDCKDCGKAFGRTS ELILHQLRHTGVKPYECKCGK TFRQHSQILHQRTHTGEKPYV CKDCGKAIFIRGLQLTVHRIHT GARPYGVLEKCGESLLDSTHS* LLHQRRIHTGVEEPYECKEKGK FIHSSEVTRHQRIHSGEKPYECK ECGKAFRQHAQLTRHQRVHTG DRPYESAED

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7902	38270	A	7957	155	1288	HTTASQTTMSQAVR/RRRSDYL SSARR/RRDPARSKPTQGGPPPN PPPTRQGRPTALTNPSPQRPRHR AHPHQHATPKPRTNEEQEGRR HTKQPNPTRTTEPRPPNRRGRPN PQTRRTKQQNTTTPQAHTSTRKN ARTPGLCP*CVKGKTEGGYDA RASARGPYMAGVSWPGEHEDP GAPEARRGRRALPG/GSAFPEM STHTESTPKTTAHTSNDRRNRE QRVKKKTYKTTRSGANRNST ERHEDGYFYGSLTTGPLPWHSA IHSVSAGQPWSLKFTVGLQQAS EGYFSQSQERSLPNRKSSVPRLR LLFLQQASRLSELPLGTGPGSL LLRPREELACTGKRRKTGGAIM GEVSVCELSLPAPAFQSPVQLC GCQPEKA
7903	38271	A	7958	1	2045	REAAAAATSPFPSSSVRPSVRAS VRSARSGPKHGRRQLQRPPGA /RWRLTRR*SERRARPTGLCTH MKMAPMTSSLQHGEKGACRSF RDTLRTTR*CTASAVSRTPKIRS AKIRAHQLGGRRC*A*CPQVRLC QPRG*GGRVLPGCRDRERQQ RGRHRRGCHRAAAL*AGATL QPCAAPTAAARG*ER/SSPWAPP TRRRMQLWK*SGLTESSSGSRP RRKKSCGRRRSGRPPWMRGSG SSRSQWSRSGRSKRSASGATGS GSSRSRSTGNSRL*KRRKPRG G*RSSLVLTIGMRKRPT*RSQ SRRWRRQQLLPSGLTTQSSSS SSRKESHRLRAAVMYPRPSTI DQAATWTATGGWRPLSPRGA RLTPAPPPPLSLSR*SGPWMRSP P/PQPPPLPPPPPPKRPRSPAPS* TVRRPEQQPLRPGPAPWRSPLR HRRLPGGQAALQRT*CSWSLQS RLSWLLPWSLPQLTPRRSTMQL TPLKLTPLLTPLPTTYPPPPPA SLTYGLATGKGPPHSRVSPGPP RHPRVLRSWPQRCPWWRWL RSHCCQQAQAVPPFSTLMSCLS RQPPSVTQRKWKGPWLP RPQ LCQPQLRSWSKSRSRPTC*PM ARPPRRRRGPRPSEGYFSQSQEEE FAQSEELCAKAPPPVFYNKASE NVIHMLGCRPSSRRGGGLRGW
7904	38272	A	7959	3	174	

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7905	38273	A	7960	3	862	GVMASRTLLLLLGALALLET WAGTHSIRYFSTAVSRPGREP RYIAGVGYDDDTQFIDAATPRM* PQSPWLEQEGPEYWDSTRNIR PAHRLTRVNLMPRRYYHQS* AGTGIFHGIRR/YIPDTCVQTHM IHHSVSDYKATLRCWALGFYP VEITLAWQ/QDEEDQTRDHE/L VETRPAGDGTQKWAADVVP GQEQRYTCHVQHEGLPKPLTL RWEPSSTPIPIVGIAGLVLFGA VITGA VVAAM/WQEEELRTFS SHR*SELTSERASSDHAQGS DV SLTACKV
7906	38274	A	7961	1	591	MVTDYAIELFLQASLILLSSTLP YNEREMGLSIFALLTLTVFLLL ADKVPETSLSPVHIIKYLMTMV LVTFSVILSVVVLTLHHRSPH QMPLLVPSDLHSQTSVAPASKK AQTRERPDAGAPSLFFSRKWLG YIARQLQEDEDHD/VAEGGLAV CGHSGPPLPVDFHHLHQRWD PSHLPGRHVPLAPSRPLSL
7907	38275	A	7962	1519	1888	ILKHPTLDKELITYLFIYLFIL RRNFTLV A*ARVQWCDLAPPQ PLSPGFKPFSCLRFPSSWDYRYA PPYLANFVFLVGTGF/SMLVRL VSNSRPQ/CDPPASASQSIGTG VNHHARITFNF
7908	38276	B	7963	280	1977	
7909	38277	A	7964	994	1651	CRGSQAPAPLTPHPNAPLGP LHSQTSVAPASKKAQTR/GDLM PEPPHCSSPGSGWGRGTDEYFIR KPPSDFLFPKPNRFQPELSAPDL RRFID/VSKPGCPASGATGGV SSISYIARQLQEDEDHD/VAEGG LAVCGHSGPPLPVDFHHLHQ RWDPRSSWSHVPLAPSRPLSL KTGGLRPGPLPVEVREPGDTPK PYPPLPNSFTNLGLLFRSG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *Stop codon, /-possible nucleotide deletion, ▽possible nucleotide insertion)
7910	38278	A	7965	10	533	DEVSLCCQAGVQLHDVQSLQT ASQVQAILLPQPEVEAISGACH HACLIFVFLVEMGFHHIGQAGL KLPTSGDLPASASQSAGITGVS HRARPASSYLFFF*DEVSLCCQ AGVQLHDVQSLQLPPRFKRFS C/PASRSS*DFRRLPPRLPNFCF/ M*RWGFTILARLVNSRPQ/CD LPASASQSAGITGVSHRARPASS Y/CIFFLRWRLTIAQAGV**CNL SSLQPPTPGFKWVSLSPSSW DYRSLPPLPANFCIFSRDGVSLC SLSWSRTPDFK
7911	38279	C	7966	312	467	
7912	38280	A	7967	31	678	TGLYFLFLFCLRRSLA/SVAQPG VQWRDLGSLQAPPGLRRFSFL SLQSSWEYRCPLRPADFLYF*S RRGFSTLVRI.VSNSRPQ/CDPPA SASQSAGITGVSHCAR/LFFSFE MEFRSVAQAGVQWRDLDSLQ PLPPGILT*FSCLSLPRLGAA/WD YRRVPPCPAIFC/IFFFSRDRVS PCWSGWSQTPDQVIRPPPSQ SAGITGVSHRARPISHS
7913	38281	A	7968	23	99	YTMTPGPCWRPL*TGPHPPHT WPGGSSSHQIPHRPPCVFG
7914	38282	A	7969	144	1239	ERTEPDH/TTTLT*P/ELPADTTA TVEDMLPSVTSVTNSDTITETF ATAQYILTSETTTLTSSIAPPAT ATPDSNSVPAQATPSKGPSAS APSPAPASAPKVAPLVDSLDT TSTPAASNLSSSVLANQGAVLS PSAPAGVGEASKAPPASKPTPA PVPTPTGAASPLAAAAAPATEA PQAKQEA PSTKGPDPPTQPGA AKSPAEEAATALASPKSEAAVS TTNPSQGEDFKMDEGNFKTPDI DLAKDVFAALGSPAPAAGASG QAPELAPSTADSSVSPAPAKTE YGLSLSAVIGLCPVVS GWEDSG LPSIKWLLGLKVQEKGLNLSGK NTASGINLGL EEERTRSSDSVLL NYGCTLES LGCF
7915	38283	A	7970	3	375	ARQAMKSLHQCFLLTRQAL EASSCNSTGWGEGTGKSGLQ RGP*NCQWEPSPAQQAFTSS* AVATAAGQGEELPLLPSTTP GKNTASGINLWLEERTRSSDS VLLNYGCTLKSLACF

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v-possible nucleotide insertion)
7916	38284	A	7971	1	2230	MFEASVGVFMRLEERTRLHDI QAQDEAVTADLEAAAGYPDIA KIIDEGGYTKQIFSVDDTAFS WKKMTLRTFIAKEGTNTDGAS SATSSLVSLCLELCLRAHHDV GFYCDLDVYQSAVYAPCTPTG YSLPQAKEESDFIPLEYEKGRIT STAGQQQDVPEMEQLEKGSIK GVTETRTGPLGCSNYDNLDSVS SVLVQSPENKVQLLGLQVLLPE YLRERFVAAALSYITCSSEGEL VCKENDCWCKCSPTFPECNCPD ADIQAMEDSLLIQDSWATHN RQFESEEFQALLKRLPDDRFL NSTAISQFWAMDTSLQHRYQQ LGSWL*KVLFKKTHRILRRLFN LCKRCHRQPRFLPKERSLSYW WNRIQSLLYCGESTFPGTFLEQS HSCTCPYDQSSCQGIPCALGE GPACAHCAPDNSTRCGSCNPG YVLAQGLCRPEVAESLENFLGL ETDLQDELKYLKQKQDSRIEV HSIFISNDMLGWSWFDPSWRKR MLLTLKSNKYKPLVHVMLAL SLQICLTKNSTLIEPVMAIYVNP FGGISHSESWFMPVNEGQFSL TWIERTNVDAQA/QCQNWMT HLGGIRWKTFFETVHVYLRSR IKSLDDSSNETYYEPLEDDWIP LRNLGYMKINTLQVFGYSLPF DPDAIRDILQLDYPTQTGSQD SALLQIELRDRVNQLSPPGKV
7917	38285	B	7972	62	232	
7918	38286	A	7973	3	258	KLSPPPPPLPPSPPLPRPGPA/GPP SRLPSP/PASASPOGVP*LGPA AELPGIRSR*PQVAAPAEATH WCCC*RSSPQQQRISH

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7919	38287	A	7974	1	1048	MAHSQNSLELPININATQITTAY GHRALPKLKEELQSEDQTRQK ALMALCDLMHDPECIYKAMNI GCMENLKALKDSNSMVRIKT TEVLHITASHSVGRYAFLHDI VLALSFLNDPSPVCRGNLYKA YMQLVQVPRGAQEIIISKGLISSL VWKLVQVEVEEEEFQEFILDTLV LCLQEDATEALGSNVVLVLKQ KLLSANQNIIRSKAARALLNVSI SREGKKQVCHFDPVILVHLK DPVEHVKSNAAGALMFATVIT EGKYAALEAQIIGLLELLHSP MTIARLNATKALTMLAEAPG RKALQTHVPTFRAMEVETYEK PQVAEALQRAARIAISVIEFKP
7920	38288	A	7975	1	782	MAVTAAACWSLRPLARRDVCV GVALASPFVKPTHWFCKTLLEP CRPTGMGAQEIIISKGLISSLVW KLQVEVEEEEFQEFILDTLVCL QEDATEALGSNVVLVLKQKLL SANQNIIRSKAARALLNVISIRE GKKQVCVHFDVIPNPWSHLLKD PVEHVKV*RCRLPLMFAITVIT EGKYAALEAQIIGLLELLHSP MTIARLNATKALTMLAEAPG RKALQTHVPTFRAMEVETYEK PQVAEALQRAARIAISVIEFKP
7921	38289	A	7976	1	300	VEQTGRGE/RAYDIYSRLRNA FLCVMGPIDDSVASLVIAQLLFL QSESNKKPIHMYINSPGGVVT GLAIYDTMQYILNPICLTLPRTVR MSPRWCRRSL
7922	38290	A	7977	2	470	RPPQRTLQNGLALQRCLHATAT RALPLPIVVEQTGRGEASYDIY SRLLRERIVCVMGPIDDSVASL VIAQLLFLQSESNKKPIHMYI/N QPSGGARGQATDIAIAEEIMK LKKQLYNIYAKHTKQSLQVIES AMERDRYMSPMEAQEFGLDK

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7923	38291	A	7978	3	864	SCRYPALGPRLAAHFPAQRPPQ RRPPRTACSLQRCLHA/TATRAL PLIPVVEQTGRGERAYDIYSRL LRERIVCVMGPIDD/SVA/SLVI AQLLF/LQSR/SMKPIHMYIN/S PGVWVVTAGLGHLTDITAVTF LQPDFTW/CSLGPGAASMSGSL AFFAAGTPGMRHFAQPLPVFMI QPALQEGAGGQSPPDIAIQAE NP*KL/KKQLYNI*RORTTQTRS LQGDRVPPMAEGTA*HEAPME GPQEFGLKTRFLVPPSPQDGE/ DEAPRLVQKEPVEAAPAAEPV
7924	38292	B	7979	1	2088	
7925	38293	A	7980	412	812	FQSLFTCVLFHFKFSLTIHHMNS QPF*RIRSTFFFLKQSL/DSVTQA GVQWRDLGSLQPPPPGFKQFSC LSLPSSWDYRRAPHPANFFYF F**QTG/FTHVGRMVPI*PRDPP ALASQSPGITGMSHCTRPRJR
7926	38294	A	7981	2	178	
7927	38295	C	7982	279	322	
7928	38296	A	7983	2	760	GVRSSGGGR/GRPGGGPRKARR GKAEDKE*MPVTKLGHLVKDM KIKYLEDV/YFSLPIKESETIDFF LGSSLKEEGLKIMPVQKQTRAG QRTRFKAFVATGDYNGHVGLC VKCSKEVATAIRGSVILTKHSIV PVRRGY/WGNKMDK/PHTVPCK VTGRGCSVLVHLIVSAPVPKLL LMMAGIDDCHTSARGCTAT/LG NFAKATFTDTSKTYSYLTLDLW KETIFTKSPYQEFTHDLVKHTH RVSVQRTRAPAVATT
7929	38297	B	7984	318	406	
7930	38298	C	7985	333	439	
7931	38299	A	7986	2	171	
7932	38300	A	7987	1	668	MGGLFWRSALRGLRCGPAPG PSLLVRHGS GTIMGVFVAVGTI PVPSRVPCIEADTLKPGGPSWT REKTLVA VKPDGVQRRLVGDV IQRFERRGFTLVGMKMLQAPE SVLAEHYQDLRRKPFPPCPSSR YMSSGPVAVMWEGYNNVRA SRAMIGHTDSAEAAPGTIKGV DFSVHISRNVHASDSV/EGAQR RIQLWFQEQ*SWVSWA/DIGGO HSSIHPA
7933	38301	A	7988	1	897	



SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/546,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
7934	38302	A	7989	1	142	MEYYAATKNDEVMSFV/GT/W MKLETIILSKLTQEOKTKHHMF SLISGS
7935	38303	A	7990	287	1086	EPWREMFISVYTLQKLGAFTI AKTWNQPKCPSMIDWIKKMW H/YTMEYYAAIKKDEFMSFER TWMKLETIILSNLTQEOKTKHR MFSLSISGSRMRIHGHREGNITC QGLLGGEVCVHTVATRGSPSATE DESCRMNVNDYGGNSPSTLQV KTSPPQRAEKGNNVRTWLYSN LVCWPSLGSMLMGKLRDRVIKR VIYTHTAGDVMHEEGFQFPLK QVSLLLCAIAFQPSLVVAAALV HITMEAYTYLEVTLTLLQIHSPLFC FLPKCHF
7936	38304	A	7991	1550	1835	DTISHQLEWQSLKSQETTALLTI AKTWNQPKCPSMIGWIKKMW HIHTMEYYAAIKRNEFMSFAGT WMKLETIILSKLTQEOKTK/HH MFSLSIRGS
7937	38305	A	7992	164	647	DLPVEPHIGKMILFEALVL/HCL DPVL TIAASLSFKDP/FVPLGKE KIADARRKELAKDTRSDHLTV VNAFEGWEEARRRGFRYEKDY CWEYFLSSNTLQIM/MKIHKAVI CAGLYPKVAKIRLNLGKKKK/K VKVYTKTDGLVAVHPKSVNVE QTDHFHYNWLI
7938	38306	A	7993	66	345	

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7939	38307	A	7994	1	2367	HRVTVISGETGCGKTTQVTQFI LDNYIERGKGSACRIVCTOPRRI SAHSSCGKSSCRKQGNLVASGN STGYQIRLPESVAQGNRVLSYT VPTRNHPSSGSDPYLSSVSHI VLDEIHERNLQSDVLMTVVKD LLNFRSDLKVLMSATLNAEF SEYFGNCMPHIHPGTFPPVVEYL LEDVIEKIRYVPEQKEHRCQFK RGFMQGHVNSQEKEEKEAIYK ERWPDYVRELRRRYASTVDVI EMMEDDKVDLNLIVALIRYIVL EEEDGAILVFLPGWDNISTLHD LLMSQVMFKSDKFLIPLHSLM PTVNQTQVFKRTPPGVRKIVIA TNIAETISITDDVVYVIDGGKIK ETHFDTQNNISTMSAEWVSKA NAKQRKGRAGRVPQGSLLFICI NGS*EASLLGWITQLPEIFEPEPF WEGTLFTK*RFLRLGEIAYFLSR *MDPPSNEPVLLSIRHLRSLNA LDKQEELTPLGSHLARLPVEPH IGKMILFAGLFCCLDPVLTAAS LKFO*SPFVPLGKEKIADARRK ELAKDTRSDHLTVVNAFEGWE EARRRGFRYEKDFCWEYFLSS NTLQMLHNMKGQFAEHLGA GFVSSRNPKDPESINSNDNEKII KAVICAGLYPKVAKIRLNLGKK RKMVVKYTKDGLVAVHPKS VNVEQTDHFYNNWLIYHLKMR TSSIYLVADCTEVSPYCLLFFGVG
7940	38308	A	7995	25	312	WLIYVITDARMYRQGRYYFL VSSSLDKVLMISFLLGWRRSSR RLRAFLVLHLRASPWAPRSFVR PVSAFSGVMCHMKTRVFENTF PFTLGHTVRYVGREIF/CRRVFT RYRESIKISLPTYLTVCPRVKGN VFSNTRVFMWHIPTLKADTGRT KLLGAQGEARRCKTKKARKRR EERLQPNKKEIKITLSKEEETKK
7941	38309	A	7996	2	417	QQIRKLIKVLIIHKPVIVHSQV GCQKSTFS/RTRKGRHMG TG* KSTANFQMPKVTWWMRRRIJL HWFGRYHESKKT DHHMYHSL YLKVQGNMFTNKQILMEHNNH LKADKAHKFLADQAEARSSK TNKASKLREER
7942	38310	A	7997	3	124	KKRPELRDLLNQARKETU/ARK EDRSASSGAEGDVSSSEREP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met box	SEQ ID NO: in US 5,406,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
7943	38311	A	7998	911	1497	SQRKARDQRRKRNRKASSIAK HKEPKRPILPSGKNSQEGVATH TKPLAQGGKVLDP/NETNEIPN ANFRQQIRKLIKDGILRHRKPV TVHSRAQGWKSLTARRKGRHL GIESKKIDRHMYHSLYLKLGKN VFKHKRILTEHSHKLDKADKAR KKPLADQAEARGSKTKEARKL REEHLQTKKEIHKLSQEEKAK
7944	38312	A	7999	34	279	EVIHAAIGKEKGSY/NA**PWVE EQLTRQPLIHHPASLHVSYY/RC RYHSLYLKVGKGVFNKRLIM EHIHLKADKARKKLLA
7945	38313	C	8000	351	530	
7946	38314	A	8001	356	921	WRATACTYPSWAPPRLVATGP AAVSAGLPSLHGTRAGPQAPCT AAVPPAPLPPHRPAS*G/MPAGP VQKGAPT/AAAAG*RLKKGQS RRQGRGGAERTGCGHAVTFQ DCFLRCFFG*C*CLSG/ERAIALE QGASHAAEQLPRLQAFKRPGL /QVNPDAQKSAASSSLKVLGS LPKHQRPRRFCQNTGS*SGP**T TGRRSAAGAA/GKPNPGSPPA PHNFKSGTNPVATTHHPVGSKP RPEPHGNSEA
7947	38315	A	8002	495	653	MTLTSIDPVLTTFFNLECLP/VFT ATASSGLGEVE*AIALN
7948	38316	A	8003	1	1433	MPESNCSLTWRHVS GRAVAAQ GGEHSSQGASLVLGEPRGGSS WLLGLEGDTGLWGGLLKEGRL TDGKGKTIDCKDAIFIMTSNVA SDEIAQHALQLRQEALEMSRNR IAENLGDVQISDKITISKNFEN VIRPILKVRGLSWHFLLEPKAHF RRDEFLGRNGEIVYFLPFCHSEL IQLVNKELNFWAKRAKQRHNI TLLWDIREVADVLVDG\YNVH YGARSIKHEVER/RVNNQLAA AL*SRTLPLGGCTLRITVEDSD KQLLKSPPELSPQAEKRLPKLR LEIIDKDSKTRRLDIRAPLHPEK GRLTDGKGKTIDCKDAIFIMTS NVA SDEIAQHALQLRQEALEM SRNR IAENLGDVQISDKITISKN FKENVIRPILKVRGLSWHFLLEP KVLTTFFNLSVLYLHGNSIQR GEVNKLA VLPRLRSLTLHGPN MEEKGYRRARGHSLHQIEK YICESDDIFRKYCNNOFL
7949	38317	A	8004	1	789	

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7950	38318	A	8005	1	409	LRLELSFCSSCLLEPPWS/TTVV CLYCRPATDTHPSGSGRVS AVLIQ*G/RPLPLRLKACHCSHTA KCPGSSPSSMSPTAEEQKSGTA EERREGASEHGEFEGWGRLE RS AVEWPNSRGSSSHSIPFPAPRP
7951	38319	A	8006	1	1787	MSKGESRKCNEENVSKSSKVV KVFI VLT PQFLSRDKDQLTKEL QKHVKS VTVSCKSPRKLLSHIT RLHPPSKGQGENLTHLVDSIKA TTWCQPPVWETVEGQRRRVGNC IDFTNGCDLVGSSSLHNMLVCS SYDINRQDTFQKDRTSEKHLID SVFTALQDSAGQWPAPRLHPQ RGEEVADPRGAPSRHIEPENSS PCQGNGEQAGKAGARALCGQ ARRSPATMPPPLTTRSLCEFAVF LLHWLFPFLFHYRKLGEQDSCY GDGGKQELDPQRLQIICNFTEV YFPHMQE EEA WRQAGGPAAEA AD/TSATSRSTSPTCRRRRPGC SGAPASTTSFRAWGWTQA AK ASPPRDNCYNSSSLPDDISLFT H DNLHKQHSCSDSLGKKQLDPS CIKLIRH*VHLLYLCTKNNRVW TLEFMGNLHWNRRGAPTSSS ARSTCWPRV*RHEELCNQS*EV QRGV*GSPAAPERSSKDFCKIPL DEVVVPH*/DFPVRSPYLLSDKE VKIVQQSLSVGNFAAGLL/LPP RTSSCSTTIFGL/DNKKQLDPTQ LRLICH*VEAVYPVEKVEEVWH CECIPSNDEQCHCPNKKCNIL

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7952	38320	A	8007	1	1475	MAVDFSLAVLMIVSSYDINRQD TFQKDRITSEKHL LDSVFTALQD SAGQQWPARLHPQRGEEVADP RGAPSRHVPEPENS SP CQGNGEQ AGKAGARALCGQARRSPA TMP PPLTTRSLCEFAVLLH WLFPEL FHYRKLGEQDSCYGDGGKQEL DPQRLQIICNFTVEVYFPHMQEEE AWRQAGPGPAEAA/TSATSRR STSPTRRRRPPGLQRCAQCIND KLQGLGLDAGSEGEPPTRQLLQ LLQPAR*HLSNQQGG*LQGRAL FTHDNLHKQHSCSDSLGKKQL DPSCIKLIRH*VHLLYLCTKNNR VWTLFEMGNLIHWNRNRGAPT SSSARSTCWPRV*RHEELCNQS *EVQRGV*GSPAAPERSSKDFC KIPLDEVVVP H*/DFPVRSPYLL SDKEVKIVQQSLSVGNFAAGL L/LPRTSSCSTTIFGL/DNKKQL DPTQLRLICH*VEAVYPVEKVE EVWHCECPSNDEQCHCPNRKK CNILKKA K KVEK
7953	38321	A	8008	1	3524	MCNNLIHLSLANNKITTINGLN KLPIKILCLSNQIEMITGLEDL KALQNLDLSHNQISSLQGLNH DLLEVINLEDNKIAELREIEYIK NLPILRVLNLENPIQEKSEYWF FVIFMLRLTEL DQKKIKVEEK VSAVNKYDPPPEVVA AQDHILT HVVNSVMQQRIFDRYLL EIQR PEFRLVLKLVGNESLPIASADSL ALTSDMVRNGLDGLFYDFRAC HTRTPPYFGEGRVDYHFISQD VFDEMVMNMGKF
7954	38322	A	8009	258	719	MTPPSVLP*PSLSY*HPDYSLPF PFSPPVLCFPHVPVQGLYSVLFVN TAAEPREKSAMAILPLSGHACS HVCLGSHQSLFQRACGRCPRL SGSLRSHCHWLLILGVKKCSPP EAGKAILTTDRTETMNISWKP RNPSHTVPHPHHICCHWRI
7955	38323	B	8010	1	1953	
7956	38324	A	8011	32	533	GRERPLLSPYMETLYRVPFLVL ECPNLKLLKPPWLHMP SAMTV YALVVVS YFLITGGIYDVIVPE PSVGSMTDEHGHQRPVAFGLG QSKMDNNINGKGLCIQAS*FTM GGFRFS*ILDPIECTKYPKTSIDS FFCSIGISSVVLLEFFPWARSNS MRNNGCPGLI

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7957	38325	A	8012	670	1052	TRDRSRCKGTWLLSVKTLAISA VKSQSKASECRFTNRSSSTAVI RVLLPGILLSKLRCSMVLATA LERDDSDVGVTISSINPQDSHFS CLLLLRISNSC*IC/CNFAIRV HLAEVCI*QTSLLL
7958	38326	C	8013	40	186	
7959	38327	A	8014	1	1216	
7960	38328	B	8015	1	1032	
7961	38329	B	8016	1	1761	
7962	38330	A	8017	108	708	LTNQKKSRTRRIHSRILPEVQGG AAADRHCPIDRLGSLQDHRRS RLLSQWSP*KSTHD*HGFSYQS AEDIRRLQQAFAAGMNTSEL LQIANQAFVNRDAVSRKENHR DNERQAQRNTDLLAAAIRGVPP KRQGGGPGKETQPGCQSLQR NQCAYPEIGHWKNKCPQLKR KPGDSEAEAPDKDEGALLNLA EGLLD
7963	38331	A	8018	1	512	LSRSSPLLPLVWHQAMVGSMD VEPAAWVLMTFCWDTPRQSGV PRERMPHTGTWRTVGIRCPKK KLRSANSSMMRGKVQPFPR/DI QAYGAAPFEDLQVDFREMPKC GGNKYVLVLGRITYSGWVEAYP TRTEKTREVTPLVLRDLIRFRP PLWIGSDNGPAFLAALVQKTA
7964	38332	A	8019	3	764	KQVLVNGDAVSREEKRKENER QARRNADLLVSCSNQSGPPKEA REELWTKDYRPGQDLRLLSQA TLTFHPTVPSPTLLGLLPAEDS WFTCLDLKDAFFPIRSAPESQK LFAFQWEDPESALAKTVRQRC VSCRQHHAGKVQPFPR/DIAY GAAAFEDLQVDFTEMEPCGGN KYLPLVLRITYSGWVETYPTRA EKAREVTRVLLRDLIRLELPFR IGSDNGPAFVADLLQKTATVLG ITRKLHAASRPQSSGK

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7965	38333	A	8020	19	1548	CIYGAQLCTGPSAPVWYICPLGT MAPTGLPGHPAVATATEPHRE RGSPL/IDSTVLVPPQDKHILRPP TVDKRGGEASGETPPLAARLRH KTGIQMPLREQQYTGIDEYGHV VERRVFGYQPF TSAHLNWK NTPSYTEKQALIDLLQTHIQTH NPTRADCHQLLMFLFNTDERR RVLQAATKWLEEHAPTDYKNP QEDVRTQLLGTYPQWDPNERQ DMQRLNRYREALLEGLKRGAG KATNINKVSEVIQRKEESPAQF YERLCEAYRMYTPFPNSPENQ CMINMALVIQSTEDIRRLQKQ AGFARMNTSOLLEIANQVFN RDVSRKENQKENGWPPCLR ALAATALLVQEAANKLTLGQNL NIKASRAVVTLMTKGHHWLT DARLTKYQTLLENPRITTEVC NTLHPATLLPVSESPVEPDCVE VLDSVDSSRPDLRQAWASVD WELYVDGSSFFNPQGERGAGY AVVTLDTVVEARSLPQATSAQ KAELVAFIRALELSE
7966	38334	A	8021	1	895	MDGAGICYLHQTNAGTEIQTPH VLTYKRELNNENMWAHRGDN THWGPEGSTNSPASASGVADV SRVGSLLQWVLGLADFKNEAKE LRLYKQEKREKAKRWKETEKG FNGDYGVTMTPGKWRTYFEID WSKLEVGWPSSEGNLERSLVSK VWHKVTGKSGHSDQFPYIATW LQLVLDPQWLRGQAAAFLVA KGQINPRKDPTPPGRGKSTPEVL FDPTSEDPLQEME/PSDPSGALP LPGKDAPHSAHSPCASTRQTY P*ATRSRQERR*SLERNPYIGSS FKTQNWDTNAPERAVVYWDR

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7967	38335	A	8022	1	1959	MLKNFKGFNGDYGVTMTPG KLRLTCEIDWPTLEVGWPSEGS LDRSLVSKVWHKVTGKSGHSD QFPYIDTWLPQWVRGQAAAVL VAKGQIVKEGSRSTHRGKSTPE VLFDPSTDDPLQEMAKVIPVVP SPYQGERLPTEFSTVLVPPQDK HIPRPPRVDRKGGEASGETPPL AARLRPKTGQIMPLREQRYTGI DEDGHMAERRVFVCQPFTSAD LLNWNKNTPSCTEKPQALIDLL QTHQTHNPTWADCHQLLMFLF NTDERRRVLQAATKWLGHEHAP ADYQNPQEYKGESPAQFYER LCEAYHMYTPDPDPSPEQRM NMALVSQSAEDIRRLKQKQAG FAGMNTSQQLEIANQVFVNRD AVSHTGAEHSVVTGPVAPLSK KTIDHIGAMGVSAAQAFCLPRT CTPGTKDYRLVQDLRLVNOAT VTLHPTVPNPVILLGLLPAEDS WFTCLDLKDAFFSIRLAPERQK LFAFQWEDPESGVTTQYTWTV LPQGFKNSTPFGEALARDLQK FPTRODLCVLLQYVDDLLLGHP TAVGCAKRTDALLRHLEDCGY KVSCKKVAQICQQQVRYLGFIT RQAERTLGSGRKQVICNLPEPK TRRQVREFLGAAGFCRLWIPNF AVLAKPLYEVTK*GDREPFWE
7968	38336	A	8023	2	367	
7969	38337	A	8024	3	687	GRRQRRSKVTSTWWQARESS CRGTLLYKTIKSCDYSLSQEQ HGPNLHLIGVPESDQNGTKL ENTLQDIIQENFPNLARQANIQI QEIQRMPPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKGRVT HKGKPIRLPADLLVETLQARRE WGPINFILKEKNFQPRISYPAKL SFISEGEIKYFTDKQMLRDFVTT RPALQELLKEALNMERNWYQ PLQNHAKL
7970	38338	A	8025	1	993	



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7971	38339	A	8026	1	842	MAEQEQLQSAVPSPLLVIPRQK GSQVDFQSQPTDLQLRDLTDOR KTNKQKGIASLTLTRSTPKPH LYVTNIKDQRPNRLIGVPESD GEKGTLENTLQDIIQENFPNL ARQANIQIREIQRTQRYSSRRA TPRHLIVRFTKVEMKKEILRA AAREKGRVTHKGKPIRLTTADL SAETSTSQKTEWGPFIENILKEK NFQPRISVPAK\LSFFISEGEIK\ YFTDKQMLRDFCHHQTCLP*K TRPALKELLERKHLNM/EGGNN WYQPLQ\NHAQICKDH
7972	38340	C	8027	320	433	
7973	38341	A	8028	9	189	
7974	38342	A	8029	26	738	VAASSFDTCADHLCALHLLQV LHYLAIQKPADLARHLLPCVIH AAVLKVKEEESLENISSVKKIHK QIISHSSKVLHFPNPEDKKLEEII HQITNVEALIAARSLKAKFGT EKCEQEEEEKEDLERFVSCLEEQ PEVLVTGAGRGHAGRIHKLFLV NAQNVA\AMTPP\EEELKRMGS PEER\RQNSVSDFP\PPAGREFIL RTTVPRPAPYSKALPQRMYSVL TKEDFRLAVKIIDGDV
7975	38343	A	8030	3	2961	MAADSEPESEVFEITDFTTASE WERFISKVEEVLNDWKLIGNSL GKPLEKGIFTSGTWEEKSDEISF ADFKFSVTHHYLVQESTDKEG KDELLEDVVPQSMQDLLGMNN DFPPRAHCLVRWYGLREFVIA PAAHSDA VLSESKCNLLSSVSI ALGNTGCQVPLFVQIHHKWRR MYVGECQGPVVRTDFEMVHLR KVPNQYTHLSGLLDIFKSKIGCP LTPLPPVSIARFTYVLQDWQQ YFWPQQPPDIALV

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7976	38344	A	8031	1	1688	MREKPCQSNCEGKAFNYSSLLR RHHIHTSREREYKCDVCGKIFN QKQYIVYHHRCHTGEKTYKCN ECGKFTQMSSLVCHRRLLHTGE KPYKCNCEGKFTSEKSSLRCHR RLHTGEKPYKCNCEGKFTGRN SALVIHKAHTGEKPYKCNCEG KTFQKSSLQCHHILHTGEKPY KCEECDNVYIRRSHLERHRKI TGEQSYKCKVCDKVFSDSYL AEHQRVHTGEKPYKCNCKGRS FSRKSSLQYHHTLHTGEKPYTC NECGKVFSTRRENLARHHRLLHA GEKPYKCECDKVFSRRSHLER HRRHHTGEKPYKCKVCDKAFRS DSCLANHTESSILGEKPYKCYK CCGGFLIQKSSLQHQRVHTGE KPYECNECGKVFNQKASLAKH QRVHTAKPYKCNDCGKPLPD QSTLFHHQSNPIGVGKRYQCN DCHKVFSNATTIANHYRIHIE/ KIYKCNCKGKFFRRHS*LVVHQ *THTGEKPYKYHDCDKVFSQA SSYAKHRIHTGEKPHKCDDCG KAFTSCSHLRHQRIHTGQMPY KCKGGKVFTLWSFHAEHQKI
7977	38345	A	8032	25	1091	IHIYSDSCSLSLQDSGDEKEFNL DDNVSFRAFLWDLAAGPGQGG GGGREKWRVAVISRTMNRKMG KMMVKALSEEMVRPADIGDGV SRGPGDRSGRM*AEKMALAFS EQEEHELPLVLSRQASTGE*GMR GTPAESGGKDWVTAVLVAGPF CGRARVHTDFTSPYDHDLSKL QVRSASGLLWSLAGCAQKGSW TEPVGSFKFIYDVLPPEEAVGH ARPSRRQSKGRPKPKTLHELL ERIGLEV*AWSSLVSSIREAQLP QGWGPGHNLNIMDPQHRAK LLTAAELLDDYDSEWL*ERPGE GAESSQEPGGEACPKVDIPRDS GCFEGSESGRDDAELAGTEEQ LQGLSLAGAP
7978	38346	A	8033	35	437	
7979	38347	A	8034	1	1845	
7980	38348	A	8035	1	212	
7981	38349	A	8036	371	915	
7982	38350	A	8037	1	2460	
7983	38351	B	8038	10	1510	

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7984	38352	A	8039	1	188	SASTTLWGLLFLIHLRLGTALRA VSSWGTIILTAKEVQWGH/DCG THWSYHHLHQPRAAHGKEC
7985	38353	A	8040	3	2332	FFFMWDPQHFTFI/VLPQQYYN SPGLYSTVLRLDENLDIL*NIKF LYFIDNIMLTGMDE*EEDGTLE ALVKHLLSRGVKINKPYRDSEV ATAVK/FLQV*WLGASRG/VPS NVKDKLLHLC/MCKGREAHCL G*ALF*VS*HHNPTCKVVS GFDP HF*VT*EECPAFEWSL/QQERTL QQIPGHGAVTILQDPLVLKVPV GGVRFGEVLNQAPVGESQWKG LGIWSKAMSSTAQKYAP/FQSR EICWKQLLACY/W*ALI/EIECLT MGHKTTM*FQ/MPLRN*HLCNS *SHTLDMPQQHPIMRWKSFL*/ D*A*IPMLTSPRKHPNLKWP*TT KQKH/WKL/GQSPSPWVSPGRVG WVHKWSKHSGRD/GGYLWVQ QY*LPPTKVDPTATSKCPTHQ HLNPMIFP/R*GSISLGDQPDPK* GVDYIALFPS*KGQRFMFTGIGT YSIVGFSCRVPVPSVSTTFWGLL IFVIHRLGTASPCSSSWGTHLT AKEVQWGH/DCGTHWSYHHL HQPRAPGP*RMLKRASIGTAQR QLAGST/LCGWEGAIQDMVHF KNQRHLYSSVISVGRTRGSRYQ GVEVDVAPYPIPSHTLSWDFAL LSQNHHSAG*KVLDSKGGYP*K ETNECPLNYTLQLP/PGE/FGQY VSRDQVRVRGVPSSPGTVIDPD PQEEAWLLSHN/GG*EEFVWNP /GDPLGGLLV/LPCPIVSVRRIQ
7986	38354	A	8041	1	1296	

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7987	38355	A	8042	498	2219	KSVKTS*DTLRTKAKTGQGHITGLQPLGLRIRQEP/SAKTEKAAAIQAKAGAEREATGVVVRPVAKTRAKAKAKTGSKTDAVAEMKAVSKNKVVAETKEGALSEPKTLLGKAMGDFTPKAGNESTSTCKNEAGTDWFWWAGEEATINSWFWNGEEAGNSFSTKNDKPEIGAQVCAEELEPAAGADCKPRSGAEEEEENVIGNWFWEGDDTSDFPNPKPVSRIVKPPQPVYEINEKNRPKDWSEVTIWPNAVTPAVLGFRRSQAPSEASP/LFVCSGLR*RKCLFFACGNSLPFF*E/PRSCSQPIPECRFDSDPICQITIDEIRQIRIREVNGIKPFACPCCKMECYMDSEEFKLVSLKSTTDPLIHKIARIAMGVHNVHPFAQEFINEVGVVTLIESLLSFSPSEMRKKTIVTLNPPSGDERQRKIELHVKHMCKETMSFPLNSPGQSGSLKILGQLTTDFVHHYIVANYFSELFHLLSSGNCKTRNLVLKLLNMSENPTAARDMINMKALAAKLIFNQKEAKANLVSGVAIFINIKHEHIRKGSIVVVDHLSYNTLMAIFREVK
7988	38356	A	8043	1	453	MEKLDELKIKIDNINGALICARHFSKCSSNAQSHLCPYLQAFPGGPG/VRGLPGWPGRTGSRGLGHGWRGCG/EGLVSGCQ/TMLSGA/PAGSPQ/PTGGTRAHAVRGRP*VPARSQGSRPLARPQGED*GAAP/DFDPGAAGVPGVPALQEAQI
7989	38357	A	8044	3	690	LSLSPSSWDYRRAPPRPANFVFLVETGTMTLTIVLIS*PHHPPASASQNAQIV/GVSHSPRPGIACILTRLDH/HQGTQSRVPALGSS*PIPHARPRGHTLKALPYRLYTQTARGFGQPRVRIPLLSLLGSLKPSELRGQVGHAFASAFASISLCVFTLLVEGKLKPPGASVRCLQSNRDLGFRATFTPSHRGHGALGLNYISQRATGTPNLWLPRFRVVLQQAACG
7990	38358	A	8045	106	299	
7991	38359	A	8046	306	445	
7992	38360	C	8047	570	926	

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7993	38361	A	8048	47	988	ASRPGSRVSLMFGAAGRPDRS SSSPGTSWPFVPEMEELVHDL VSALERELQSKPRGGFAEPGDP FSEVY/PCPLKRPARKRRGRKR RFV*CASPVGGLVTA*SEGSDS SFRRTKSKKRKLKIRQGPQIQD EGVVLESEETNQTNKDKMECE EQKVSDLMSESDSSLSSTDA GLFTNDEGRQGDDEQSDWFYE KESGGACGITGVVPWWEKEDP TELDKNVPDPVFESILTGSPFLM SHPSRRGFPTKTQSAFMECLQRI LKNLEGLQLQWYFFLAQWVTR EWFIFRILITMTIGLALGLGQS MTSISF
7994	38362	A	8049	3	476	LTRPV D* RFGTHLGRGV RAR P ANRRQRARRGA AISPPGCSV AGFLRGR LG/PEPGDNGQHLGE PWLGCGLFA*RA*CSRSTRCT* RRRAPGDRELPRAPATWAPPIK LVPRVFSSKVGQGVSLVEAM CLQGDSILNQSNKHNSVASSNT ITVIG
7995	38363	A	8050	2	143	
7996	38364	A	8051	1	161	
7997	38365	A	8052	3	1189	ESPLLGHSSSDAARRRSVSSFP VPQDNVDAHPGSGKEVRVPAT ALCVFDAHDGEVNAVQFSPGS RLLATGGMDRRVKLWEVFG EK CEFKGSLSGSNAGITSIEFDSAG SYLLAASNDFASRIWTVDDYRL RHTLTGHSKGVL SAKFLDNA RIVSGSHDR TLKWLRSKVC I KTVFAGSSCNDIVCTEQCVMSG HFDKKIRFWDIRSESIVREMELL GKITALDLNPERTELLSCSRDDL LKVIDLRTNAIKQTF SAGPKC GSDWTRVVFSPDGSYVAAGSC *RALLYIWDVLTGKVEKVL SK A\HSSHQCGWPWSPSWARTF VSVDKGCKAVLWGTVLTGLSG LGGPQCPPEEAHGLLPWSW QVNVLGYSMDLPELKKANVGH

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7998	38366	A	8053	116	921	LKSNRCW*GCEEKGLTIHCW WEC/KFNPLLKAI*RFLLKELKVE LPLDPAIPSLGLSKIGTGKKVW QRLPNCPTISLFSFFHKNNRHTGT YRRRFLDSLAVRCPNCPATFGS KSDVCNFWVMPSTGKKCALPS HPLFPNGLNADVVCLSDSENLS QKILLILEVSDSVILGKLSHKNI QHDCEEPLTLLRNTQQFRFLCI ACHGCTSQYSTFLVKASWTRS QGLIQRQPSAGSGYPEKLFSEG AGDEGVDLLPLLAKPASPDQL
7999	38367	A	8054	35	422	SCSEVTEASWGSVPFLRDAQLG VGLHSPTYRHPHRETLTCCPAG TLQAWPFCGRIRVRVPVSWLGE PGRGLIPGSGSAASSECLPGLHG RAPLGTSCRPGRPLP/WNQPPPR LAQPGHRDPDADAATERPGLQ RPSRTACERFPMGVSVRRRVEA HSQGVPELRD
8000	38368	A	8055	3	277	GPPRPPA*RGHGGRPENT/PAPP RWPPPP/PRSPAIPPPRRACADV THPPVPTPGKRTPPPIGGAPAA AAPRRPAPSCFSAPTPGCSLTG
8001	38369	A	8056	3	179	PPHPQGP PPPGRPPGC*RPI/QG RQVFSMKPGRTPERTAWS/PPY PGCLGSRPRRPSAPA*SGAHCV VAPYPGCLGSRPRRPSAPA
8002	38370	A	8057	3246	4682	ENTLSFASFFFFEMLSLCPGW SAAAPCQLTAASTYVVKRFSC LRLPSSWDYRRAPQHANSFCI FSRDRL/TMLVRLVSNS*PQVI RLPQPPKVLGL*ACCGFCGSS GMAPGCGRVVSHAGAPGGGTR PP
8003	38371	A	8058	3	718	LTRLVLSPADP/RATHLIAA/R AGTEKVLQ/AQE/CGHFHVNP DWL.WSCLERWDKIEQLFPLR DDHTKAQRENSPTLPDREGIPP TALSHMPILPKAQPSPEVRIYD SNTGKLIRTGARGPPAPSSSLPI RQEPSSF/RVDDILGEGSDSDS EKRRPEEQEEEPQPRKPGTRRA RTLGA PASSERSAAG/SRG/PRG HKRKLNEEDAASSESSRESGNEY EGSSSEADEMAKALELNDL
8004	38372	A	8059	273	468	NVGKTAANGD*G*RGEAAPAG RSRARVPEDAASSESSRESSNED EGSSSEADEMAKALELNDL M

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8005	38373	A	8060	1	2886	MEVPAAGRVPAGAPTA AAVE VRCPGPAPLRLLEWRVAAGAA VRIGSVLA VFEEAASQASAGAS QSRVASGGCVRPAPRPERRLRSE RAGVVRELCAQPGQVVAPGAV LVRLEGSHPVVMKGLCAECG QDLTQLQSKNGKQQVPLSTAT VSMVHSVPELMVSSEAEQLG REDQORLHHRNRKLVLMVDLDQ TLIHTEQHCCQMSNKGFHFQ LGRGEPMLHTRLRPHCKDFLEK IAKLYELHVFTFGRSLYAHT
8006	38374	A	8061	2	680	
8007	38375	A	8062	658	1657	PGILSLRNALLTGVDCKVVVPV PPGHTHPQLRLFHFHPKTCSGW GEWGDHGVVWAGPAPA/YHL HRDVPQALWTNDHALAWP*AM TSERTLWPGHELSARPGRSWRI SCPTGLPQGGDDRTRGHWVTA TCCSADGLRLCRYGD/GVRRGL PTVAWP*LTGCSLRYGSGQQC CYTADGTQLLTADSSGGSTPDR GHDWGAFFRTPPRVPSMSHW LYDVL SFYYCCLWAAPDPGKD RAGLGCTPT*PSTLTASA FGD HFVTFDGTNFTFNGRGEYVGM G*NQGGRLPSGSRSAPTTAGT ETRTGTLTAVAVQEGNSDVVE VRLANRTGPER
8008	38376	A	8063	873	1791	RCAGCPHSSSFERRGQ*AAVGP CCHGGTYRKASSV*RVSV*HPP HDRGSRK/QSLSGR*STGLS*MP SGVASSASV*FVNVSLSASN*L AQSTARFPFGSVRGLGQGRAG GG*APGHGADHPTGRQHS*GSP APVTWLWWPPRHQAALAPAP STTPYDNSPLHCRPSGSPQSSHP HSALPGT/VPGSSPLEIVPGSSL YVS*SLIRALAAPISSSSVGKNC RCTERLAIKPAESCRTRSSSAG QSVFSRFTSL*AFTG*AR*PSAS AADLLVKASILLAQLLILESAS STRMYSFRDCTSSFSA

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8009	38377	A	8064	2	935	YSPARGSGRGLSRRPGAGRRA GQGPQVVGAPKPGGA EYVVRWA AGGMKGAGGSSGSGSGSRE AG*PGVPRGRRGWRTPAEPPG WGPGRRAQACGA*G/EGRAAAQ VGGAPAAAGGVAREEAPS*P GDAAGSGTPGAASVQVSAPP AQPINLSAGARAGVARRCVC RGAES*GPGDPGPGSRR*PPAA QSGPPPCPSALFLHPSGFLCRRP QPSRAQGGVEVGALRAVPRLSG GAGNLAAALPCQLPGSGGLTPGC /QASQGLGVGLVRAGPAWSPL DGPLDQKVFSPTSLWNQRCFS LAAAGPVIIIR
8010	38378	A	8065	3	367	
8011	38379	A	8066	2	1246	TPAWSREILAEELCTPPDPGA VVECPDESFQICENATFQRY QKGADAPVALVHHMAPASVL VDSRYQQWMERFGPDQHLVL NENCASVHNLRSKIQTLNLI HPDIFP/AAHQFPL*EGGPHQC AHGSG*MPQVPAPFQE/WSAR GMPLLLAILRNS*LRRCSFPTSS RALQEYRRSAQDGPAPAEKRS QYPEHFLGTGSAIPMKIR/NVSA TLVK/QSPDTSLLLDCGEGTFGQ LCRHYGDQVDRVLGTAAVFV SHLHADHHTGLPSILLQRE ASLGKPLHPLVVA PNQLKAW LQQYHNQCQEVLLHHISMIPAKL PSGRWLRSPLQWKD*FSSLLR TWIWEFQTCLVRHCKHAFGC ALVHTSG/LKVVS GDTMPCEA LVRMGKDATRKADELISFQG
8012	38380	A	8067	121	880	GAAASQLPAPQPVPGGPAPH QYDSCQMPSGRG*DLQSCSGKI DQFA/AWTTCDLEEFQTCLVRH CKHAFGCALVHTSGWKVVYS DTMPCEALLVRMGKDATLLIHE ATL/EDGFRKREA/LEKTHSTTS QGHSAWGMRMNAEFHY/VLN HFQARRY/SKVPLFSPNFSEKVG VAFDHMKVCFGDFPTMPKLI LPP LKA LFA GDIEEM/EERREKRELR AGAGRPSCSRGAGRRPLEDGE P QQKRAHTEEPQAKKVRAQ



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8013	38381	A	8068	1	607	SPGSWETRLVWVSFYRSCCKHS LCPCLVGEFLVFNSPMQSGSAG EPPRLQF/GAPLPGAAPGNYRRT GRGREGPWPPPLAPSLFAFSDL GSSPGRTSWRPPAVSRRLGPTFP PPAPGRGRPRRAA*TGPSAQ/PP RSLSTLSPAAPAVRTAPPVAS PRAAPAPLRAITLLATKSEELPV VSFFSSRLVLAKRPKRLAQMH WGH
8014	38382	A	8069	1	290	QFLDAESGSAGEPPR/LAVPAPF PGGAPGNYGRTRGRGREERSWP PPLAPSLFALSDFGSSPGRTSRR PLAVSRRLGPTFPPPLPPAPGR GRPRAP
8015	38383	A	8070	1	565	SPGSWETRLVWVSFYRSCCKHS LCPCLVGEFLVFNSPMQSGSAG EPPRLQF/GAPLPGAAPGNYRRT GRGREGPWPPPLAPSLFAFSDL GSSPGRTSWRPPAVSRRLGPTFP PPAPGRGRPRRAA*TGPSAQ/PP RSLSTLSPAAPAVRTAPPVAS PRAAPAPLRAITLLATKSEELPV VSFFSSRLVLA
8016	38384	B	8071	475	913	
8017	38385	A	8072	145	275	
8018	38386	A	8073	1	310	VEELTARTGGGAPPGCQADAK RMPQFPQRTPWGHGFAGAPFP ISKPHGPPAGQL*PG/PSCEQT/E PPSPVNVTVTHLRANSATVSW DVPEGNIVIGYSISQVQV
8019	38387	A	8074	1	483	GSHRVGRWAALCDRAAPRGLT NRETGGGAPPGCQADAKRMPQ FPSQRTPRGHGFAGAPFPISKPH GPPAGQL*PG/PSCEQT/EPPSPV NVTVTHLRANSATVSWDVP NIVIGYSISQQRQNGPGQRVIRE VNTTTRACALWGLAEDSDYTV QVRSIGRL

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8020	38388	A	8075	2	854	RPPAARARRWLKPKSPARRSRR PAHRCRRRRRTCTPQATRPGMR *APAAACGPTGRRS/RLPALKI. ALEYIVPCMNKHGICVDDFLG KETGQQIGDEVRAIHDTGKFT DQQLVSQKSDSSKDIRGDKITW IEGKEPGCETIGLLMSSMDLIR HCNGLKGSYKINGRTKAMVAC YPNGTGYVRHVDNPNNGDGRC VTCIYYLNKDWDKAVSGGILRI FPEGKAQFADIEPKFDRLLFFW SDRRNPHEVQPAYATRYAITV WYFDADERARAKVKY/RNR*K RCEG
8021	38389	B	8076	1	205	
8022	38390	B	8077	1	806	
8023	38391	A	8078	1	2279	MKVGLDQIIEVVPVSHSVTSAGAA AGECGGVHCDSVCAEGRWGP CSLPCYCKNGASCSPDDGICEC APGFRGTTTCRICSPGFYGHRC SQTCPQCVHSSGPCHHITGLCD CLPGFTGALCNEAYSQ/SCPSGR FGKNACIGICTCTNNGTCNPDR SCQCPGWIGSDCQPHCADKC VHGRCIAPNTQCCEPGWGGTN CSSVKKQSTVCFES*KCEPWEER PCGGLHWDIAG*/P/GKHGGYL NELGAFGLDRSYMGSLSKDLG KNSEYNSSNCSLSSSENPYATIK /GPTCTYPEKLRVWLCGDEIAG TKRFPICRDQ*LNFSQQECL*S* TYSECCPRSIQQ*WASFPQSI*PP KNSHIPCHYDLI.PVRDSSSSLK QEDSGGSSSNSSSSSE*/APKDR LGLLV**RS*SM*TNRLAKHPK QPGRKGPKI**HGTWKSSQEK/ HAEEQSGKLAATLCCKDWLIQ REGWPYILSRMFL/CFISTDGRE SESLWRKSNKSKFK*WGRPG KCGL*EGQREEVWGLGNSLYC LAGQL*CLDCECHH/GFQECPP VLGHSWGYKS/CLNRNPLKGLS SRCAGLAVRDSLAPNSQGWKA TFDFPSLECPSTGYGYGCRQICD CLNNSTCDHITGTCYCSPGWKG ARCDQA/GCYHSWKSEQLKPN QYCSPC*FLPDRGHCRHHHSCP SCSLPTGIVHYL*TAEGKGKIKH
8024	38392	B	8079	1	2909	

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8025	38393	A	8080	332	602	NSLSNRWLKGLPGAPGIQEIKE MWRCMSSICQKEGWRTAGS LGHHRSLLHVQG/AGNDVDRT GSLPASVR/QHAYYTASSVEGR VSYKLYT
8026	38394	A	8081	2	422	FNISLGFACPLRIDFFGWFFVF LSWSFTLFAQAGVLWCDLGLS QPPPLGFKKFSCLSLPSSLDYRC LPRLTNF*FLVEMGFHHVGO AGLELLTSGDPPASASQSAGITG MSHRAQSAALSFK*SGISKNRY FIFWA
8027	38395	A	8082	1	951	
8028	38396	A	8083	1	924	
8029	38397	C	8084	271	738	
8030	38398	A	8085	1	575	
8031	38399	A	8086	2	332	
8032	38400	A	8087	1	897	
8033	38401	C	8088	181	804	
8034	38402	A	8089	1	1923	
8035	38403	A	8090	294	2340	EKCRHNCSRVWQSLVSQSVW ATEGQYGRKTNARPVQVKIDS ASFPYQRRYPLRLAEAQGLQKI VKDLKAQGLVKPFNSPCNTPI GVQKPNQGWKLVDLRINEAI VPLYPAPNPYTLSSQIEEAE WFTVLDLKDAFFCIPVHRESQF LFAFEDPSNPTSQTLTWVLPQG FRNSPHLFGQALAQDLSQFSYL NTLVRLYRDDLLAAHILETLCH QATQKKTGIALGVLTQVQGTSF QPVAHLSKEIDVVAKGWPHCL WVVAAVAVLVSEAVKIIQGRE LTVWTSHDVSGTLTAKGDLWL SDNLLNQALLFKRPVRLHTC ATLNPATFLPNNKEKIEHNHQ VIVQTYTIQGDLLLEVPLTDPDL NLYTNGSSFVEKGLRKAGIHPS RQWTPLPKAGPEMLSKRQVL ESGILKAFVLPYLLVAVLGSIDF NGKPPVAVFSLSQAHFLCAT WLLGYGEVWIHSHTAIKTYQ RRRSQDGRIGTAPVYSSQRRR RRRVISAFPSEGIPDLQLRVLS VRRKTNKQKGHPHQPICTSPS SRPKVDKTTKMGKKQNRKTGN SKTQASAPPPKERRSSSPATEQSW MENDFDELREEGFRRSNYSEL EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKARELR EECRSLRSQCDQLEERVSAEMD

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8036	38404	A	8091	158	865	NPAARTPFVVIKKGGKRGEGL AKAGAIHILNIG/GTPVCCPLE EGINLEDWATEGQYGRKNAR PVQVKLKDSASFPHQRQYPLRP EAQQGLQKIKDLKAQGLVKAC NSPYNNPTLGQKPSGQWRLV QDLRIINEVTVPLYLAVPNPYIL LSQIPEEA EWFTDLDLKDAFFCI PVHPDSQFLFAFEDPSNPMSQL TWTVSPQGFRDSPHLFGQALA QDLSRFSYLGTLVLWYVD
8037	38405	A	8092	1	748	MNQSDQEMTGAFVHMKSYTG LISGVAVKMERHIYQDRRIAIEK EFNSCRTGCMGDSWFTITQIRL LENTGIRVFKDNLVEAEWFTV LDLMDAFFCIPVHPDSQFLFAFE DPSNPASQLTWTVLPQRFKNSP HLFGQALAQDLSQFSYLDTLVL RYMDDLLLAAYSETLCHQATE ALLNFLATCGYKVSQPKAQLCS QQVKYLGLKLSKGTDRDITFLP VNEEKIE/P*LTSTNCSKLRCRSG TSRGS LG
8038	38406	A	8093	194	1377	NPAAQTFFVVKGGKRGAGL LHRQYPLRLKAKQGLKKIVKDL KAQGLVTPCSPCNTPTLAVQK PNGQWRLVQDLRIINEAVVPLY PAVPNPYILLSQIPEEA EWFTVL DLKDAFFCIPVHPDSQFLFAFED PSNPMSQLTWTVLPQGFRDSLH LFGQALAQDLSQFSYLDTLVLQ YMDDLLLVTHSETLCHQATQV LLNFLATCGYKVSQKLAQICSQ QVKYLGLKLSKGTALSEERIQ PILAYPHPKTRKQLRGLLGITGF CQIWIPRYSEIARPLHTLIKKTQ KANTHLVVRWTPAEAAAFQVLK KALTQAPVLSLPTGQDFSLYVT EKTGIALGVLTQHYGEERNS*L PTEYLSNIRKPLGDYYWLYRNL KRWQSYTARVIRKERKGGK
8039	38407	A	8094	3	521	

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8040	38408	A	8095	1	3203	DSPLSTKAMLGMLVKDHWSPA AQTPEFVIKEGGKRGAGLHGGQ LILKDKFITQSAADIKEKLQKST LGPERNLKTLLNLATSVFYNRD QEEQAERDKRGKKKATTLVMA LGQADFGSGSTRKAWANRMP NRAYFQCGLQGHFKKDCPSRK PQVCLTIESQEVNCLLDAGAAF SVLLSCPGQLSSRSVTIRGLGQ PVTRYFQPLSCDWGALPFSHA FLIMPESLTPLLEREILVKAGAI HLNIGEGTPICRL
8041	38409	A	8096	13	183	VHLHPQGHVPVKHTPTGLGYS SCRHLLGRACY*KGEVGA GMQVSDALPRLGGVS
8042	38410	A	8097	1	2427	MSKFSCASLTATESDGTPLMEQ YVPCPVCEAWAQTDPSEKS EDVQYFDMEDCVLTAIERDFIS CPRHPDLVPPLQELVPELFMTD FPARLFLNSKLEHSEDEGSVL GQGGSGTVIYRARYQGQPVAV KRFHIKKFKNFANVPADTMLR HLRATDAMKNFSEFRQESML HALQHPCIVALLIGSIHPLCFAL LAPLSSNLTVLSENARDSSFIPL GHMLTQKIAYQIASGLAYLHK KNIFCDLKSNDILVWSLDVKE HINIKLSDYGISRSQSFHEGALGV EGTPGYQAPRIRPRIVYDEKVD MFSYGMVLYELLSGQRPALGH HQLQIAKKLSKIRPVLGQPEE VQFRRIQALMMECWDTKPEK RPLALSVVYSQMK/APDFCHLV *TVLWEADSLLLIPGPGVHRGV LGWKRGVQELHGGNTEKGLM EVQRMCCPGMKVSCQLQVQRS LWTATEDQKIYIYTLKGMCLN TPQQALDTPAVVTCFLAVPVK KNSYLVLAGLADGLVAVFPVV RGTPKDCSYLCSHTANRSKFSI ADEDARQNPYPVKAMEVVNSG SEVWYSNGPGLLVIDCASLEIC RRLEPYMAPSMVTSVCSSEGR GEEVVWCLDDKANSLVMYHS TTYQLCARYFCGVPSPLRDMFP VRPLDTEPPAASHTANPKVPEG DSIADVSIYSEELGTQLIHQE
8043	38411	A	8098	1	1641	

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8044	38412	A	8099	1	1075	VLHKFPYRMVLPALPKRMLGA DREFIEARRRALKRFFVNLVARH PLFSEDVVLKLFSLFSGSDVQN KLKESAQCVCVDEFLNCKLATR AKDFLPADIQAQFAISRRLIRNI YNSFHKLRNRAERIAS/RAIDNA ADLLIFGKELSAIGSDITPLPSW AALNSITWGS/LKQALKGLSV E/FALLADKAAQGGKQ/EENDV /VEKLNLFLLQSYKDLCE/R GHEKGVF/HTKHQALAQSTA* LKRPD*LSATGAEPSPPEVRGS KLKSRIRGARENAQTMELRN YVFSLYCLHQETQLIHVYLPPTS /HILRAVFNVSQIQGHKEMSKVW NDLRPKLSCLFAGPHRTLTTPPC SPPEDGLCPH
8045	38413	A	8100	1	974	MPQVPAP/PLPSITSGHPGEP/PA RPSCSCLFSPQPCNSITPSSLLLR QLAVAAAGCGGHGAPALSST GWQQVCKSPQVRSVPDNPTTA DSTASLWKFGVLRSHINGCY K*KQQPLLVPVHAQRRRAQVAP/ APPAGLSCGQHS/LPQPPRCSDLS LGLHPGR/LPCDRGHCPPLPPVT PTPDKAGPILDPAQSCPCPSIPA PPKQSPPARFPPEMKRKKTLM MPPSEGSLSLASGMEASVFQRL LSRCTCLDQATVIWGFYCMQV QASQGIQPCRGKDELLRLAPLPV KEARRTKPRSPGKHAKAPPSSS ACSPHLCSSPILQALD
8046	38414	A	8101	1	460	SLQAPRRNSRAEHTRTLNSECP RRRRCCIKGCTYT*LDVAPPPP VLDWLVPKPRWLGNGWLL DGPPEVLQAEACSTTIDGAEP LCPSGYECHILSPG/DVAEGIPN RGQCQVKQRQADGRILRHKLY KEYPEGDSKNVAEPGKGQQRH
8047	38415	A	8102	3	219	NNHRLDRTLPRDYCHAATAYT THELAFGDFRLPTEGHQELCHN SHLIYFRDK*THCTWRSVDSL TGVTHR
8048	38416	A	8103	230	555	NVRPS*ALQAPWGRHHLCVTP MQLRMTLVVSSLGKGTGGLSL AQ/CAPVQEGTHGSGPPVEGWL AATRTCEGCRRENTMKNVGSR KYAFNSLQLKAFPKHYRPEDL RKS

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8049	38417	A	8104	23	304	KGFLYLFNKQTIEQTNNNGSKSFA KRNTTEGHDDLQLQGFQGSQTPTS FLSSSGRCYSWGAIGPIQFGALS GfSPFPFSAANRQSSALDFWIT TSISF
8050	38418	A	8105	99	375	VLEFGALSGSLISPLCTIPALVE PPCGPQPSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSPQGVQ LPLGPRRLKMNTEPTTRP
8051	38419	C	8106	5	376	
8052	38420	A	8107	545	990	GLCHVLQPCDPCLPGMTQEAQ PPEVLKTAGKAGGQEPG*.*RIP *GSLCPPCPVAFGAAELPLPSS DPVSRGTGAPPQG*WLGFGYFS SNEGSPQAGG
8053	38421	B	8108	252	801	
8054	38422	A	8109	169	1226	PNGLRPPCPSPASETPGNAPVCD PGSSSQGAQKKLKPGGI.PGWL FPFFAQPSPEGL/CPCPCPVAFG AAAEPLPSSDPVVRTGAPPQQ GSW/PI*SPGSRSGTRADPVKGE VAGRERCLPIE*ASPPPPHSG* AGQVPVGAAPRTAG*GV*TGTA PCPKAOPRK*QR*RCSS*VG* ESAEIVCPQGDAG*RGKSP*/G/ SHRRNVPS/RYSNSHGPYDSNQ PHRKTITFEEDKVDSITLIGSSS HVEVEDAVHIIPENESDDEEEE EKGVPVSPRSPKRP/PSATRAAA SRLRGS*TLGGLLGCIFAFFAPP SPTEGACAHQAQSLSGPLRSFRC HLRLCPARGLHQGRDDG
8055	38423	C	8110	58	504	
8056	38424	C	8111	203	1874	
8057	38425	A	8112	32	1026	KLLEQCLHSVSTWETPQYRRPP SPS*RGSRQPCSFSSPRDTPGE NHWLSLPQRD*AGPPVR/PSAG GFMTTP/PPRGVPTVEVPPDPTC/S PNHTRPFRPPFSKNPCFRFEPL RAPTLVPGPLPPTHGVRVPHLE RNL.SALGLGKSEGLKRNPCVEP /PAPTPIREFPKITGTLPLR/PAADH ALLGMRDQSLSGQSPGPKSPDA DDQLQNRDHTETEQRISGRSS ALAPESQLQQGCAGIHFRGRFC KAPPLASGPA/RPPCLSLPPPWW APVRPKPPR*APPAP/PVPSPIN HPRAEECGRTARDWQAAPLAA LVRDPLDEASWAPESGGDVEN LYV

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8058	38426	A	8113	3	909	TEGGASHRAHPVGPAPRG/KRH SGATEPANGTWARRRGPRGRDS SNQSSGGGERSQLRHRGWRL SRPLLPPGAASPLAGEDPERNA G\GWRRGGAAPMRPKRGPMNGG GCGPGAGSGAGGEALGRGRGA VSGCRPAPPVRRPPPPPPPPGG WLRRTAGSGPEYV/GSRCARGS GQVSAGGGLCARAARGGKLAP RLRALRGRSPWPAPLGRSPAR APARVPAGRCGPGA*RGRCAL GGQGEAGPAGSEGAGRPLGRP GCPGTSRLLPRRPVRKTDVGN RSSFFPRAPGRAPHACQPTQFLII
8059	38427	A	8114	1	454	
8060	38428	A	8115	2	172	MFIYTSAFI*QFTNSINIPITSFC *TASVHLSICIVAFCHPCQCSS SFIQCTTN
8061	38429	A	8116	1	594	LAPVFKLIPMPVS/YGIFLYMG WAALSSIQFTNRVKLLMPAK HQPDLLLLRHVPLTRVHLFTAI QLACLGLLWIHKSTPAAIIFPLM LLGLVGVRKALERVFSQELLG LDELMPEERSIPEKGLEPEHSF SGSDSESELMYQKAPENISV N*LE*ESGSGDPRKQHEVLTQE VRTFLAFLGTSRCSVGLGKD
8062	38430	B	8117	1	3402	
8063	38431	B	8118	1	4614	
8064	38432	A	8119	3	435	DHAKLGTRTSGMRPHSLSLCFF SSSYDILMRITKDRVKNLTCITY TILPTDLQPGCGLPRSFYPPSSKP TSFWLWACKLFPPLPISFNPSPA HSKTAHGHSKGKHTAAGM*WS* TGEGITGRCCFVSIKAPLPSSG PVGGPVGG
8065	38433	A	8120	1	525	MALLPTVLCLWAQAQFLVDLG QNSKHHQEHQLAPDVAFKMK GACVCAAGFRGWRCCELCAFG THGKGQQLPCQCRHGASCDPR AGECLCAPGYTGVYCEELCPPG SHGAHCELRCPCQNGGTCHHIT GECACPPGW/IG/TV*GPPSPGSL LGCLPRETSLIISLQLCLYLLL



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8066	38434	A	8121	1	1050	MLIMTFHGLLPCMQMACKWQ LRVLVAGIRCDSTCPGRWGP NSVSCSENGGSCSPKDGSC EAPGFRGPLCQRTVHILYPRGCGI RDVGESGNRKQKAVEQYREH WTVSPEVQCSASHFSSVRPKSA CPPGFWGPACFHACSCHNGAS CSAEDGACHCTPGWTGLFCTQ RCAPGTFGYGCCQKCECMNNS TCDHVTGTCTCYCSPGFKGIRCDQ GIMLL/CPHCGAAGPICLASAA AEREGRPGSPCLLHTCHEDDQ HRLPLSGANSIPTYR*SGRPDS PLRTEALILPQCKQKFGSGQGEV CAVSCAAGTYGPNCSICSCNN GGTCSPVDGSCCTCKEGRILCLQ
8067	38435	A	8122	3	732	IRCDSTCPGRWGPNCNSVSCSC ENGGSCSPEDGSCCAPGFRGP LCQRICPPGFYGHCCAQCPCLC VHSSRPCHHIGICECLPGFSGAF CNQGIQAPTGNPSGWYRS*EM TDPRCSCR/CLSGESTRHTSPVL LGTDASETQVIGFVNLAQFLIIC PRKLHYKAQNSKKSNGSDASS DWKDWGIWDRESCCELCPPGS HGAHCELRCPQNGGTCHHIT GECACPPGWTVGA/HC*ALCCP
8068	38436	A	8123	77	864	PAVPEL*VFQAKPERKSRYWQL HFPFHSSSPTS WRKSLEPMYRC TCPPLTPYGCTCPPLSPYRRTCP PLTMYRRICPPLTPYRCTCPPLT PYRMFSSPLHKEITSAQRSPEPS SRPHSSKAAALR*QPRIMEKQRI YGPSPTSVQPASPPCLDDPRKK AERPDHRATGKRHLPETSL/YA ELVRRAPENPEDSEAPAPAPAA LSPASEHRTDPIQETKKARKSSD NDGSTPLAQTPTRRSSQWPRLG QFQQQEDDSSGLYSTG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
8069	38437	A	8124	314	1188	KHFLNFCPLPYMILNKYRNQYCT FNDDIQGNKIFTAYGSITCLKI.V HNCIKKIWL.VDSKGLIVKVRIC HF*PE*R*LCHSGWPSNLEAIVQ EIKPTALIGKHFLLSLLPYPLF*P DCFFNERPIIFALSNPSTSKAEC AEQCYKITKVK*NYNRYFNNOI FIHYREATLYPGQGNNNSYVFP VALGVVACGLRQITDNIFLTTA EVL*NPLSLPRV*NTKCAQPRN TIRDVSLKIAEKVKPLLKLIHYF SFLFLNNMQEAFVRSQMYSTD YDQILPD\CYSWPEEVEQKIQPQ
8070	38438	A	8125	1	1115	SPAQVMFQCLWKSCKVSLSTA SAMQRHRLVHLGRQAEPEQSD GEEDFYYTELDVGVDTLTDGLS SLTPVVSPTAS\IAACLPPPGAAR AAGAPSPA*SPAACPAAPAP CPEHRC*PPVLSQ*PCLPRAA*R PPAWSRMPRRLEPAHPPCPPGS ESS*GSPAATRISAGM*YGMEA PGPPGAQPAAGRKP\PAVPLGL SGSFKNIKLPSPSPPPGPGAET ARRNKPGGAGSPAAAGSAFNW VGVPDLTLEPPPPGPEGSPPT QS/SPLKKPSFLH*SPNPHLSPF TPKGGGSHPSRLSARRFIKGV MGPAALGGQSRCTLRGVGEGTP PLALNSTALGPWGCIFYPCFLFK LQVSHVWAATRRREKLKI
8071	38439	A	8126	116	333	KLRDRCLSH*K*NGASPPRPTN YSIMRPSLV/SLVHHSGL*FPQM LRALS*LRVFGVA/VSSP*MVPL NPCIIH
8072	38440	A	8127	5	829	KPSQPQPCPRPGPPRARFLRRSP DVEKIPFA*RPCDVRGRPPAGG ARRRAASLG/PWVRRRLQARPG /LFRPRDFYLRSPRSYGRTP*KSP QSSPRGSARPD\GPA\PPPEPPV KRRARGVLESSRHAAPRRVFHL GREREQSQEGPAWPKRGRPAPS PQRTATWRPAAGGGK*GSAAT S*ARAGPARRGKRRG*EPREN RAGRPA TRGRPGRRCPPA*S PRPSKRSSPLCSPPRSWPTRPS KSSYGASLARTTTLQWKFSVNL IRKQIRDAQ

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8073	38441	A	8128	5	844	KPSQPQPCPRPGPPRARFLRRSP DVEKIPFA*RPCDVGRPPAGG ARRRAASLG/PWVRRRLQARPG RFAPGTFTCGAPRSYGRP*KSP QSSPRGSARPDGPAAASARATR EAQSARGLGELAAAGSQAGLP LGKGARTEPGGSS/CSQGPAPW KRGRPAPSPQRTATWRPAAGG GK*GSAATS*ARAGPARRGKRR G*EPRENRRAGRPATRGRPPGR RCCPPA*SPRPSKRSSPLCSPPPS WPPTRPSKSSYGASLARITTLQ WKFSMNLIRKQIRDAQ
8074	38442	A	8129	795	914	RGIRLASEMYPLTCFWRs*LYR RGLARIALVNCRRNAL
8075	38443	A	8130	4073	5350	YSLKSGSVTPLALFFLLKIDLA MQALFWFHVNFVKVFPNSVKK AIGSLMGMTLNL*ITLGSMIAIFT ILILPTHEHGMFFHLFVSSFSLS NGL*FSLKRSFTSLVSWIPRYFIL FEAIVNGSSMLMIWVSVCLLLVY KNACDFTLILYPKTLKLLISL RRFWA/GQWGLFDIQSCHVQTG TI*LPLFLIEYPLFALLPNCPOQN FQHYVE*QW*ERTSLSPVFKG NTSSFCPFSMILAVGLS*IALIIL RYVPSIPNLLRVFSMKGC*ILSK AFSASIE/YNHVVFVFGSVYMQ FLLVPLVEFGCESIWSWTFFGW *AIDYCHNFRSCYWSIQRFNFFL V*SIGRVYVLRNLSSSRFSSLFA *RCL*YSLMVVCISVGLVVISPL SFFIASI*FLSLFFFTSLASSLSILL IFSKNQLLDSLIF

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8076	38444	A	8131	1	1715	MDGISGGKRALRERHSKSKAL GRCPFWTNIPTPALPGITNDTTI QQGISGLIDSLNARDISVKIFEDF AQSWYWILVALGVALLVLLFI LLLRLVAGPLVLVLGLVGLV AYGIYYCWEEYRVLRDKGASIS QLGFTTNLSAYQSVQETWLA LIVLAVLEAILLVLIFLRQIRI AIALKEASKAVGQMMSTMFY PLVTFVLLLCIAYWAMTALYL ATSGQPQYYLVASNISSPGCEK VPINI\SCNP\TAHLVNSSCPGLM CVFQGYSSKGLIQRSVFNLQIY GVGLFWTLNWVLALGQCVL AGAFASFYWAFHKPDIPTFPLI SAFIRTLRYHTGSLAFGALILTL VQIARVILEYIDHKLRGVQNPV ARCIMC*FKCCLWCLEKFIKFL NRNAYIMIAIYGKNFCVSAKN AFMLLMRNIVRVVLDKVTDL LLFFGKLLVVGGVGVLSFFFFS GRIPGLGKDFKSPHNLYYWLP MRNPITPTGHVFQTSILGAYVIA SGFFSVFGHVCGRSFLCFLGK DLGVSNNGFPGRPY\Y/MVPRA FLKILG/KKNE\APPDNKKRKK
8077	38445	A	8132	1	208	GTRASSAPCPSSSAPAHSEAC CCRMSLWGSCGGSGDGSSACG SGWNLSMAGTSCSPAMCSPSR APS*RSASRPRTWRATTSAA WAPRRCWCGWA*SAT*PSSTTT ISSSPHCGWPCPASCASAAAWL SSTWATASVAGSCWGPIM*SSA PAHSFEACCCRMSLWGSCGGS GDGSSACGSGWNLSMAGTSCS SPAMCSPSRAPS

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8078	38446	A	8133	28	1956	SRAARERGRSDSGGRSDPGCPA VPACVPRSRPMTAPAGPRGSE TERFLTNPNGYGTQAGPSAPPT PPEE/VRPSPSS/TNTFS*VPATSF EPRAASPAS*CCKWSRSWWSR CSSSCLGSVISWL*HSGKRTPSP SDTSSCWATRTERMTSPQPTRG SSCTRPSSMLWT/SAGGRAGAG GQAGAVPGVA/WTCHWAGLLS ASGTTTEATWTRPTTHLTLIRW WLLTASRWIPPSGPLRPPATISP SWKAAPVTRTSRSNSTSTACSL EGGPGVSTWQGTALALGAGRDP KTPLTLTRASCLGWSMSPSTSG *RPLTSRASSIMRSRTAIPAS*S RLTTKHTVGGSPSAWRPRPTSR SVSTPVSSSTGGQLPGSCLTW WSYSPACTSSSPLTPSRLPAA EQSLWGSCGGSGDGSSACGSG WNLSMAGTSCFVTSVDLHHLG HHS*RSASRPRTWRSRRAAAS SWAPRRWCOWA*SAT*PSSTT TISAHSPWCLSACSRSSMGTTTC L*RSPPCRRSRAAAA WCGSSPS STFTPSSSLFILHGAQPLHRAHH RAPTYTIKHSRRRRRRKRASC PYIAQCPGPHLRQVPPRERAR PIAILLLLRKGPLGGAFAAGELI RPDCRWTVGPGLQRPPPTPLIY L
8079	38447	A	8134	1	2994	MQRPCLCVEPMRLCFDSFLLLV NQEEEEGVVPCLEENGRAAA DPGPQDQDCLLPTLTPSLSGDE APDRTOSSGDPRERCGYLSVTC EEGDNRFAAFCLCGSWRLNHG HADWCDQRRSQISNRLPASLGII VGTGRSRHLLAALRGVKEDRQ TKGCVQTPASLPWLPGLSSET RAQKTCVLLIDYATFLKLAND DDDGCLDCLQPGVRTA WASSQ HGIRAPRKSVQGSASSPSLRTW ALTCTQNWFCVLLVK
8080	38448	A	8135	215	418	

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8081	38449	A	8136	767	1458	WREHLTKFNVWGKQHLESLSN QQKNMRCPVRSQTRPPTDVKP VSRSGRRDRRAAGGEGGADR QGPGTARARAPGSPQRGG*GR NLRIQAGPPGKHGRGIPPPQTRG RSRGAPPGTPEGPRHPPRPA PGPATGAPKRPQPQTQRQGHIA RDSRPSSDPVPLRETGAPPPWD A\SQGQAARPRATQTPSSAPVA TRQSGRRADSRRRGVTRRTER CAQPSLAVSRVPTR
8082	38450	A	8137	3	424	
8083	38451	A	8138	1	813	MVQKELEEEGRKSTPQSWGRE NMEKALNSSLKASLGGSGVMI CASVKALLTVVIKVLGRLLAES LFLLLQTQTAL*QTL/RHTNRNI SHQYQDEIHLDGSDLPMSRPR KYEPVPFGRKTYKISIRGKAN KKCEEARQEKEAMVMKYVRG EKESLDLRKEKETLEKKLRDAN KELEKNTNKKIKLSQEKGR LHQ LYETKEGETTRLIREIDKLKEDI NSHVIKVKWAQNKLLKAEMDS HKSFKNPLVR CNFAATFGYVK KLIPEIKTGSSH
8084	38452	A	8139	3	808	NVRVEPTDSSFMEIEFAQKGA FDAYVAVGGGSTMDCKA/AN LYASSPHSDFLDYVSAPIGKKG PVSVPLKPLIAVPTTSGTGSETT GVAIFDYEHLKVKIGITSRAIKP TLGLIDPLHTLHMPARVVANS FDVLCHALESYTTLPHYLRSPC PSNPITRAPYQGRNPISDIWGYS TRWGFVG*VS*RRAVQEIPMDL *KARSHIMHLASAFAGIGFNGA GVHLCHGMSYPISGLVKMYKA KDYNVHDHPLVPHGLSVVLTSP AVFTFT

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8085	38453	A	8140	2	1154	IDPLHTLHMPARVVANSQFDVL CHALESYTTLPYHILRSPCPSNP TRPAYQGSNPISDIWAIHALRIV AKYLKRAVNSTDK*RRRMSLR APSWEWPSRSGPARCLPRRFY IT*GS*QRYLLWPLETVDEKY VSLQFSFRQGVV*ITCLIFLPT *HFFHHHIF*GSSLFCRNCQC* CVIVRYLYHSQGWQKSR*S*RO GLIWHLGKCFLLGIGFGKCWVF ICGHGNNV/SYPISGFRWKDVIK KGIYNVGIHPTGWPPWAFSVVP HVPQRCFTFHGPRCFPERTPWR WQEILGADTRTAQ/RSQDAGLV LADTLRKFLFRSG/IVDDGLAA VGYSKADIPALVKGTLP/QER VTSFAPRQSEEDLAALFEASN ETVLNVHLN
8086	38454	A	8141	2	990	WENWISIC*RMKL/DPYFSPYTK IKSKWIKDINVKQPMKLLQEN IRETLQDIGLGEDFSQAQATKA KVDKLDHVFKFNCTAKETIN KVKRKPKEWEKILIFADYPSDK GLITRILFIDHSWVFLGEGNLAG SSDNSGGKAWKHLLPLLASRCS GTHSNLRAKLRLSQGTVAWTP VLKREGEKSCGPSESPDLGAPQ ARDVTPCLGICSSWLLQASGHH HIPWCQLWKLFFVYLVQLQPH REVALVPAPGAHPTTASVPVC AQWLDPMVIHSHTLCCSEPDSP LAGMGFRPVAQAKHNPARPSG WNESRPEQNLDKGATSHRGF WLAR
8087	38455	A	8142	1	196	GQYPWPLETNPRFLRE*TLPKS LQKSL*DSPVPE*SLCGTCQQA RSLSEEVDESSISQVCCPT
8088	38456	A	8143	3	413	ITLGKDCIMHGYML/KLGNPFL TQWQRRYFTLFPKNI*WRRRGE SRQNLLTMEQILSVEETQIKDK KCILFRIKGGKQFVLQCESDPEF VQWKKELNETFKEAQRLLRRA PKFLNKRPSGTVELPKPSLCHR NSNGL

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8089	38457	A	8144	705	1983	EIKVDSLLKSF <sub>LDL</sub> MNGKQNL ENLNALKDFAMMLNLSYATEH LGLEHMHNRFVYVYRDLKVRTI DRILHSRYCVNGPLEDKVTEK DFPGNPEIKPSIGKWLGCPS*KS PTLSQRGLMTLPCQTLGSG*LSF PE/VLDLP*WTNAHFADWFSLG CMLFKLLRG*VEMHPSSAVLM AAGAWMKT <sub>TV</sub> VRGFKTVFLSV W*LSCFIPSKRDVSKRLGCHGG G*AIVPAFRYLQKSKIVLN <sub>FQ</sub> YPPPLIPRGEVNAADAFDIGSF DEEDTKGKIVHM/CHLFLYFYF WM/VMISVGKQEVTTETVYEA NADTDKIEARKRAKNKQLGHE EGKIAHVSQNISNAVNQNF <sub>LY</sub> LTQWQRRYFYFLFPNLEWRGE GESRVSLRQPHRACFPVRTMAY GYWLLRAPKFLNKPRSGTVE LPKPSLCHRN <sub>S</sub> NGL
8090	38458	B	8145	156	281	
8091	38459	A	8146	2	181	VWCCSR <sub>TAL</sub> TRTRNCARRRCS RGSRTWKRSGRSSRRRAH/SQ YDLERLRAAQQLEREQE
8092	38460	A	8147	3	670	ETGLKNEGRV <sub>LV</sub> VRHSAWCPLL WGREGSRSSLS <sub>SW</sub> PELQGSPLC ASQGVVLQQDSYIEDQKLV <sub>LSE</sub> RALTRSLSRPSS <sub>LIE</sub> QEKQRSLE KQRQDLANLQKQQAQYLEEK <sub>R</sub> RREREWE <sub>DR</sub> ERELR/DGRPSWP SARRRCSRGSRTWKRSGRSSR RRAH/SQYDLERLRAAQQLER EQEQLRREAERLSQRQTERDL CQVMGLPAESN <sub>LM</sub> MILKTPCV LSKVRK
8093	38461	B	8148	47	699	
8094	38462	A	8149	1	242	MNRGGFAVKILALLDALSTVCS QRVQAKKQQH <sub>LQ</sub> NKEHFKFA LLKQKEKLKQ <sub>QED</sub> L/RKKLF*IQ GIRCPQATPHHGQCSL



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8095	38463	A	8150	3	929	ASSCVVRAVPPG/SGVWGFRG LCGPDCESGLISGRMFAGPQ G/PPGAGTAVTLAAEGEGL STAQHSGSLCSEEPVVRHA WQKSYSRNWLPPARPRPALA MSSDTRGQAQLSPSWQLEKKG LSSSTAQRGCRALQGRAASARR VQRKANPTAGTWLRLAPGLP LLCPQTPGGRHSCPPG/K/PGK EGLEQFYSSARLQGFAGKSRQV PDVTRKANPTAGTWLRL/HR GPRGGEACAMAVRGPRSHEQR CPWSAGADSVS*GHCEGTIDGR VASGACLVDSRGSAGQNPLP DPEHWHVFCDFP
8096	38464	A	8151	2	1749	WVQGASLCVRASRAPLPLAR* VQGAELTHPWGPAHP*TRNQ KPALGSSGPHSPHIGNPQTPTQA GQP*PHTARHGVPQEHGRQR GPHLHKTETPQEATP*EVGSIAT EQAWLPHLCL*RPFFHQLGLFP RGPCMEGAQQRVGESSAAGT QVCMGPKTAGDWDGPWLVCW FH*GEEAARILRPGLGGLSGHP LWPQGGQMTVGYGGASEAC GAGELLMRRAPPQSPGKARGL PA/HYWHQGTGPRKAEI
8097	38465	A	8152	1	583	MAAVVAATALKGRGARNARV LRGKERDPGEGRTAEDPFSFTS SPTIAGGILAGATA'NKASHNR TRALQN/HTASPEGKEEP*/DPLS PELENTFPRKEGQRTPMESCGN LPWAIIGFPLWFLPLSSFTQAG KWDK/VTVLKAD*RLRAEHCG FSNTGRV*RARRFRAFLPEVAPF PLMFGSGVSGGADLRVSCDPP
8098	38466	A	8153	141	341	GTRGSPSKKGERVRRDAQQT TW*TRSPASGCFQICEGNKQDE ACDVRGLQHCERHSLAGPREY
8099	38467	A	8154	1	521	MKNRSRNKGNVEWQAEGIRSK RSVGKQRPSPKAKIPSGDKNGVS LTHNEVINNDNPLESNDEKEGQ EATCSRPIQV/EFQQ**LFRPE* WRRASGNLQIPKKRVS*A*GTR GSPSKKGERVRRDAQQTATW* TRSPASGCFQICEGNKQDEACD VRGLQHCERHSLAGPREYMP

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8100	38468	A	8155	1	619	PEAELHNHGIQINSCSVRLVDIK KEKPPSNSKVECCQAQARTHNN QASDIHVISSEDESGSTDVDEPLE VFISAPRSEPVINRATPCELCX* KEG/QEAI/C/SRPRDVPRALGFR KFSPPFEESFRKGLLGQDPDFPD SIEKKPPAEASSGALRSKHGEK APMTSRSTSTWRIPSRKR/RFS DSDLSNGKELQETCSSSLRRG SGKE
8101	38469	A	8156	362	1043	PTTPPSAGSSWTTASPPS*GKA WLGTRPPSPWRRMSASMRT/S EEDGRLQPQLPL*AHPSESSGQ DRGNQVSVGREADCGQD/SPVS TMTRSHPGRPCAEGC**PCCSSR P*PCPCGSGSLVTSPLSLPAPSF WLPLRPSISPPGLPPLQSSLSFPP PPPPVPQPPAPPALQWGLHLPG VPQPGVPAGRRVVRSLAKHLPR LPDHSV*GAPGRRSLREHLPOH RPGDQ
8102	38470	B	8157	52	633	
8103	38471	A	8158	15	3054	AGPDGLAAPASCQGARGQTRV PGAFSWLAPGSHHASEGLAPG VPPAGGVSAQELTAPPQEGWG LGAPPAAPRPESDEKRAAGSDAV RSFSRGARDSLGQRRLGGTRGA GPAGKGAQRTMGPSAGFSFPP RPHQEPSRSCWQHLLWHCP WPQPSRLPRLTPAQLLQGGPGVL AAPPG*HVPGLAQSPWPLPS GPRSP*DPLHQGALVPLPQGGG PHTAPHCLPSVLSPI/QQPLPT AST/SRSPASTMAP
8104	38472	B	8159	748	3111	
8105	38473	A	8160	1	463	GGGGGRGQRGRSPRPRYLCPGP GPTG/GPGACAAGGVTVGPS NGRPLLPQRHPPVGVDFSRRC RFRLPKHKERSPDARFKEGPGG AA/GPGARGQ*DSARTPDSALK LVRPPLPIPTGRPSCASGGP*PA GKRGHLSAPPRPGRSSPGPSQP

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8106	38474	A	8161	1	2733	MALRRAGAGRTGCFIAIDTML DMAENEGVVDIFNCVRE/LRAQ /RVNLV/QTEEQYVFVHDAILEA CLC/GNTAIPV/CKLQNLFQNTK CTAMSNYTLTQGLLQHWSL*T T*FIWLAGTMRLLCLSLCVDAAS APWVLKTLNIVT/PRVRPEDCSI ARPNHDKNRSMDVLPLDRCLP FLISVDGESSNYINAALMDSHK QPAAFVVTQHPLPNTVADFWR LVFDYNCSSVVMNEMDTAQR GQSFFVGPLEFGGAQL
8107	38475	A	8162	1	307	
8108	38476	A	8163	3	969	GLFCSRKTPPSK*KHNVIASDK AAEKSVVHEHSHDHTQLHA YIGVSLVLGFVFMILLVDQIGNS HVHSTDDPEAARSSNSKITTTL GLVVHAAVFYVSLFPNIADGV ALGAAASTSQTSVQLIVFAIM LHKAPAAFGLVSFLMHAGLER NRIRKHLVFLAALAPVMSMT YLGLSKSSKEALSEVNATGVA MLFSAGTFLYVATVHVLPEERL KLVTVLGAGLLCGTALAVIVPE GVHALYEDILEVVPSPFYCHLY VVEYLMFSSSHFCSPDPWQDQL LTLRVCSSTSASLGEGLGVSSI RKGMELSVQAQHHVEVAKA
8109	38477	A	8164	164	240	
8110	38478	A	8165	2	417	QQIRKLIKVLIIHKPVIVHSQV GCQKSTFS/RTKGRHMGTR*R KSTANFQMPEKVTWMRRMRIL HWLFGRYHESKKTDHHMYHSL YLKVQGNMFTNKQILMEHNHK LKADKAHKKFLADQAEARSSK TNKASKLREER
8111	38479	A	8166	1	86	RTRGCLSHNNHH*HLHRHHLH HHYPYSY*HHHCLNYH/APYLF HWLYH/APHHLNQHAHYLHLY YHHHYNHHHHLHHHHRSHCH HHHHHLTIHLLCQHHHHHHPHT KHLLLAHPQALQTHHNNHDM/ HHHYPYSY

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8112	38480	A	8167	50	1156	LLLQFSRATFILFQPPANTFTSA FSQTRARRGGSGRGGGQESAEE TSEFGDRHAPEAAAAATRGSAR APEPKHASSCGTRGQCACARRE VEAQVRAKGDIVAERARRGGR WLTRSGMEHLERCEWLLRGTL VRAAVRRYLPWALVASMI.AGS LLKELSPLPESYLSNKRNVLVN YFVKVAWAFTFCLLPFIALTN YH/HDRQGWLGPAAD*/CTLLV GTAIWYICTSIFSNIHYTGSCY QSPALEGVRKEHQSKQQCHQE GGFVHGFDSIGHSFLLTFCALH DCKKRCLCLQ*R*KTDRLSHCLH TAITTLVVALGILTFIIVLMFLC TAVYFHNLSQKVFGTLFGLLS WYGYTGFVWPKAFSPRTSSPEL
8113	38481	A	8168	2	926	
8114	38482	A	8169	2	1053	TRERFSVANRVGTSETVPKAEA GPESAAGGQEEEGEDEEELSG TKVSAPYYFSFWGTLEYHNAMV AGTEEARDGSAGVRVLYLYPT HKSLKPRPVSLGKCRFKENC FSHGQVVSLDELRFQDQDPLSS LQAGSACLAKHQGWPLERQHA SPMWDNGYLSQV*LAAA\RE AVVGGGRHPAPTAKRPQESD SDS\EVVRTFAMPEWVGQMLW TLGPAALPLLGWVHTRGIGSR LLTKMGYEFKGLGRHAEGRV EPIHAVVLPKGSQDQCVETLQ KQTRVKGAGTNKPPRCRGRGA RPPGRPAARNVDFLNEKLQGGQ APGALEAGAAPARRSKDMYH CQCECQAGP
8115	38483	C	8170	166	419	

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8116	38484	A	8171	55	1157	ALDEPHGAGASEERAGDVFGPP RRVPGPSLWPLEAWPTSSQKV MPQVRCRLHLHQVWGQRGGPPR IKRWAWAARGHTGLGPTPHGP SWTHSNFLKEKIF*KMFAKQV GPEAKQSLPNGFPGVATAWSP VRSSVCPLFIKARPC*QLQDSC WDPGGTETADPGHTGLELRFFE PPKPTLPLALSEAPVPQREEKTQ GRGHYPAPQCLPGDPCSPHHPA PQPHQPHPAR/HN*PPPPRPSSHP PTTVPPTRPQPWQPGCCAQPPR PCLH*RGGN*VY*GMQLHQKS VSWPHSQWPQKREGNGSSHEI HPSCPPSGFHGSPPEGRMPTQA GALHSWVPGLSLSHGSGPHPPP RWTATVQAARPRVPLTLNL
8117	38485	A	8172	1	362	LFDNTVYCPRTERRLLKNDTKH QRHAQSACQLSTTLVCSQHRK VSDFIQHKHSAPLPQKSKRKQ NQQSFMKLTLNKLIGIDEMYRA IYDKPTANIILNGQKLEAFPLKT GTRQGFSLSPLL
8118	38486	A	8173	1	655	MIISTDAEKAFDKIQPFMLKTL DKQGIDGTYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPF SQLLFNLMLEVLTRAVREEKEI KGIKYLGIQLTRDVKDLFKRN* KPLLNEIKEDTKKWKNI PCSWI GRNTNVKMAILPKFR*WTR*RQ FSTVHKD*KLSETVSHSYLKIKF WKLKRPFLHSEPLKERQQDSV SLMNWVCMSSKTGQY

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8119	38487	A	8174	2	1936	DKPTANIILNGQKLQAFPLKGT TRQGCPLSPLLFNIVLEVLARAI RQEKEIKGIQLGKEEVKLSLFA DDMIVYLENPIVSAQNLLKLIS NVS/KV*GYKINVQKSQAFLYT TNRQTESQIMSELPFTIASKRIK YLGIQLTRDVKDLFKENYKPLL N/IEKEDTNKWKNIPCS WIGRIN IVKMAIL/PKVIYRFNAIPIKLP M TFFTELEK/ITLKFIVNQKRARI AKSILRQKNKAGGITLPDFKLY YKATVTKTA/WYQYQNRDIDQ WNRTEPSEIMPHIYTLVFDKPE KNKHGGKASLAFIKW/CWENW LA/ICRKLKLDPFLTPYT KINSR WIKDLNVRPKTIKLEENLIGITI EDIGVGKDFMSKTPKAMATKA KIDKWDLIKLSFCTAKETTIRV NRQPTTWEIFATYSSDKGLISR IYNELKQIYKKKTNNPIKKWAK DMNRHFSKEDIYAACKHMKKC SSSLAIREMQIKTTMRYHLTPV RMAIIKKSGNNRCWRGCGEIGT LLHCWWDCKL/VQPLWKS VWR FLRDLELEIPFPAIPLGIYPND YKSCCYKDTCTRMFIAALFTIA KTWNQPKCPTMIDWIKKMW/HI YTMEYYAAIKNDEFMSFVGTW MKLETIILSKLSQEQT/KHRIFS LIGGN
8120	38488	A	8175	2	1105	LPTKKSPGPDGITAIFYQRYKE ELVPVLLKLFQSIKEGILPNSF YEASIIIPKGRDITTKENFRPI SLMNIDAKIP**KY*QN*IPA AH QKSLSHHD/KVGFHPPGMQDW FNIHKSIMLIQHINRAKDKNHM IISIDA EKAFDKIQPPFMLKTLN KLIGGTYFKIIRAIYDKPTANII LNGQKLEAIPFEMLKVMYRAF RQNKQIKGIILEKEEVKLSLFA DMIVYLENPIVSAQNLLKLISNF SKVSGYKINVQKSQAFLYTNT QTESQIMSELPFTIASKRRKYL GIQLTRDVKDLFKKNYKPLLKE IKQDTNKWKNIPCS*VGRINIVK MAILPK*DVLASPSPTMTVTC RKQVQVL
8121	38489	B	8176	120	2036	
8122	38490	A	8177	3	316	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, v=possible nucleotide insertion)
8123	38491	A	8178	1	1447	MSIRVTQKSYKVSTSGPWFSS CSYLSGSPSAHSSLSFSRAGSSSF QGGGLGRGYGGASGMVEITAVM VNQSLSPINLEVDLNIQAMHT *EKEQIKTLNKFASFIDKVQFLE QQNKMLENKWSLLQQQKMAQ SNLDNMFESYINNLRWQLETLG RKKLKLEAELGNMQGLVEDFK NKYEDEINKYTEMENEFVLIKK DVDEAYMNKVELEYRLEGPTD EINFLRKLVEQEIRELQSQILD SVVLSMDNSHSLDMSIIAEVK VQYEEIANRSWAEARMYQN* YEELQMLAGEHGDDLSTKTEI STINQNISWLQAEIEGLKGQRA/ SLESTITDVEQRGELVIKDANA KLSQLEAALQRAKQDMALQLH EYQELMNFKLAQDIVITTYRKL LESEGSWLESGMQSMSIHMKT TSGYAGSLSSAYGGLTSPSLSYS LGSSFGSGAGSSFSHTSSTRAA VVKKIEAQNGKLVSXSSDVLPK
8124	38492	A	8179	272	1813	KCGLRSRSFSAPSRIAWFGPP ASTPASTMSIRVTQKSYKVSTS GPRAFSSRSYTSGPSRISSSSFS RVGSSNFRGGLGGGYGGASGM GGITAVTVNQSLLSPLVLEVD NIQAVRTQKEQIKTLNKFAS FIDKVRFLEQQNKMLETKWSLL QQQKTARSNMNDNMFESYINN RRQLETLGQEKLEAELGNM QGLVEDFKNKYEDEINKRTEM ENEFVLIKKDVDEAYMNKVEL ESRLEGLTDEINFLRQLYEEIIR ELQSQISDTSVVLSMDNSRSLD MDSIIAEVKAQYEDIANRSRAE AESMYQIKYEELQSLAGKHGD DLRRTKTEISEMNRNISRQAEI EGLKGQRALEAAIADAERQGE LAIKDANAKLSELEAALQRAK QDMARQLREYQELMNVKLAL DIEIATYRKLLGEESRLESQM NMSIHTKTGGYAGGLSSAYG GLTSPGLSYSLGSSFGSGAGSS SFSRTSSRAVVVKIETRDGK LVSESSDVLPK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
8125	38493	A	8180	1	3519	MIHKELPALAACGLVADFDPVG EEETADFGPLVLDSDSDSDSDR DIEEAIQEYLKVGSSKDQGSASP VMSRADSFQESIRAEIEQFLNE KRQHETQCKDCGSEVKKPDTHE NSAKSLSKSHQEPATKVVHRQ GLMGVQKEFAFCRPPRLAKTN VQPRSLRSKVTITTTTQKEGST KPATP/TRPSEAVQNKSGIKRSA STARRGKRVTSVQQAPEASDSS SDDGIEEAIQLYQVQKTHKEAD GDPQQRVQLQEER
8126	38494	A	8181	208	445	AACVWREHHRHAECCGCPGVH LPPLLHP*KSXWPGRC/RLRGN AAHPPWGGQATPALCCGLQ QPESSQ*GLSSLGSSR
8127	38495	A	8182	1	1607	MDMFRSGIRRDGGLGDGIVRA RRRRQGALAGSSQPIQAAVPR GPAGPAPRDRSPWPCQSSGEA *PYWKLEGAGLE/RKRGTEIRA VGEQLESWRSWRKDVAGCSP TPIPEFGAAAPTKS/GPAGPSSTQ QPSRSIWAAPKRLAG*DTAHH NHP/SAAP*PAPODRARPK*PPR ADPQRSVTPPRSPKGS*GSPFFP KQ/PRIPKSGAASEASNPLLAITS QVVGGESESTRVEGLMKESV REGNAAFSRFLRKSIV/ACKPPAS EKDRGSRAAEGDEHASSNLQEP IPHL* <sup>2</sup> TALGERPEARGGPIRFRP PGEPCSHPRSVNELGTGEPHTF QLGCLQRHPGAVDQAGPRGPG AGSRARETGKTGTNSEAAVRQ EPKQRILSKIHTSSTPGHRL/EPT AFRTRSARSPELASHGHQAGKVV AGPRVVRARGA/PPTGRPGLAAR PTEAERASRAPCP/PPQTDARLFI TARPRGKSGCRLPAHSPDPSPSR LPGPRSRSLSPA VRVVAAGEK EASGAETAFPAWGTMAFWSL QPRALQAL



SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,406,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
8128	38496	A	8183	3	683	ERGITAGPPGVHPPTARSAGAA LPVWDSACVEGVPPAPAMDP *EHQLRISGLGCQDTLMLIESGP QVSLVLSKGCTEAKDQEPVTE HRMGPGLSLISYTFVCRQEDFC NNLVNSLPLWAPQPPADPGSLR CPVCLSMEGCLEGTTEICPKG TTHCYDGLRLRGGGIFSNLRV QGCMPPQVCNLLNGTQEIGPV GMTENCNRKDFLTCHRGTTIM THGNLAACI
8129	38497	B	8184	230	252	
8130	38498	A	8185	29	316	GRVSRCLPFKLVTPVLCFLWH RSY*EYRNF*MNQISKTLQKQR PTRFTG**QPWPRWW/PAPPRPS QGRLAGREWSTQAHPRDSQGP RLCGEGRGA
8131	38499	A	8186	1	57	SRPVQAGPKATGTPQPPPS*PEP VERPLSMASGTHAQGSPSPSW PQLTGAVAQDPSPLPPRDT APAPSMPTADGVQRCARQSGN TGPRVAT*PVAPTSFPAGPDSGE MG/ESCRRRPGT*PTPFQSLFR RRPSASRIYGLLGPCVISL/HKK QKSLPPLAPPGTITVDILFTWAS SLFSLNATEGHTVVRHV*CSRRN YQKANAPRTPTASPNTRSHSLG NAKTPPQTVPHRDHPTQEHTG DTSSCVAVLSANTRERAAVEC GVTVLNLD*LK*TARSSMSA STGVAGSVQGKR/LRTSALSSG G*GPKATGTPQPPPS
8132	38500	A	8187	1	3564	
8133	38501	A	8188	154	256	
8134	38502	B	8189	1	1206	
8135	38503	B	8190	1	1311	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
8136	38504	A	8191	2	2491	EAGWEEGPSQNGLVLQGEKL PPDFMPKLVKNLLGEMPLWVC QSCRKSMEEDEQTGREHAVAI SLSHTSCKSQSCGDDSHSSSSSS SSSSSSSSSSCPGNFGDWDPSF LAEHKRLGLWNSPHSIGAMPGS SLGSPPTIPGEAFPVSEHHQHSD LTAPNPSPTGHHPPQA/LSNP/AL TPAPLAP/APHPHLLPTTAAAPFP AQASECPVAAA TAPHTPGPCQS SHLPSTSMPLLKMPPPFSGCSHP CSGHCGGHCSCGFLPPSSQPLP STHRDPGCKGHKFAHSGLACQ LPQPCEANEGLGEEEDSSSERSS CTSSSTHQRDGFCDCCYCEFF GHNAPPAAPTSRNYTEIREKL SRLTRRKEELPMKGGTLGGIPG EPAVDHRDVDELLEFINSTEPK VPNSARAAKRARHKLKKKEKE KAQLAAEALKQANRVSGSREP RPARERLLEWPDRELDVNSFL SSRLQEIKNTVKDSIRASFVCE LSMDSNGFSKEGAAEPEPQSLA PSKLSGSSEQPDINLDLSPLTL GSPQNHTLQAPGEPAPPWAEM RGPHPPWTEVRGSPVFVPENG LVRR/HEHRAQPIPGDLGQDQT AGHPSSEEASSKEVPSCQELP EPVSSGGKPKQKGRQGSQAKK SEASPAPRP/TSQPRGSCQCGPG RWP/TSSQAGS*SLPK*AAVLKL ERGAGGAGQDQVGLAVPKLRR
8137	38505	A	8192	277	434	
8138	38506	A	8193	4	168	
8139	38507	A	8194	26	219	PRLQCIGQPRLTLPPGFK*FLCP SLPSSWDHRTPT*LANF*KNY F**IWGFMTLMGMSGTCNP
8140	38508	A	8195	1	498	
8141	38509	C	8196	105	251	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, **=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
8142	38510	A	8197	1	1620	MWGVGKIDTPKDVDTLIPGTC GCVTILHGERHFVDVIAKPTRS VQGNPKLGSKKMEVSIMKTQE SIKLTVKATTQRRNRNESNGPT TEFHQSTMTNTHSDTWMVVLD PMKPGPFVEVMAQQTLEKINF LRVHDLVFGDVVWLCSGQSNM QMTVLQTLSCGVVTVIFIMTLA GAHGTLSSGIFSIYQSDSLKCK SGRKAPVGPVRVLRGTYSQS NSTGNPDLFVQDHTWQFCCKH SGSYVASMETVDETAFILSTHT SFRTDWELKCFITVRRQLGRQY ERTCYLSFRPVANTVEYICGFRF ASYINNDMLVQKEPAGAVIWG FGTPGATVTVTLRQGETIMKK VTSVKGLISLLVCLSQFEIVPED DPQNAIVSSADACHAELLRTIS TTMGKLMPLNLLPAGADFFGFS HPAIHNLIQSCPGARKCINLPAS RPVGLSIGPLSPLDSYQWVKFD VCKPGDGLPEGLPENDAAMS FEAFQRQIFDEQNDPLL*SSL* PWLVIIMVPL/WSSGIFS/TISK*L FEV*VGSESGSGSPAEDRLHM VSRKFHRKSRPVCSSGYLA/VLH *ALRILCCFHGNSG*NCFHSLHP H*/HSALTGNSSASSQ*DASLGG SMREHATCLLDPLLT*STVLV FALLHTSIMIWCCRRSLLGQ*Y GASVHLEPQ*P*PCAKVRKPS*R K*PV/CKGLISLLVCLSQFEIVPE
8143	38511	A	8198	1	900	
8144	38512	A	8199	915	986	IIIDTRPGFHDESAIYPVGYCSTRJ YASMKCPDQKCLYTQCIKIDGG VQPQFEIVPEDDP/RNAIVSFFW QMLVMQNISQDYKALLWGKL MPNLLPAGADFFGFSPHAIHNLJ QSCPGARKCINQYQWVKFDVQC TLEMGQLPEGLPENDAA/RALK PFQRQIL**RIDKRNLLKIKQL KVFPGKTITTRTFHDEIPLVSSLP SELLPSFIYPKILV
8145	38513	A	8200	3	414	
8146	38514	A	8201	1	2445	
8147	38515	A	8202	1	248	ENGNLGPQAEVKGATGECNIS ERKSPGVKISLRELDGSLVH KIAEGFSESKRSEDENENKIE FRK/KGGF*GGGFLRRK
8148	38516	C	8203	70	324	
8149	38517	A	8204	1	675	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
8150	38518	A	8205	692	808	
8151	38519	A	8206	1	1954	PGTGEETVRLGFPVDPKRVLIIV AGHHNWIAAYAHFAVWYRI KESS*WQVFTSPYLDWTIERV ALNAKVVGGPHGDKDKMVA ASESSIIILWSVQDGGSGSEIGVF SLGVVPDALFFIGNQLVATSH GKVGWVNAVTHQWQVQDVV PITSYDTAGSFLLLGCNNGSIYY IDMQKFPLRMKDNDLLVTELY HDPNSDAITALSVYLPKTSVS GNWIEIAYGTSSGPVR/VIVQHP ETVGGSPQLFQFTTVHRSPVTKI MLSEKHLVSVCADNNHVRTWT VTRFRGMISTQPG/STPLASF LSLEETESHGSGSYSGNDIGPFGE RDDQVQVFIQKVVPITNKL FVRL SSTGKRICEIQAVDCTIISSTVTR ECEGSSRMGSRPRYLFTGHTN GSIQMWGSGPLLDWMVNKSE DKDVS GPTVEELLKLLDQCDL STSRCATPNISPATSVVQHS ESNSSLQLQHHDTHESATYGS MRPYRESPLARARRTESFHSY RDFQTINLNRNVERAPENG GPIQAEVKGATGECNISKSP GVEIKSLRELD SGLVHKIAEGF SESKKRSEDENENKIEFRKKG GFEGGGFLGRKKVPYLASSPST SDGGTDSPGTASPSPTKTTPSP RHKKSDSSGQEYSL
8152	38520	A	8207	2	383	
8153	38521	A	8208	13	332	SKGFIVLLKCLQILKTPSLGPGN QGLNAGKESRGGGLSVKA*RA RPDSWRPGPPLSISITLRLKEG RRHHRALPLCCITLLASSPNCI AP/TSVP*IPRLHPFWL
8154	38522	A	8209	1	1839	
8155	38523	A	8210	1	364	
8156	38524	A	8211	3	3723	MIPAGGRAPGPPYSPVPAESEL VNGNHTPQTATRGPSACASHSS LVSSIEKDLQEIMDSLVLLEPGA AGKKPAATSPSPMANGGRYL LSPPTPSGAMSVGSSYENTSPAF SPLSSPASSGSCASHSPSGQEPG PSVVPPLVPARSSSYHLALQPPQS RPSGARSESPLSRKGGHERPPS PGLRGLLTDSPTTVLAEARRR ATVETPRLGGLPVVAISLSEYP ASGALSQPTSIPGSPKFPVPVPA PRNKI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
8157	38525	C	8212	398	415	
8158	38526	A	8213	3	45	
8159	38527	A	8214	1	929	IAAAPELLERSGSPGGGGGAEE EAGGGPGGSPDGDARPGPSREL AVVARPRAAFTPGPSAAAMAR PLVPSSQKALLELKGLQEEPV EGFRVTLVDEGDLYNWEVAIF GPPNTYYEGGYFKARLKFPIDY PYSPPAFRLTKMWHPNYETG YVCISILHPPV/DTDPQSGELPSE RWNPITQNVRDHSS*V*SSLLE RRPNTFLRPANVGRPLPWLQ SWEREQGGRIELHRTSFRKQV LGTKVDAERDGVKVPPTLPEY CVKDQGRRAPDEGSDLFYDDY YE\DA\VE\EEADSCFGDEDDDS
8160	38528	A	8215	80	430	IAQGFYPPGWPCSGPGGNTSSP RPPPTGGKGK/PGGPQK/PLAPRI PAVFTRGDSG*RSCPATTPLSA GSPSLPHRIPEKPPHRIPEKHLH RACAHAPDPGSGGLRIFLTAHV HGKL
8161	38529	A	8216	3	645	FSVSHLLDLEEAGDMVAAQAD ENVGEAGRSLLESPLTSGTAT PQQDNDQLNSEEKKRKRQRN RTTFNSSQLQA\LERVFERTH*T PSSLFFLSFLMPSCLLTILQVWF QNRRAKFRNRERAMLANKNAS LLKSYSGDVTAVEQPTDLQLCE TNACYSPCSLPCPYSAMATYSA TCA\NNSPAQGINMANSIANLR LKAKEYSLQRNQVPTVN
8162	38530	A	8217	3	907	RVDDFVAVQLGRPIGSCFGGRA QLQEGVQKQAMAVGNINELP ENILLELFTHVPAQQLLNCR VCSLWRDLIDLVTWLKRCCLR EGFITEDWDQPVANWKIFYFLR SLHRNLLHNPCAEEGFWSLD VNGGDEWKVEDLSRDQRKEFP NDQVKKYFVTSYYTCLKSQV DLKAEGYWEELMDTTRPDIEV KDWFAARPCGSKYQLCGHLS DAAQGPHGTFQPDATIQKQSD AKWREVSHTFSNYPGVRVYWF QHGGVDTHYWAGWYGPRVTN SSITIGPLP*HPLSPHLLNPDW
8163	38531	B	8218	117	398	

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8164	38532	A	8219	1	3063	MSLEVDRSVETMCSGDEILLPD LPKADVADPLWGFPPVQNCLS LARSDSREQGLVLMESRNRRE VVPPGVSYSKDGAKSLKGDVP ASEVTSKDSFQSFPISSAEEC GDDEKIKVDDPLTRRTCNQASG SAPQQDYDKLKAFGGENSSTK GLSPSGNMEKNKVVKREAEAN SINLSVVEPFKVRKAEDKLKEN SDNVLENRVLDGKLSSEKNDT CLPGTAPSKTKSSSKLSSSSAI MALSAKKAASDSCKEPV
8165	38533	A	8220	1	1188	MPLDEDPSKLCRHNLCLECN IFQDKTSLATHFQQAADMSSGQ KTCTICQMLLPNQ/CQRHIIQHKS P*TCPECRAICR/SHCEVFYKCP CPMTFKSAPSTHSHTYTQHPSIK IGESKIIYKCSMCNTVFTLQTLL YRHFDQHIEQKRDVYISHVRK EHGKQMKKQPCCQRDKPFSSS HSLCWHNRKHKVIRKVVYTCSH CSDSRGTFTKQLMLEKHVQLT HGKIDPDLKE/TDRRHQ*GGR NKRPPQGPQSQVEVERTGSGV QASQGAITQPKLEINVFKVHKC AVCGFTTENLLQFHEHIPQHKS DGSFYQCREHLFVAHKLKEPOP VSKQNGAGEDNQENKPSHED ESPNGAMSDRKCKVCAKTFET EAALKTHMQTHGMFAIKSKRM SSDEK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/546,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8166	38534	A	8221	842	2687	KGECLPSALSLNGNGRESLES! ESLSLEGFTTRAGLRTCSPCL SLPAPPWAPVLPPEPRGAPPAP RRPV PSTTQGLRSAGARRGTGR QLHLRPRC/ADPLGEASWAPES GSAPAILKVRIKTIKMSSGEIKR TVTRVLPEVDLDSGKKSSSEQTA SVMASVTLLSSPASAAILS/SSP QGASPVHGHQCSFTC/SSSPLN RAPA/GAIIKAANAQQQT VVVP APSRANAKLVPKTVHLANINLL P/HGSATN/ISRQ*SMQQ/RSQPP KKVSRVQVVSSLQSSVVEAFN KVLSSVNPVPVYIPNLSPTNAG ITLPTRGYKCEGDSFAVEKS LTQHYDRQSMRIEADTRGQK TCTICQMLLPNQCSYASHQRIH QHKS LYTCEPGAICRSVHFQT HVTKNCLHYMRRVGFRCVHCN VVYSDVAALQSHIQGSHCEVFY KCPICPMASNQNKEDTKSMNG KEKLEKKS PPKSVETKKVA SPGWTCWECDRLFQRDVYISH VRKEQKGQMKKHPCRHLCQH NRIKHKGIRKVVYACSHCPDSRR TFTKRLMLEKHVQLMHSKDP DLKE/TDRCHQ*GGNRNKRHH QVPQSQAPLHCTQVKGTASV QAKWSWGR
8167	38535	C	8222	1	438	
8168	38536	B	8223	98	463	
8169	38537	A	8224	1	2679	
8170	38538	A	8225	1	1209	AADTRGQKTCTICQMLLPNQCS YASHQRIHQHKS LYTCEPGA CRSVHFQTHVTKNCLHYMRRV GFRCVHCNVVYSDVAALQSHI QGS HCEVFYKCPICPMASNQNK EDTKSMNGKEKLEKKS PPKV KSVETKKVASPGWTCWECDR LFQRDVYISHVRKEQKGQMKK QPCCQKDPFSSSHSLCWHNRI KHKVIKVVYTCSHCDSRGFTT KQLMLEKHVQLTHGIKDPDLK E/TDRRHQ*GGNRNKRPPQGPQ SQVEVERTGSGVQASQ/GAITQ PKLEINVFKVHKCAVCGFTTEN LLQFHEHIPQHSKSDGSFYQCRE HLFVAHKLKEPQPVSKQNGAG EDNQENKPSHEDESPNGAMS DRCKVCAKTFETEAAALKTHM QTHGMAFIKSRMSSDEK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
8171	38539	A	8226	58	391	FAKNDGFLHPCPEPL/PWSQTRTQSAAWA*GCNYLQPTGAADLLAYFEFLGPEGKGTG*QGLDRDATGAPSPPTARQ/RVGKALGTAAALPSFIPL*SKKMARETAAWSEW
8172	38540	A	8227	993	2235	NGGPHLWRLPTAHRACGERHGGAVACGGAAVEALVGPAPT VGLRRGCPHSAPGGYACPVSSSTYSGLGQRQCVFPHYSPRAVPLVPALGAPKP*MGPSAGL*GDMPLPAASVKRAPTAAGPWMLYPYSPARLDSAA/LQALSTKKVASDSSKEQVANSRESSLSKEVNDSPRAADKSPESQNLIDGTTKTS LKQLDSPRNISSENSIKGTPASPAGSTPPPKVRIKTTKTSSGEIKRTVTRVLPVEVDLDSGKKPSEQTV SVMASVTSLSSPASAATLSSPARVPLQSAVVT/KQFPLQSPPLNR SQSSLWLLSSQCLL*RQQDPKSLI*SSLTTPR*KPRSYLLPLSRVPAAPSLKLANAIQQQTVMMPSA SSLANAKLVPK/MHLANLNLPLQVAPATSELCPVSIKTPQI
8173	38541	A	8228	1	3370	MIINTIITTTTTIITIMSSSPITITNIITIIQHIIHHHNDQRPSLGKCRGLYIRVRKVPGERATANSRC PINAQIESCWNGVMALWLGPNSTCSRPELTDSEDCQIYGDTERKRRHSRKTCTWEYQVETKDTFLEELLFEPALRTGIQSKQGGPL LQLAANNYNLEPKQHFGSWFG TMKQLGETESIFSAYEVCLTVYEIFGLPGIAPSKTKSFNLSCTAIAALSTKKVASDSSKEQVANSRESS
8174	38542	B	8229	1	438	
8175	38543	A	8230	38	597	VPCGPHCRLPASAWRTSPRLWN DTTSRKWKSGVAKSSCYNL*PSAGMRKRKF*LRAPSTLSGSALL *NRLMRSRFCATSSCAS**CEQRTSLSFEGSLWRSTITSRPPPSAARISSASAPTRRRCASESAACRRSTGRAGPGPGGGKQQMKAGR/ RGTAQPSSPHPLGIPTHPDTRGASRQTGHL
8176	38544	C	8231	1	1062	



SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
8177	38545	A	8232	3	595	WSSAQPRASRAASRSSRLHSS RRLLCLRCRAPRRPQLVASAKGR ASSARSRGRSRSR*RGARSR GGGMSPLAQRRLK*ASSSSGRG AAWSRASGAARGSGPLTGRR SAPLHSSSTVPCSPRYARPGPPR ATA/RGPTRATCLPSHRSTITSRP PPS/LPVA VQPALPPGAAAPSP PRAGGALAALGPGLTVGAGR
8178	38546	A	8233	2961	3005	SRLQQTQADAFACAKGCWP GGM/DELEAETSSSLFLLAMQV WMCGRMEDIPCSRVGHIYRK YVPYKVPAGVSLAR/SKNLKR AEVWMDEYAEYIYQRRPEYRH LSAGDVAVQKKLRSSLNCKSF KWFMTKIAWDLPKFYPPVEPP AAAWGEIRNVGTGLCADTKHG ALGSPLRLEGCVRGEEAWN NMQVFTTWRDIRPGDPQHT KKFCFDAISHTSPVTLYDCHSM KGNQLWKYRKDKTYHPVSGS CMDCESDHRIFMNTCNPSSLT QQWLFHTNSTVLEKFNRN*A ALLFDESQFDSSNCQHSCYPR
8179	38547	A	8234	203	314	VPASSPALGSTLEFQLCEPINS FCLNQID*GFGYL*ARFMSWPY WSLLSPFFLIPLH
8180	38548	B	8235	1	1008	

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8181	38549	A	8236	2	1495	CLVVTSTDSIRFQIIPWAGTEMK QE/IKLKDGSMEEHLKKPLEDY MALFPFSVRIIRTKKREGLIRTR MLGASVATGDVITFLDSHCEN VNWLPPLLDRINRNRKTIVCPM IDVIDHDDFRYETQAGDAMRG AFDWEMYKRIPIPELQKADP SDPFECQLVRDITLGDADSQQH DVSHLARCQADFLFPWSPVMA GGLFAVDRKWF/WELGGWAFS HGDPPQPPWKESLFFPSSCTSPQ VESHWAPGMPPIPEQYCNWSP AVTCPVTAGRVCLGWGW*RK *WGTDLLGARWKSPP*SP*T NQDVKNPHDLIEQFQRKEHFC TESAWLGCPOGNSWLLQSORS HRERWNHGIFMTVISAVSCGLH GVVCGGRMEDIPCSRNLKRVA/ EVWMDEYAEIYQRRPET/GHL SAGDVAVQKKLRSSLNCKSFK WFMTKIAWDLKFPYPPVEPPA AAWGEQKDMPLSQYTSKGAGI KSYLGSCTHHWGHRGRQKQG NILIAHQ
8182	38550	A	8237	1126	1603	TIMKITGRAGDAIMGADICH/N KDRKVRRKEPKSQDIYLRLLVK LYRFLARRTNSTFNQVVLKRLF MSRTNRPLSLSQMIQ/MKLP GRENKTA VVVGTTDDVRVQE VPKLKVCALRVTSRARSLILRA GGKILTFDQLALDSPKG*GTVL LSGPRKGR
8183	38551	A	8238	504	737	QLCWAGGKILTFDQLAVDSRK GCITVLLSGPLKGRKVYGHFGK APGTPHSHTKPYVHSGRKF RARG*RAS*GYKN
8184	38552	A	8239	1	360	MLGFALLPAPPGGLV/GSG*SP DDQIGRTGPALAPSLSRPSPAT LNSAGSEIHDRPSGAPPTCLR GSAQASTSACSPGANGPEPKPG LGTLRQQLHIMATNRLDEAG WVACYPTDVR

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8185	38553	A	8240	3	666	MSFRQLFQDLKRYVQDADVR WEYCVRAKRQGTDTSLGRLFQ QGPVGPRHRAHSATSPDHRFP VADLTGGQVL*GCGPPAAPWG AG*YPGAPLHAGLGTLPAAAG AHGHQHPAG*GGAGSPATRLM SVEGCSQRPWTEAPDRPLEHEA VCSVRPRPRCFLGGVGRAGAFL EEEWQHQSVCVPCQPPWGLGT CSSMSGKLSRPPASSLLSRGKA WGQEEES
8186	38554	A	8241	2	443	RTSLEFFFFFF*DGSTFLVAQA\
						GVQWRHLG*LQ/RRPGFK*FS YLSLLSSWDYRHALSHLANFV VYVLCFVETKSRSVTKAGVQ WCDLGLSLQAPPPGTFPSCFSL SSWDYRHLPPHLVNF.CIVSRDG VSLCWSGWSRTPDYK
8187	38555	A	8242	1	354	VSLQPVSQEGVSQRTLGQSSRS SGSG/CPGELNSPIFGVPHRW AA*EESRAAGVPWPSSQISGMC SKFRI*NW*DVSWAGWSEDLRS *VDLSHGAKSRRTGD*SPKGGP PIRV TAP
8188	38556	A	8243	2	241	WSTGLLRSSGS/NQSSAGKPRR SQSESPG/PSRSSSGCQESGT CH*G*RRRG*GVLAPAPGKRDL PPRVKDQVRHPCVV
8189	38557	A	8244	5	282	AKKESVREPWARVPALGVAA R*VEQSDFCGPAQMGLGLGG IPGCG/PFLGLVVRFLALVASSC PPPRKAGLAAGGEGPRQASLRG LTPLKRG
8190	38558	A	8245	1	302	LSREGVGQKALGQSSRGSGSVC /LGELNSPISSGVQRWDTA*EE SWAAGIPWPGGQIDFWHL*QA PCPRKSREGVETRREGVGVLAP SPEKRDLPRLVKD
8191	38559	A	8246	1	200	LSPKGVSQRALGQSSRGSGSG/C PGELNSPISSGVPHRWDTA*EES WAAGIPWPGGQISGTCCKLHS
8192	38560	A	8247	23	187	
8193	38561	C	8248	1	1764	

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8194	38562	A	8249	115	872	LRRGRTYPPP*ELPKARHP*WS TGLLRSSGSISLQPVSQEGVSRQ AFGQSSRGSGSG/SPGELNSLISS GVPHRWDMA*EESWAAGIPWH GGQISGTCS/RAPGGGGSGGMP GCCGSGVWKFLCASRKAGKGS GHRDTRSGCGHKGLGRRDMRL GCGNKSGSHRDIRGWGTCPPF RKAGLAAKGEGPQASLRGLT PDLKLVRCPWAGWSEDLRS*V DLSHGAKNRRITGD*SPKGGPPI LGRPLRACSAAVHF
8195	38563	A	8250	85	529	SGSISLQPLSREGVSQRALGQSS RSGSGG/CPGELNSPISQSGVPHR WDTA*EESWAAGIPWPGGQISQ TCS/RAPVGGSGSGGTGRCGSG VWKFLCAGDVAGVCLTVEAR NCNFFLLLYTLKARLIKSCPCPR KAGLAAKGEGPQASLQ
8196	38564	A	8251	1	552	MEARETPGWKEGNVERVASVL IKKGITGLPSTVRVTGSSASVMV YGASEAIGQHQSAAKPRRSQS ESLGPEFQGLWEWLPGPRAVK RLRVIFDEKEPKRYLIWDKEKG ALTLTMPLAPATFLRVNCWAG GGGLVTERNCKP*WSTGLPRRS GSISLQPLSREGVSQRALGQSSR GSGSGCQGLGL*SVLIKKGTGL PSTVRVTGSSASVMVYGASEAI GQHQSAAKPRRSQSESLGPEF QGLWEWLPGPRAVKRLRVIFD EKEPKRYLIWDKEKGALTLTM PLAPATFLRVNCWAGGGGLTVT ERNCKPDQMKMGIEIKRRERLK CGSKIERKKLRDSEGGWRRVE
8197	38565	A	8252	535	710	KCFPACHHYHNHHHHHHYHHH HQHHHHHHHHHHHHHRTIITITIF TIITITIIIIIIITITITIVIFMRVR VKRPPNRLCVSNMAVYFTWQV KKKSSLA FSSVVTSDLKSKRRR LSGKSLETSSASLMVYGASEAT GQRQSSAAKPRRSQSESLGPEF QGLREW*YDGGDDDDNDGVD DGGDDSGGGGGCGSGGKQESI SIFD

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8198	38566	A	8253	54	563	AEKESVREPRARVPGARGVAA RPSA/RPR*GRLLCSPTYPKH* NCAWHQQAGCWLGTGPAAPA SPPACAAFSWGYGGLPAPIQTA FQAGW/GAPGQGRSKTTRPGV QSVSNPGEPAPEPRAAASSGLSS GAFPAATDPGICSWAEGVLM GKGHHIRPSISARIPCFHV
8199	38567	B	8254	232	987	
8200	38568	C	8255	1	1812	
8201	38569	A	8256	1	1035	
8202	38570	A	8257	2	664	SLIKLIPPPRPFGRNRHLVIRQN ERTQRGKRRGTRYMFSPRF*/R KHGVVPLATYLCEIYKQRCDP VDIQGEWGTCSKKGMP/HHKC Y/HGKTGRSLTIVTPACLPLFN TTQFRRKILAK/RINVRIEHI*AL LRARD*LP*NRVKENDQEKERS PKRKGTVGST*SRQ/APPR/EA HFLPEPNEGALSCWEPFPHYWI SLGLLGVKKKNKD/LWATKK
8203	38571	A	8258	1	747	MSESLKPLPEVDAGAILLVQP AELYSKASRLDDCYQKDSYTH RCQEKRTCHTTGGHSGKHQSL SGASVSPTCsAKTRDKINCFDFS PKSEVITLSNDDSIIVLSDCQEG KPKPCSGPFATFKMQYDRTCE WTALKISNGGKLILISTNVSFIR LIGAFKG VVIHTFGSYANSEAV TLEASFTADSQFVIMIGSEDGKI HVVNEESG/KK*LGWMVNTQA QLPVCNSTPSSMTFASACSNMA FWLPTIDD
8204	38572	B	8259	50	260	
8205	38573	A	8260	1	541	EVWGPGLASEGAVGITHGPFPK AKRNPgKVRSKRDPPIQFQNL RRS*WRSIPRKPGRQTGSRRSL WT/ALHPGAGTAKHPPPA/CA GRET*CKSKSPAGRKWSFHRSS SRRASE*DAQFAVPAGVTSRE PFGSRRGTGPTGTGTPTRTAR SRTWSSSWVRLSGRTGAVGYS RSPSCSS
8206	38574	C	8261	177	236	
8207	38575	A	8262	1	417	

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8208	38576	A	8263	2	475	GIHTRLNSELLKEEESNKRLEAE IEYQSRSLTAAISKHSESVKTER NVKLALAE*TDVSVQVKMSSDI SEVEDKNEFLTQLSKKQIKFN TLKDKFRKKRDTLRKKSLALET L/QNDLSQTQQQIKEMKEMYEN AEAKVNNSTGKWSCVEERICQ LQHEN
8209	38577	A	8264	3	518	IFRAPFRICLGILLSPNTEQAQY KKQLEQ/FKQGYNTASLNKKEL TLKDVECKFYKMKATAYEEVTT ELEEYKEAFAAALKANSSMLK KLTKSNKKIAMIS/TQLFMEKEQ VKYFLSTLRARRGRESPCDENL TSIGL/NRKYIPQMPVRIPTS/SPQ TSNNCQNYLTVSHMTVSL
8210	38578	A	8265	1053	3733	NGRSCCERSSTKKECTDIESSEF VNRKSLTSGLEEEQQRRESEK KQPQDFHNEEVKDLMDENCI LKTDAIPRQEICTMKNDNLEKE NKYLKDIKIAKGTNAALENCIK LNEEMITKTAFRYQOEIENDLKA ENTRLNSELKKEKSKKLEAE IESYQSRSLAAAIKHSENVKTER NLKLALERTQDVFEQPAGLEEA ELVLSRLSCGEATEGAARRALA AEEAGRWRRGVG/DSWLAPES RLHVLKTCGSCW/WENLELGRH H*LCLWA VKNFQKRFLPGQKK SPFQLMSQREFQHTL*ITQKQN RVMNFIKKYLRMLSSV*CMP LT/KHSIDKEVRSTASRLPCLGS EEICPAALSGKYKKLLEMTIN VLSVFGNEFDCHGDLKTDQL KMNILIKKLKHKFDDLTAEKEA VSSKCVDLAKDNQVLQOELLS MKKVQQQCEKLEKDKMLEE EILNLKTHMEDNMVELSKLQE YKSELDERAMTAVEKLEEIHLQ LNKGNTASLNKKELTLKDVEC KFSKMKTTYEEVTTKLEEYKE AFAVALKANNMSKKILTKSN KKIAMISTKLLMEKEWVKYFLS TLPTRRGQESPCVENLTSIVLNS KYIPKMTGRIPTSNP*TLNNWQ NYLTEEDMVSGDLISGTWSME EWSLGASSLGTWSAAVGGYLA RWPLCDLSVTVAESPSPLCCGA
8211	38579	A	8266	2	209	

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8212	38580	A	8267	1	1431	MTQKAAASVEHLAIRCHWSQR PAVTGVDVLQVYSGSEGTAIIFCE TQRSVTEIAMNPHIKQNAQCLH GDIAQSQRREFTLKDFREGSFKV LVATNVAACGLDPEVDLVIHG SPPQDVE/SYIHRSGRTG/FVTM TLESLEEIQDVSCAWKELNRKL SSNAVSIQTRMCLLKGNVRVCF DVPTTKSERLQAEWHDSDWIFS VPAKLPEIEEYYDRNTSSNSRQ RSGWSSGSGRSGRSGSRNYF AVDTASAIAIALMTFGTMYPMS VYSGKVLLQTTPPHVIGQLDKL IREVSTLDGVLEVRNEHFWTLG FGSLAGSVHVRIRRDANEQMV LAHVTNRLYTLVSTLTVQIFKD DWIRPALLSGPVAANVLNFS DH HVIPMLLLKGTDDLNPVTSTPA KPSPPPEFSFNTPGKNVNPVIL LNTQTRPYGFLNHGHTPYSS MLNQGLGVPGIGATQGLRTGF TNIPSRYGTNNRIGQRP
8213	38581	B	8268	128	1497	
8214	38582	A	8269	1	618	
8215	38583	A	8270	1	334	LFHSIFGYLPFARQTLLPGSILVF TYTQPPKIQFANGTKGLPDPLM TPK*QK\APLMPLLVSLGLSAST IALGTRIAGISTSVTTFCSLSNDF SASFSPYLHRCFLPWSSL
8216	38584	A	8271	1	2919	
8217	38585	A	8272	1	4192	MRIPVDASTSRRFTPPSTALSPG KMSEALPLGAPDAGAAAGKL RSGDRSMVEVLADHPGELVRT DSPNFLCSVLPTHWRCNKTLP AFKVVALGDVDPDGLTVTVMAG NDENYSAELRNATAAMKNQV ARFNDLRFVGRSGRGKSFTLT TVFTNPPQVATYHRAIKITVDG PREPRNNECVYGNYPEIPLEEM PDADGVASTPSLNIEPCSPATS SEAFTPKEGSPYKAPIYIPDDIPI PAEFELRESNMPGA
8218	38586	B	8273	385	3930	
8219	38587	A	8274	830	906	

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8220	38588	A	8275	483	971	ATMPGHHFYLCETGSNSVSQAG VQ*HDFGSLQPPPGFKQFSCLS LLSSWDYRHMPPRANF/SVFL VEMGFYHVGGAGLGLLTSGBP PASASQSVGITGMSHHAGPTM KLLNPQSEVIFSPRNSHSTLLTP LSRHLPHPISISTWCIHYAPLHT VSISAEAP
8221	38589	A	8276	1	2088	
8222	38590	A	8277	1	1822	MMTKDGLVFLGRQSGPILYVQ GLSRFRSFSVASGDSKRTRHRE KLPLLEAGERDHNCYGSQPILA FQAICKIAKPGKEQSCSKLVGH TFDPLLEIARKPEERQKLPDPVCV KWGGVGNFPVKRVGDRIFFVS QGGKFSQAPEGPEVTSQSQGLE SKTLEVYPVFYCTVAELALNHN VQPSHSTLPPQAEEPHSVATTT GPWGVLPGCCQCSLKAQGLFS QLVMNAACTGIHTSGQWAPLW PSTVPEMPSSKSGLESPTRTCF VLYPAVAKLLPRGTLAYSGKG CQNSSANHWDTQIHSPCHAA AAREYGGKSGISDSRLSPTLFSA SFSNMNKLKDFKVFYGCFCF EATAGANVLKIIRESKYKNTD DIDILSRQATPVIAQLAHEHSGH VAGMEVVFSGNSNTDFHLPRQT WLQPLSHASLLAAETNTESKND TTPQGDQPATWRLNSGYGAF PACNASAKTIHGLTEVLYTVLV DGNHNLLTKLSLEEENCLQLK CENLQKLEQMAAIE*KSLRRK RATQEECLMHSNLKFKESAE YTALARQ/LEAALEEGRQKVAE EIEKMSSRESALQIKILDLETEL RKKNEEQNLVFNKNEQ
8223	38591	A	8278	1	5103	MDESSVHSSVGDHVDVRVSTS QVAERTRCNKMWRIETKSPSG DNEGTVIEKTRLSGQGFCFL QLSEGLQNLQAQRRKIKFREME DPSSRPLCSSLDIALCASVKPSA GFPQRPVKVPLCVLGSAGGTG DAERSLQSSDPLKKQQPLARSL RGLCERIVLGGSGCGARGRLG AGGGTALSVPGASRGFEGMFG LDQFEPQVNSRNAGQGERNFN ETGLSMNTHFKAPAFHTGGPPG PVPDAMSALGEPPIILGM
8224	38592	A	8279	1	783	
8225	38593	A	8280	888	4915	



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8226	38594	A	8281	94	757	APTGCLACNLLLCGLGVTSPL *ASAPKCVTVHN*PLCKALPRR *SSAWELS*MRKLRLRGVNFRL TDGLCFICISTRATPPSARARCV STSLKPASLQLAVALYHHGSRSQ GCHLPAGREVCTSQSRGVRETS PWGCEKGSPIAEGFPAVISLNP PSSSTAHDLPANKASASQPGSH LQCLSVHCTDDVGDARASV PTWRSLHSDISNRFGTVAALT
8227	38595	A	8282	2	374	
8228	38596	A	8283	260	500	
8229	38597	A	8284	98	828	RWASVFPHPFPYILPALLEKKT AERRGGAFSRNKQTAGPCGGT LQEEGSARTVGDSYGEASAGG FSCNKEEGNQRYREG*VTEML GVGYHRALLQLRGLDPS/PALS VT*SRTSGPRPSRLNKITYCIPP RQDCYNNLAACLQMEPVNVE RVREYSQKVLERQPDNAKALY RG/SGVAFFHLQDYDQARHYLL GCRE*AALKMPNVRYPPLRTR VRTQQPTHRKEKQLLPWACL V NKEERCSS
8230	38598	A	8285	396	602	GNCGPEKERTCLRSPSWTPMPS PKQAVPVSSWPPGPHHQ/RCVP SRSSNFSKSSKSNSCDGNSSSS SS
8231	38599	A	8286	3	156	SVVSLSPHR*AIQILSGVAAGW GLSDGFPSSPPSPSGARDTGSPG SSLGL
8232	38600	A	8287	32	515	ARGSWGPGAGARPPGTARRAA RCATGCGSRSSSHAPVSPRRA APSSVHPGGCHGPALPPSPRR VTQAADARRAAPPLRAASAA P SRRWSQAPT/K/RRLGYPPPRP PAHPGPR/PPLRRMVSRSSEDP PRRLT*TGSETPKSTWRELSRR RSLQSKAATR
8233	38601	A	8288	30	460	RRCPAQRGEIWQSGH/RALLSC SGLHFPQTSWLPVYTVRVKLP T QALAMVDAPPPTKLECPRLISV CCYAGSENFKPVLDLSSIGGS GGVGTGRNLLVCELRRPWDKR SIWAGVSRFLRSPSRFLA*LG LSSYLTRTKT

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8234	38602	A	8289	2	1094	RMSRISDDSRITASQLDEFQEC L SKFTRYNSVRPLATLSYASDLY NGSSIVSISIEFDRDCDYFAIAGV TKKIKVVEYDVIQDAVDIHYP ENEMTCNSKISCISWSSYHK NLLASSDYEGTVILWDGFTGQR SKVYQEHEKRCWSVDFNLM DP KLLASGSDDAKVKLWSTNLDN SVASIEAKANVCCVKFSPSSRY HLAFGICSDHICVHYADLRNTK QPIMVFKGHRKAVSYAKFVSG EEIVSASTDSQLKLWNVGPPIY CLRSFKGHFNEKNFVGLASSG DYIACGSENNLSLYYYKALSKT LLTFKFDTVKSVLKDREEDD TNEFVSACVWRALTQMGESIN VLIAA*QFRVPIKVLELV
8235	38603	A	8290	1	667	MRIKATSEDTGTVIAQAEYGSVD IGEEVLKKGFAEKCLASRTDI CEEKKLDPGQLVLRNLKSPIPL WGHRSNQSTFSRPGHLSSEKM TLDLKDENDAGNLITFPKESLA VGDFNLGNSVLSLEKIKQDQKLI EENEKLTETKDALLESYKALEL KVEQIAQELQQEKAADVLTN HLEYTLKTYIDTRMKNLAAM EILKEMRHVDISVRFKGLSDAI QVLG/SKGALLQLL*MD*R*Y GQNTVWLRRILKLSEYVSEGN LIAQRNEMQKLYMSVEDFILE VDESSLNKRKLTLQDLSVSLEA VYQAKKEGANSDEILKKFYDW KCDKREEFTSVRSETDASLHLL *HGSKEP*RIKVMQTRR*FQIHI VKYCKRFIQRKGSIPQYKLSTR TVLS/SKKQIEYLLKIPSDVHL LSIK/TDIEKLSSTQMEIG*KE* FGKSQMLMALKLK*KKK*LK KGFAEKCLASRTDICEEKKLD PGQLVLRNLKSPIPLWGHRSNQ STFSRPGHLSSEKMTDLKDEND DAGNLITFPKESLAVGDFNLGS NVSLEKIKQDQKLIENEKLT EKDALLESYKALELKVEQIAQE LQQEKAADVLTN HLEYTLKT YIDTRMKNLAAMEILKEMRH VDSVRFKGLSDAIQVLG
8236	38604	A	8291	1	325	
8237	38605	A	8292	1	593	
8238	38606	A	8293	1	2013	

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8239	38607	A	8294	2	1427	LLARGAGRTNPAPPLMSCGPW GKFLKCCVEYKSGPYKVQ*EEI TIHSRAEAESTYQIKYEELQTLA GKHGDDLRCAT/T/EISEMNQNI SRLQAETEGKKGQASLEAAIA DAEQWGELAIKDANTKLESELE AAMQRAKQDMA/RQLGEYQK LALDIEIATYRKLLGEESRLES GMQNVSIHKKTTSGYAGAPARI VSLLQNELLSLEVGVKLGHPPTG KGEELGAPYSECSFGLCRRTVM LTQAPSSVVRNSNRNHTVNSG GSCLSASTVAIPAINSSAAMSA CSTISAQKRTCTACEPARKYK DTASHQEPACVQACQLETADP KGGGVLLALPQPPSPGMLCWPY CRAHATDYFLANFFSEFPCHFL HRAGAAQTATGDMEHGQS RELPKRKAPREESETSEEKSPNK WGPVSKQKKQLLVILTTIIRPT RGNAYTGLSTRKWKPRSEENA LMQPNKKDEKGLTLTKQLGL
8240	38608	A	8295	301	462	
8241	38609	A	8296	2	825	YPPSPPGRSAAHVSCTLYRTTP* WPDQRSAPPTAAWAAS*SPSAR RRPSAESMVPREPL*YRPSAATS AATPAISPARALGAGAPCPLFR RRSGPFGRTSAIRPPSSAGKAVL FPPHGRPVWPVGRRLARYATAS GWGAHI*ASSGASE/PAVVSVLP AGSGASPFHSASWDPPAHPAAA ASAAAIVIPAL*RSGDRPPVLSFQ PLFWFLIRGDNVSFVWLLRGLP CPSQAVTTTRHSRQKEKLKRNR KSCVNFMQSQVSVSKYNSLVK HHHFCIRPL
8242	38610	A	8297	3	251	
8243	38611	A	8298	208	307	
8244	38612	C	8299	18	197	
8245	38613	A	8300	1	1866	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8246	38614	A	8301	2	2558	FEVLWSDSSITSVTKSSSEVTEFI SKLCLQYPEENLEKLIPLAGPD AFYVERNHVLDLSGLRYLASLP SHVLKNDHVRRFLSTSSPPQQL QSPSPGNPSLSKVGTVMGVSGR PVCGVAGIPSSQSGAQHHGQHP AGSAAPLPHCSHAGSAGSALA YRTQMDTSPAILMPSLQTPQT QEONGILDWLRKRLRLHKYYPV FKQLSMEKFLSLTEEDLNKFES LTMGAKKKLKTQLEKEKESE RRCLNPSAPPLVTSSGVARVPPT SHVGPVQSGRGSAAELRVEV EQPHHQLPREGSSSEYSSSSSSP MGVQAREESSDSAENDRRVEI HLESSDKEKPVMLLNHFTSSSA RPTAQVLPVQNEASSNPSGHHP LPPQMLSAASHITPIRMLNSVH KPERGSADMKLLSSSVHLLSL EERNKGSGPRSSMKVDSFGSA MMDVLPASAPHQPVQVLSGLS ESSMSPTVSFGPRTKVVHAST LDRVLKTAQQPALVVESTAA TGTPSTVLHAARPIKLLSSSV PADSAISGQTS CPNNVQISVPPA IINPRTALYTANTKVAFSAMSS MPMGPLQGGFCANSNTASPSR HPSTSFANMATMPSCPAPSSSP ALSSVPESFYSSSGGGSTGNI PASNPNIHHHHHHHQPPAPQP APPPPGCIVCTSCGCSGCSGSSG LTVSYANYFQHPFGSPSVTFPF
8247	38615	A	8302	2	266	YCGPL*SVWVARNPPGFAFVEF EDPRDAAGV*ELDGRTLCP/ PSWGHPR*DDYCRRGLPPRRRP PRRRNLSCSRSLYSPWTLSL
8248	38616	A	8303	37	535	ESWLVLGRRKAGRLIGACGFEP PHFLTLDLEMRDSCPL\CKV YVGNLGNNGNKTelerAFGY GPLRSVWVARNPPGFAFVEFED PRDAADA VREL DGRTLIGC/RV REELSNGEKKK/SRNRGPPPS/W GRPPSENDNRKEESFPFR/RRSP R/RRSFS/RSRSLSLF

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8249	38617	A	8304	2	668	EIAERRITQPAP <sup>1</sup> GPSRPSQGP GELGGPGTGRALCPADNGGLC CGCPLAVP/GPLAVPR/ALKPQR TSLSHPTSVTNGRGVSQGPGR RHPGLPTQASTKPPQSRDDAA LGGAGRGPGSMAAARTPRGG GH*GVDGPGRRPRDASRLGRL RPRSADPVPG*P/PVAIGRDLPS PDDNGQRP*GAWKVSE/CPERR RVERLAAIGRLVFILPDFAVGRE
8250	38618	C	8305	101	183	
8251	38619	A	8307	329	399	RERET*SSINTTFIPGSVLQPDAS PSKTGTLT <sup>1</sup> SIPVTIPENTSQSQVI GTEGGKNASTATSRSYSSIIIP GVIALIVITLSVFLVGLYRMC WKAHPGTPENGNDQPQSDKES VKI.FTGKTISHESGEHSA*GK
8252	38620	A	8308	192	537	KFPSTPENGNDQ* <sup>1</sup> PQSDKESV KLLTVKTISHESVILNQNMDEI TEIEFRIWMAMKITENQKIETHS EESEEFNKTIQGMKYEIALRKN KDTLTELKNSPQEFHNTLEVL TAE
8253	38621	A	8309	1	789	
8254	38622	A	8310	1	423	EDIWFDDVDPADIEAAIGPEAA KIARKQLGQSEGSVLSLVKEQ AFAGEELEVVQKEVAEMLKG RILVGHALHNDLKVLFLDHPKK KIRDTQKYKPFKSQVKSGRPSL RLLEKILGLQVQQAIEHCSIQD AQAAAMRLYVM
8255	38623	A	8311	1	1077	MGKAKVPASKRAPSSPAKPG PVKTLTRKKNKKKRWFWSKA REVSKKPSGPGAVVRPPKAP DFSQNWKALQEMGSKKKPKII QQNKKETSPOVKGEMPAGKD QEASRGSVPSGSKMDRRAPVPR TKASGTEHNKKGTKERTNGDI VPERGDIEHKKRKA/GQPPH PPR/DIWFDDVDPADIEAAIGPE AAKIARKHLTRALALDCMVG VGPKGEESMAARVSVNQYVK CVYDKYVKPTEPVTDYRTAVS GIRPENLKQGEELVVQKEVAE MLKGRLVGHALHNDLKVLFL DHPKKKIRDTQKYKPFKSQVKI QDAQAAMRLYVMVKKEWES MARDRRLLTAPDHCSDDA
8256	38624	A	8312	3	640	

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8257	38625	A	8313	1	1274	MGKAKVPASKRAPSSPVAKPG PVKTLTRKKNNKKRFRWKS REVSKKPASGPGAVVRPPKAP DFSQNWKALQEMGSKKKPKII QQNKKETSPQVKGEEMPAGKD QEASRGSVSPGSKMDRRAPVPR TKASGTEHNKKGTKERTNGDI VPERGDIEHKKRKA\GQPQPH PPR/IDIWFDDVDPADIEAIGPE AAKIARKQLGQSEGSVSLSLVK E\QAFGGLTRALALDCEMVGV GPKGEESMAARVSIVNQYGKC VYDKYVKPTEPVTDYRTAVSGI RPENLKQGEELVVQKEVAEM LKGRILVGHALHNDLKVLFLD HPKKKIRDQKYKPFKSQVKS RPSRLRLSEKILGLVQQAHC SIQDAQAAN*GCYVMVKEGVG RAWPETGAPCLTASRPLQ*RRL SSPALLAACPPRLQRC
8258	38626	A	8314	2	414	
8259	38627	A	8315	1	621	
8260	38628	A	8316	1	885	MGEKPGPILLFSSAKPKNPQEGE HKDEGDHPNNSFSPCSAHDHRR LQKHFAKIRDSTSGGKMKVN GAPREDARPVNKGTYLVSTGG QTVAFITGSDQDDSESLGC QEDSTALHPTSTSPGPSETVPPS LLPEATKRLLSLDFESFGQTQR NLSCPLCPAGVWQEKTLCEWR DAGGNRQAGVPQAPCMKSN ALIVILGTVTLDAVGIGLVMPV LPG/SPALLQRQAEEPSGRRTQG /RRVTPTTASAPVAPMTAGAC RSTSPKFETGAPVGAR*RSMGR PGRMPGL*IKAPTWCPOVGRLL PSLLAPGKTKTTQSPA/SGCQEDS TALHPTSTSPGPSETVPPSLLPE ATKRLLSLDFESFGQTQRNLSC PLCPAGVWQEKTLCEWRDAGG NRQAGVPQAPCMKSNALIVIL GTVTLDAVGIGLVMPVLPGLLR DIVHSDSIASHYGVLLALYALM QFLCAPVLGALSDRFGRRPVLL ASLLGATIDYAIMATPVLWY
8261	38629	A	8317	1	396	

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8262	38630	A	8318	186	2123	CPAHCWQEAMLSAWRLVMSP GGPCTQHPAPACHPSVLTTTPRK AGEPRP*WPPCPAWGLADSSK PHRWPKPPASCRPLVRRPWGP QRTLTPTLTSHWRASIR*SWNW TPSSCFPQGLGAPRLSWPRAPC Q*ERRRNLKPWT*STSR*PPDQ GATMAPSTAPAPLSRPSAPFA VVASSFPETSPERHEAAVRASS LGTRAGGTSALCPQVRVSP/HRP PNSPSISIPCMGSKASSPHGLGSP LVASPRLEKRLGGLAPQRGSR SVLSASPVSDVSVMFGRTPHSP PLAKEHIAVAAPHSPSTPWWTY PLC*STAAQN/RGSSPPQRTPGH QNSVQPGAASPSNPCPATRSNS QTLSDAPFTTCPEGPARDMQPT MKFVMDTSKYWFKPNITREQG CPGGA VSI DSRIVPAIELLRKE EPGAFVIRDSSSYRGSGFLALK VQEVPAQAQRPGEDSNDLIRH FLIESSAKGVHLKGADDEEYPFG SLSAFVCQHSIMALALPCKLTIP QRGCHTLYLSSVSVELTGA VQKAISTTFFERDILPTPTVVHFK VTEQGITLTDVQRKVFFRRHYP LTLTRFCGMDPEQRKWQKYCK PSWIFGFVAKSQTEPQENVCHL FAEYDMVQPASQVIGLVTALL QDAERM
8263	38631	A	8319	15	909	LHVSHPGHADARGGLLQPCAA PPLWLCRIQCPRWFQTPSQVF YHAATEHGKGDVYPGQCLWE GCEPFQRQRFSFITHLQAANC/ EAQ/RSTPRAQKAIVNHPSAAL MALRRGSRNLVFRDFTDEKEG PITKHRLTAALILKNIGYSEC GRSWPRASRYQQGHQDLFILRS DLPSQVFIRDKLMERRNRRTGR TEKARIWEVTDRTVRTWIGEA VAAAAADGVTFSVPVPIHIFR HSYAMHMLYAGIPLKVLSLM GHKSISSTEVTYKVFALDVAAR HRVQFAMPESDAVAMLKQLS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, \=-possible nucleotide insertion)
8264	38632	A	8320	189	4419	KPGLFP*RVY*EYVFRLSQSLGE FHQF*FKRGQY/ATTSPPSPW ANIIRKATRC*CRWRFRFIMPV MASMSA/GMLNELQQYCDWE QGGAAVVAQHVAAPPGIVEIDS EKFACQWLNHAEVFNPDSCVS RAEMYSEYLTCSKLARGGILT STGFYKCLRTVPNHTVKRVED SSNGQAHIHVVGKRRAIPLPI QMYYYQQPVSTSVVRVDSVPD VSPAPSPAGIPHGSQTIGNHFQR TPVANQSSNLTA
8265	38633	A	8321	27	674	GPQNTMPMPSPSVRVQGPQNSS QPSPFSGSSQPGDPMRKPNQNF MCLWQSCCKWFQTPSQVFYHA ATEHGGKDVYPGQCLWEGCEP FQRQRFSFITHLQDKHCSKDAL LAGLKQDEPGQAGSQKSSTKQ PTVGGTSTPRAQKAIVNHPSA ALMALRRGSRNLVFRDFTDEK EGPIITKHTPTNSCP*Y*KISGKY SECGSADWLKETMENNLSA
8266	38634	A	8322	16	341	PPGRGSAHPAARQLQTPGSAAP LS*HQGPASRGTPGPGIKARAP SKSRARGLRAAQRARLSARAR AGCA/PP*ARGAARKLGAPGTF QETLPPGTRDRKCCSGDAVVH
8267	38635	A	8323	1	400	MAEGMAMLRWTRLGTWPDDS FDEMDSTLAVQQYTQQNIR/AQ DCSNTDKNLEPPEQGDADCHG F*APRWHCASASYVASSEFAGDD RR1*IPLDPWVKKFCECWCSGPT PFRE/CPRELN*HLKDGCSCRYL RARN
8268	38636	A	8324	3	179	ISWPSPLLQGTAAALCANGAGP AGTPPGRGPVSARFGRGGAAC VCSPPSPPLAPLSR*RFVVMW WQEA*RRGPRLPLLSLPAAG SGRAAAAAELPGGRAGAR/P L/LLTPAQVQGESARG/AGAEG GRGTPG/GCPLPAGRSLCQPIG PRSPPTAALCANGAGPAGTTP GRGPVSARFGRGGAACVCSPPS PSPLAPLSR



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8269	38637	A	8325	1	1744	DFQERLSMKDQLIAQSLLLEKQQ IYLEMAEMGGLEDLPQPRGLFR GGDPSETLQGELILKSAMSEIEG IQSLICRRRLGSAANGQAEDGGSST GPPRAETFAGYDCTNSPTKIV EAPGTES/DPRLPTVLESELVQRI QTLSQLLNLQAVIAHQDSY/V ETQRAAIQEREKQFRL/QSTRGN LLEQERQRNF/EKQREERAAL EKLQSQL/RHEQQRWERERQW QH/Q/ELERAGARLQEREGEAR/ QLRERLEQERAELERQ/RQAYQ HDLERLREAQRAAQPPS/HPPSF NGEGLEGPRVSM/PSGVGPEY AERPEVAR/RDSAPTENRLAKS DVPI/QLSATNQFQRQAAVQQ/ QIPTKIAASTKGGKD/KGGKSR GSQRWESS/A*AGPPLRLGLEG ATGQALAAAGSQEIRDTCAILW RGNQKAQLASWLRPPHTGPVW SPGPKLR*STLHLLTSTLKTGV WGPALERARARRQRSLATWD QHSRTGTASFDLKQQLLNK/L MGKDESTSRNRRSLSPCTCGRH SPAPPPDPGFP/APSPPPADSPSE GFSLK/AGGTALLPGPPAPSPLP/ ATPLSAKEDASKEDVIFSKRAV TQANH
8270	38638	A	8326	147	536	WAQEGSGRNTHQYQKILDVML KGLFKVCAGRGQLMAGPVFDL GTDG*TGVLQKDG/WSALRPV LRTTRSSLAAPSLF/YFDFHNS NWNLLIRWGISFCNQGTGVFNQ GPHSPILSLVRTGVEVAREPSVG
8271	38639	A	8327	59	339	
8272	38640	A	8328	43	510	LLLWGLRELTIMVEDEGEQM SIWVLDKDLGAPHLVLVGSML TARSRCWTPWRSSSHATAATSE GEGWGVGVLIADRPGWASDEG DGEAGGGGLLTSAEFGELAAV GEAGSAHPMFSFRPRYSTWCLT HIGQGGLELTL*STRSASQSAG VTGMSH
8273	38641	A	8329	98	493	FFYFLFIYFFETESRSVTLAGVQ WYDLCSLQLPRLKRFCSLSLP SSWDYRHPPHPANFCSFLVVT GFHHLGQAGLELLTS*/SIPSSAS QSAGITGVSHHARPGPLSLANN PRSQTRTSATVCPEQLGLD

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8274	38642	A	8330	3	328	HSAARRPSSRRSSPRPETSANS VNAGWNQDPHTHIVIRFMSMAT AGSTRYR*GLHAAPSPPHPRRP RSPPGAE*A/RREARSLKR*SPPC HPTKKATMCRCIIVPLIJK
8275	38643	A	8331	24	593	FEQQWGWAAAAAPPKKAHTR *TGRSPHRPHRTQPR*NPSGTA APGPVPS*AGSSH*AGSG*RAW GPGSSRR*RSCT*RLRSRGRPPR *GPSRR*VRSARPSRA*RAPPGS HRPGCGAAAPAPAAAPARAP WAGADSSAPRTAD*SLPTRVC CSLSALHTGESGDLGPGTQIEG KQNYSVTVWFLAR
8276	38644	A	8332	24	832	FEQQWGWAAAA/CSSRQSTYSL RTGRSPHRPHRTQPR*NPSGTA APGPVPS*AGSSH*AGSG*RAW GPGSSRR*RSCT*RLRSRGR/TS MRAFSPLSAIRSPKSGRDAHHQ ASHRP CGAAAPAPAAAPARAP APWAGADSKRASSYSRLEV LK VIPEAAA WTSAGSFRT*/PENLPI PVNEIMLLSNCPGRMGSVPLKR RLILGVRVLGERGPGIAWCTCG PPTSMCTGALDLVSWAGRGMP WASQRR/PQGRDRVRDKPGTCFL PSAVPVLPCV
8277	38645	C	8333	153	269	
8278	38646	A	8334	615	1275	QKRKTFNTTKCYNKEKGSWPR WPTGSS*CAQLSWRGMEGTSK YRTE/ILKHGQEIPISEPTPPGP/S SLTCRA TWLSRAAPQPHMKPR EP*ILSIYVAPSPSTIEKPSIGERF AIFITLLMRNGDLGEASCDV K ALRQPWVGKAQVEKNQLSQT KC PAMWHFESQNPALLIVRECLEG WKAYPQSTKEERLLHPEEGAG FTSSSQEKYVRVRGQRLWPTPF FSLQMDRKRHLIPPVVIKKR GVGQDGRLEAVSVHSHGEEW KGQVNTPESTTSRSGDPI MNP LHQGLKSDMQSYMESQSSPS ATHEAQGALDTQASWKKQQQ LRKSRAISSPADGVQHGHGA RHCHDVLKRDRQTSWPCKMSS LAEEVVAADTWLLDNGT MQA TGRAAQVREQGKGMDLGQYIS CYLMTLSRAIKQKENKKVCFQ RLGKPRVKTASVQKK

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8279	38647	A	8335	423	998	PPSAVPHDHSSPART*PQSLSVI TAELEPVRAPSLIAFFHGSAC MCPFRWRYSRFSLKQQRILAH PVNTFGIDRRHTIKFCLSAKQRP YPTITIRWQLSDNMVYTEKH ISVTTAAAIHPVIGSFPIG/PIRA RALSTFLPVHIQRL*GVHFP SCRAGAGVL*SASWRQQVQRQ EQPVLRRRQQ
8280	38648	A	8336	2	218	HPSPSPGLKHRSSLGSV/PNPLL LPSGFSLLPAGHSHGDGPSAS QMH*FQNQTHPVP*PDPASLPA VQSHQ
8281	38649	A	8337	76	129	
8282	38650	C	8338	1	410	
8283	38651	A	8339	651	741	
8284	38652	A	8340	1	612	
8285	38653	C	8341	1	729	
8286	38654	B	8342	1	313	
8287	38655	A	8343	705	990	TRSSCWGKEASLGDGNGRVVA ALHHFTGAAARQHSGSPLERGP HPQL*SPRS*VEGHWLEI/LQA* S*VLPQKQPHQPARCWQLLSH WLPRLALLC
8288	38656	B	8344	1	588	
8289	38657	A	8345	220	678	MNAIPVASPCMVCSLIVHVLGS RPM*PW*RPPTRFQWSEVQE/V MELTTMRPQPPPPPPPP*QQ QQQQQQQQQQE*L*LAATPR APGTLAQGSLTPSQIFSA*RLKT DAAGSP/GSPQTITDAELRVTLT VEGKSVFVAVLPQSFTDSPH
8290	38658	C	8346	1	411	
8291	38659	C	8347	1	534	
8292	38660	B	8348	1	774	
8293	38661	B	8349	1	705	
8294	38662	A	8350	1	297	MPGHQKAPLRPAVSKK/ESMLE KGKIK*LLKPEGILPISEPPSNRIF ACWGKPAWTACCNLRARR*R AISCCPSHW*KEKPPWRPIRKPP LPARWPIH
8295	38663	A	8351	616	988	DPQLQAGSGHIPGRNVCPGERI CWRGTPD/SDPSTPTY*PPLEKE VAQGRDLIHASGLWS*IPLEA LQGPQGCPCQFSQVCCIPVIPTVE MKQGRQQLASDFQDQDLEFY EILSWKGILIIIP

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8296	38664	A	8352	1	1668	MELVPEEATAVSARAYTGRWP LDAAARTILVTPAGVGHNTIVL CGQASLDAYIKSICLKEGRKE GKKKGRRKRRDKYGGKEKK RKKGRKKGRKKKEKKKKEREK ERRKEEKEGGKKRKEKERKKE KERKKLSIGKGVVYCLSSNTQK KQVSQTKIRVISTILFILAGCIVF VTIPAVIFKYIEGWTALESIYFV VVTLLTVGFGDFVAAHPSDHL CWVIVTCKGKYLDPSPQEKAT DFSGVAQKRNEPQKPLIWC/W ELRSYPTALMMQERVV*KEKP KAAAPNRRGLGTEKLEF*R*EV AAAVEPHAVLSMIGDWLRVLS KKTKEE/VCRPPLFKSPSNLRL LGVAAHVGEIKAHA AEWKAN VTAEFRETRRRRLSVEIHDKLQR AATIRSMERRRLGLDQRAHSLD MLSPEKRSVFAALDTGRFKASS QESINNRPNLRLKGPEQLNKH GGASEDNINKFGSTSRLLTKR KNKDLKKTLPEVDVQKIYKTRFN YSLDEKKEEETKMCNSDNSS TAMLTDCIQQAELENGMIPTD TKDREPENNLSLEDNRN
8297	38665	A	8353	1	418	
8298	38666	A	8354	251	394	GAQVPTLLVGVLTVTISTVQNL AISLLGKAK*GEGILSVSGRMY RVL
8299	38667	A	8355	107	250	EEGHLLDPRMVDPMMACTM QLEKLQTLNASL*KQLGGGLYL AKPQG
8300	38668	A	8356	331	893	SITENCENKNIPHVENKDIGTK YNSLKLPEHIRAEVMQPSKLD* VNP/LPSTCKERFVMQSHLART VGSSICNL*MSP/CFGIW*QLAE ANPAKCFP/GCWTNSCTSSML CSKYVTPNGTVV*ITREGPISDD SILRFLLSMETKRMQGLLVSTA QPKGHQSSYQLHKRGPEHIERS SSQPPVAAFGIH
8301	38669	A	8357	2	416	SGFRYGSDIVPFSKVDEEQMKY KSEGKCFSVLGFCKSSQVQRRF FMGNQVLK'PFMEDLRQYMFSS LKNSKKYAPTEAQLNAADALI DSMSLAKKDEKDTLEDLFPPT KIPNPRFQRLFQCLLHRAHPL PLPSIQQ
8302	38670	A	8358	1	2130	
8303	38671	A	8359	1	1152	

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8304	38672	A	8360	1	320	FKGTAAPWPLSFARAAAGRQA GTDTRPSLRVRFPREARSQKQ RGRSVRLSAKSPPAKVETKPSG GSRTA*IFRQRSKQGKMGAKG KQAKWLLILRALICFSLSER
8305	38673	B	8361	1	1231	
8306	38674	A	8362	1	2276	GGRPKRLRTGNMVRSGNKA VLCMDVGFMTMSNPISGIESP FEQAKK VITMFVQRQVFAENK DEIALVLFGTDGTDNPLSGDQ YQNI TVHRHLMPLPDFLLEDIE SKIQPGSQQADFLDALIVSMD VIQHETIGKKFEKRHIEIFTDL SSRFKSKSLDIIHSLKKCDISL QFFLPFSLGKEDGSGDRGDGP FRLGGHGPSFPLKGITEQQKE GLEIVKMVMISLEGEDGLDEI YSFSESRLKLCVFKKIERHSI HWPCRLTIGSNLSIRIAAYKS ILQERVKKTWTVVDAKTLKK EDIQKETVYCLNDDDETEVL KEDIQGFYRYSIDIVPFSKVD EEQMKYKSEGKCFSLVGFCK SSQVQRRFFMGNQVLKVFAAR DDEAAAVALSLLIHALDLDL DMVAIVRYAYDKRANPQGVG VAFPHIKHNYECLVYVQLPF MEDLRQYMFSSSLKNSKKA YAPTR/EAQLNADV DALIDSM SLAKKDEEGQTPLKDLFP TTKIPNPSIFRGLFQCLLA QELLHPR/EA FYPPISGRHI WEYAGILPAEGGQRKSSGF PLS*N*RTLFFL*FEAKEK GFKWTAQGI FQGPWKVGPT AKKLTGARG EPTFSVSSLA EGSVTSVGSVNPA ENFRV LVKQKASFEEASNQLI NHIEQFLDTNETPYFMKSID CIRAFREEAIKFSEQRFN NFKALQEKVEIKQLNHFW EIVVQDGIT

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8307	38675	A	8363	624	1992	GRKVVVVLPPLGNQSTPGGIC LSAQLPL*RD**SASARCSSPGS *TSPPSYFLDPDRGPGRALQRFS RSPSSPGGNPAISAA PPRSKLLL GPPGVAATAAAAGAKPELRH RLPPSSATTASRV RACHFLAS AAATPAFSPPPPPPASPSQRT KEVQRAGKAAESCPAAPELLGF GGSRDSAGELGGLSSDACV/PD SSEPGVRRPARRRTLALHALTHA STHTRTLPGSCARVAVPVALCK GGFT*PIFSPQYVTNTYPGEEGA RLGVLIGREQTVSAILLGGSRSK APTITTVAVASAPPVTAAGRITP HASIRIPRMLSKPSPPPQAL*K GVMAPAQCPPARRGQAGLEGT VGFKSPTRPHQLTAASSPCNGL IRIRQGQGGGKRRWRGSSGDP GAWYCFRGRRRGSPCPSLRTAT LIPGLGGHGGSGDAASPLLGT RDGGPEAHLGKE
8308	38676	A	8364	123	248	
8309	38677	A	8365	1	540	MLEALGALNKPESSRPLIPELHL ASTAAANLGEHPNQRLKFAS QETPEESANAVPHYHKL CNRVS HVWGNRRQGHIRNTMDNRP/ GKTTFV*IIVSPALLALTHSW DSQVRPAVL/QP/YSHTGTGP*W RSSSPCAASST*KSPYP*CH*QR LSQSPSA/FRPTLRRLSRSTRCRS WRRK

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8310	38678	A	8366	31	1429	RETRSCWAHYHAESSKHQKAK LKDSRKARRSIELIGPGSSQKGG DICSLIHLSSKLGILCYSKTGNM GGWEGGMQLRVSSSENSMGKSS RERAAADLPQGSWCWHELPGRLI NTRISLKRPHVWNLSSVLCQVV KKVKSMQMFHMPITSAMQGD RLGICVTQFDPKLLERGLVCAP ESLHTVHAALISVEKIPYFRGPL QTKAKFHITVGHETVMGRMLMF FSPAPDNFDQEPILDSFNFSQEY LFQEQLSKDLTPAVTDNDEA DKKAGQATEGHCPRQQWALV EFEKPV/YLPSAVPGDWLQARC GHS/PNTCLRAFHGQSCSTG*RT GTTPATASCPG*RCTS*STSMGLV ERAMDDYSVIGRSLFKKETNIQ LFVGLKVHLSTGELGIIDSAFGQ SGKFKIHIPGGLSPESKKDPDTP PSKTGPGWVPVGGQPGRRRSPSG ANPHKMGWLTRPFKRYVFDTH KRMVQSP
8311	38679	A	8367	3	119	RSPREGGHRGPSSGGGRCRRR PGWAGNEAM*PDRRARVVGIE VPAEEGGAAVAQDGLGMKR CSLLRDL
8312	38680	A	8368	3	389	SFATHTAGPQPPAA/PAPKRMA ARASWGRNPPRAPVRTSAAAA RAAGTRRPAPARVACPLPAGPG SPRRPPRAARTRRARRRPGPGR AAQQSAGRRWTPPAPAPSGASF AAPAAGSASPSSHRRAPGGGS TQSSLLSPSSALHSSPPSRPWA ARHERSSWS*/PRSALEPTSTEP/ GPGPRRAPVLGTRSCGRGAGQL E*EA*GAA*APPPLGWTP*LLCV HVTLGNAVSHVSCGAAPPFHG GVGVGYRARSREGGHRVPA/ RTREVPSPRMGWNEAM*PFK* VSSRWPLRLPSRGMAAPRGA AAGGARRVEGWEGASLLSGSA PGSARWPRAAPASQVVGARC AAGAPCLPRVWRRGAVGAE NAPSELAASTPAG/GGRGAGSG SSDLAARGGAVAAFPFG*GHSR QQHGAEKDGGQGFGLSQPPPR SCAHQRRRGACSGNAAPSSAR RMSASSRSRQPEKATQSRNSA RSSAARPRSRSTAVSRAQVDTA SSCAFWRVFCSSCRFFCESAEP TVSTRWW

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
8313	38681	A	8369	3	1130	LDFQHINYKAMRKLKQVQE QCPNITRIYSIGKSYQGLKLYV MEMSDKPGEHE/LGYWHGEW GEVGTGGQPRHEPAASPHVSPG EPEVRYVAGMHGNEALGRELL LLLMQFLCHEFLRGNPRVTRL SEMRIHLLPSMNPDPGEIAYHR GSELVGWAEGRWNNQSIDLNH NFADLNTPLWEAQDDGKVPHI VPNHLLPLPTYITLNPATVSILR AAVEVLWGADPCLCLLPLLTCP IQVAPETRAVIKWMKRIPVLS ANLHGELVVSYPFDMTRTPW AARELTPTDDAVFRWLSTVY AGSNLAMQDTSRRPCHSQDFS VHGNIINGADWHTVPGSMNDF SYLHTNCFEVTVELFCDMFPH ENELPHEWENTDA
8314	38682	A	8370	1	2229	MWGLLLALAAFAVGPALGA PRNSVLGLAQPGTTKVPGSTPA LHSSPAQPPAETANGTSEQHVR IRVIKKKKVIMKKRKLTLTRP TPLVTAGPLVPTPAGTLDPAE KQETGCPPLGLESRLVSDSRL ASSSQSFGLPGRGRNLNQSGLE DGDLYDGAWCAEEQDADPWF QVDAGHPTRFSGVITQGRNSV WRYDWVTSYKVFQSNDSRTW WGSRNHSSGMDA VFPA NSDPE TPVLNLLPEPQVARFIRLLPQT WLQGGAPCLRAEILACPVS DPN DLFEAPASGSSDPLDFQHHNY KAMRKLKQVQE QCPNITRIY/ RIGKSYQGLKVYVVEMSDKPG EHELGEPEVRYVAGMHGNEAL GRELLLLLMQFLCHEFLR/GNP RVTRLLEMERIFLLPSMNPDPGY EIALH'RSS*LVGLSEGRWNNQS IDLNNFADLNTPLWEAQDDG KVPHIVPNHLLPLPTYITLNPNA TVAPETRAVIKWMKRIPVLSA NLHGELVVSYPFDMTRTPWA ARELTPTDDAVFRWLSTVYA GSNLA MQDTSRRPCHSQDFS/ NGNIINGADWHTVPG'SMNDFS YLHTNCFEVTVELSCDKFPPEE* ICPKEWEWNNKDALLTYLEQVR MGIAGVVRDKDTLGIADAVIA VDGINHDVTTALGPGIWRLA* PPGDYIMVDLPSSEGYHSVTRN



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8315	38683	A	8372	409	517	HFRSAGVCW*PPPLSVHGPR*H FRSAGVCWSSTDPVCLGITSR GCRTAKIAAFSL
8316	38684	A	8373	957	1230	
8317	38685	A	8374	1	2658	MVEEVLDDNILKSVFRLGSILPI TFSFPDSQGPLLQVCRSLLEIH SRPCLPGYHQWRLQNSKDCCL FLPLEASSQRGTCQMPAGALFY KVSVDPFWEVSSQETWGSIGIH LRRQSVPYQSSSAVLGDLFFSS EPACKNKSAAEAVPTAAPSPRDA LSREESREAVWPQLSHAPM GSAQLELPGGFVYTVRRKLPTQ ASVMLDAPPATKLEHPRSSSDC CVGSKNFKPVDLSLLGSMGVG SVELDHLAPWLQPPFQESERFC LSGVVPSPPLSEEINHALPKATV MASLGAVARKDNADSLHVPPP TPLFASRPVTALKYWQAPREDL QPFTRTLHWGKGNDQTFWGL VDTSELTLTPNDPKHHYGPPIK VGAYGGQVINGVFAHIQLRVN PMGHWTRPLVIFPVPERKISIDI LSSWQNHIGSLIGRKTGDSWR MTVGVRKLNQVVTPIAAAVPD VVMLEQINPSECECLKMSHQI TMRPELPIMNVWLSDPSSHEL G YAQQHFIIKWKWYICDRAPAGS ESTTSPFITQWVHEQSGYGDRD GGYTWAQQHRLPLTKNDLAM AT/AECPISQQ/QRPTLS*HGV/I PRGDQPATWVRVDYIAPLP SW KGQRRFFTRIDTYSYKFIYP PAP NASAKNTICGLMECLIHCHGIP HSIASDEGTHFIAKEVQQWAHA YRIHSWYHVPHPHPEGWGKVLQ
8318	38686	B	8375	1	3258	
8319	38687	A	8376	3	196	DWESCQNQC*PQQPRLHGTHW DPC*DME/CPSVCPCQSPCLSR DQWTIPCPDPLSPQIMAAAGR/W
8320	38688	A	8377	248	423	
8321	38689	A	8378	407	683	LSSYCVHAGCYPREAAARMISF SPSQIRWKPFGESWRPPARRGT CTPGAHPRPSPRAAGPAHRP/ PPP/PSSELPRAPQRPGRNRRPG NSGPV

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8322	38690	A	8379	11	888	TGKLHTSVICNSTELTSDWSRR LFLKGKPLLSAGAGVNVMPST APFPAPCKGSLRGNPSRPTH* RSPQLERDTGGASFRVDEGEER GASSGGSIRDTEGSGGAVPFGE SWRPPARRGTCTPGAHPRPSPS PRAAGPAHRP/PPP/PSSELPRAP Q/GPEAPTLGQPHGRGLFPPLFK LSKLYWPLGETRSRPRPRPYCQ SPGPGVTERGRWSAPRAPGAP RSPRWRRQSGPGALPRPRVNPC IQHGSEASYAPAL*WALRIPQG GNTSSADEPADFTPNQADQDM PCLHSCSG
8323	38691	A	8380	1	3135	
8324	38692	A	8381	44	2279	RQTVGDQAQPHHPPQPPRPSFP PPPALPCTAPAPQLPPSPSCREEF PSSPMQGTPTGWSSGGPWTSP PHSSSRRLASPLAPLSVIPSTSQ MARSSSQSTTRFSPTPTHSQQ ASQAGTLWPWWLRSGTMLTSP LVGGPHFIRNTRSMVNTAC*S SRPSLGLERSQTTGATRPGGP*R SRGSMPTPLPSGPGSATPTKPS SPRTGAGPMPCFSTRAVGCST WPSAQATRCWSASLVEMAISK TAH*CPSCQGRGIALIDS*IPTQA SKGCSSTGYTGKKGPTTVSSAC SG*RASLGGPAGAGTRSPALVP GSRDDGTYSNPSA*VAGASA VGSCAASPLGEEACAAATGPGE SFSEGWHEQ/TSLA VGP GTGAT ELVLPLEG/HSPTSVCTSRGGP TWAVATYRPPSPPGCSGPTSP PWMVSVTPSMGWGTSCWSGP KTGTPPSCFRAAPPRLAQRPPT SSPLRLST/ASSLGPVTQWLL EPHDAIRVLLDNQVTVFQPDHE DGGGQETFNATGVLLSRNGS/G SRPASTAGPPSR*SRSPSTSTPPP ASRPSTRTARRGSGSGITQRT TSQCPMAPPPQGALRRCFSTL E*PGRSTGQASLARGMTSCLPT SPLFSTHNCKKTAAGLNI*SPTV TEIAHASMTWPACTQASDFTR GKSVKTTSRTPPSISTRPPSMV VV*LKPTRGRPR*FSTPAMLRM

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hud	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
8325	38693	A	8382	1	2900	MVWGFTCS TTATLEGQSTAA SRTSNQDISASSQNHQTKSTETT SKAQTDILTQMMTSTLTFSSPSV HNVMETVTQETAPPDEMITSFP SSVTNTLMMTSK TITMTTSTD TLGNTEETSTAGTESSTPVTS SITAGQEGQSRRTS WRTSIQDTS ASSQNHWTSTQT TRESQSTSL THRTTSTPSFSPSVHNVTGTVSQ KTSPPGETATSSLCVNTNTSMM TSEKIVTITSTGSLGNPGETSS VPVTGSLMP
8326	38694	A	8383	3	468	SSPPLGHPRPISQSCPRPAVSCSR GPSALLCRPLLGPEADP/P*GSS WP/EGPLWGPYPSPSVVGNHG WSGAGVADE/PAAPSRPAGARR APSGGRPAAARCSRRRASRSSR PGPPAGRAGR*ACPAARSAVA AAPRPPGAP*CGSASSATAPAA APP
8327	38695	A	8384	3	1319	DSSRLCSRRSSRGHTVGLWGQS PGLGTGKRGGGG*EDPPPGTPR GQQDPSHSAKQ/PPAGLPAGVK WGPS/SSPPSPPP/PAKRELQGR PKFGRCSSEGRAGDPGPS/GCPR AKQTHSLGTAVPVVVIYYPVH ALSPAANRTL N*NIISSQPLGTPP MVPGE*HGPRGHA*PRHPLK DPPQG/PAQR*RGCRSEVQRRP GTLP*GSPP/GNSHNGLPAMP *PPTAR/PQFPNPQDPRPLGQSS EPLPRCPKTLCKTRHPDLRGRG KQPRGWAQVPPGEVFGGNGA QLEA*EGARMSASP*P*SLESD TTASPPSQGLFTAQKGLWGPQR RLGALWLGRRSEKTSWRRRLQ SQVYWSCREEVEKCSRQGARL GQRRGWENVLGKSGSASECLS CPFCASLAMPSCGPWELSKVA QCFPLKTGHGPQEGSNNLKV TQQS

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8328	38696	A	8385	1	771	HSLHSLTHSLSPVPVQSPA WLR PLCLSAPAT*ATA/CRVCLPGSC DSCSDSWQVDDCPESCCEPPCC APSCCAPAPCLTLVCTPVSCVSS PCCQAACEFSPCQSGCTSSCTPS CCQSSCQFACCTSSPCQACC VPVCKPVCCVPVCKKPVCKKP ICCVPVCSGASSCCQSSRQPA CCTTSCRPSSSVLLCRPVCRS TCCVPIPSCCAPASTCQPSCCRP ASCVSLLCRPTCSRLSSACCGLS SGQKSSC
8329	38697	A	8386	1	453	AQSLGRARPWGASSGRVPDS\ RLE*TPTVCLA/PEHGIVAATAS LGTFFLTQWEGHNGCYQRSFPP PQSMPTPPCPASETP/PVFRYRPP PSPGSSPRSITAHVPVLSVSNP PHPEVWNLCTWKRLATSLQ KFTFGPKLGTINVDSDLS
8330	38698	A	8387	39	630	IGTWRFGGSDRQEGQSRQNC EANDWPVSTALA/KPRGATGK NKSPGNDPAAAIATAGAAATA GPGSPCSLQ/NRPHLLPFIS*APP EG*TPSTQDRPWYSAGAA*ASV KCRGTGAVQKQLL*NRRRFP PAPAQTADPGRGGGRGTGS/GV PSTGSSDWQERPWPCCGMEPP RLRCLLRCSGSIHSPTALQSLRN HQ
8331	38699	B	8388	1	2673	
8332	38700	A	8389	10	281	TTSDPYHPAPEIGLG*SPN/GGP MQGDLPGASGKEVSFL*GNVN EDIHNSGCVWQPSCDHLARQP KNKAVTMETKKRQKDTGSSLF SSSCS
8333	38701	A	8390	3	416	EYGGQCQCHKRPRGPFHFSPG PRGGSYISDLGGQESPEAGGGFP PRISAL.RPKSNCSFLRPRGRGS* YPAAGRPRAPGGPALQLSPR/PH PAAPPRAAPQPKPPRRDVEPA P/PKLPHP/P/GGPAPRRQGDLP GRLQP

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8334	38702	A	8391	98	1286	TMPPTFLAHLDPQAYVFCV EGKERNLSRSKHTSPHSSTPAH LLSKPPRSSEVVYHSQVLP RPTSQLHLELVLPVFARLP GIEREQSSPY/RRGHHRGYTEE D*VNS**DGVEPYGKVA AAGPQRGRGYCCPWRQRHGRH R/RRPPIALQRRQ/PARTPSARPP IALQRRQ/QARTPSRPPIALQRRQ RHGRHRPRP/RHRSAEKTTART PSPRPPIALQRRQRHGRHGRH H/HRSAEKTARTPSRPPIALQRR QRHGRHRPRPPIALQRRQRHGR HRPRPPIALQRRQRHGRHRP WPPIALQRRQRHGRHRPWP PPIITLQRT*RHCRHGRHPL/PLQRT*Q HGCHRPWPPIALQRT*/PAWTP LAMATHRSTKKITAWTPSRPP IALQRT
8335	38703	B	8392	128	457	
8336	38704	A	8393	348	1355	GNEGKAGTSSCWDPKPAAPAV ASSLAS*GASNSTPSAAGSTVA SASWLVEWSPGVT/VGVTEG SSKLGPMLLSTSTPDEAWSP ESSCLLLVAPGVWLLPEAGFL LGIHSQGAAPPSPSSCFSTSS FLSSSSSSSSSLPMATPCDLG FSKCGSRLSPPAKALLEDALTP RGA*AWMRDRASIGADPVWLC PSLPSSFLCFLSKAVCTSSA/PP CYTTFGLSPTQKTKPSKQGLG VCSQVSRHPALGQLQDIAEDK SPPHSGSTICSLWSSSRAPCD RCTSRPSSKVQGYLCQQDSR SRTAGWKTPTVVGRHVPVKIE KESIRP ANFG
8337	38705	C	8394	154	219	

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8338	38706	A	8395	3	1054	LYLKVCYI*KELFEFSNLYKHPS GEEVWERILRV*DNNGRN\KLI YQAEFIDLGPVSRDSAFNVAQ GVKKGSRNLFPLAEIWITRW TVSELEMPDLPWFNVVEEIKRL REIGMVWISHFRCTHPSWKGP EDIPLTNALQNRVRAAPASLK SLVIALFCMSDATAAGTAVTQL QNLNTMGIIIGSRGVDRDQVVAL NHQRQVGVANRQGTPT/QRGT KKRTR*PGQAKRPGPKERGTRS HAYAHTSVTTPKNNRHDTRPS QRTFQQKRDAQHQTETPTTTP NTSRPPSHVSFFRSKKRRRRPQ HIEERNKRTRTEEEARERNRAN KDDTKRQPPKKTRENRRLWS
8339	38707	A	8396	140	398	
8340	38708	B	8397	15	192	
8341	38709	A	8398	1	1167	AGTARRAPESSRRRAVAAGHPE TMGKLVALVLLGVGLSLVGEM FLAFRERNVASREVEPV\EPENC HLIEEESGSEDIDILPSGLAFISS GLKYPGMPNFAPEDEPGKIFLMD LNEQNPRQALEISGGFDKELF NPHGISIFIDKDNVTYLYVVNH PHMEVHCGRIF*ILREQRSSGY YLUKTIKTWNFFKSVNDIVVLGP EQFYATRDHYFTNSLLSFFEMI L\DLRWTYVLFYR/PREVK/VVA KGFCSA\NGITVLSQTQKYVY VADVAA\KNIHIMEKHNDWDL TQLKVIQLGTLVDNLTVDPAT GDI\LAGCHPNPMKLLNYPED PP\GSEVLRIQ\NVLSSEPRVSTG YANNGS\VLQGTI.WASVYHGK ILIGTVFHKTLCYEL

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8342	38710	A	8399	89	1685	KGPLLLSLPCRAGAMAETSVAT GACGEAMAAEAGSSGPAGLTL GRSFNRYRPFEPQAFGASSPS(WA RLDGA FSGNERAEGCKVPQEG RLLKLLAGLTRPADVRPPILGRG LVGGQEEASQEAGLPAGAGPS PTFPALGIGMDSCVIPLRHGGLS LVQTTDFFYPPLVEDPYMMGRIA CANVLS DLYAMGITECDNMLM LLSVSQSMSEEREKVTPLMVK GFRDAAEEGGTAVTVGGTVVN PWDLLIGGVATCSIANQFEFI(M PDSAVVGDVLVLTKPFRNPGL LFNAHQWLG*FLERWD*S*RW WFSREEVELAYQEA\MFNMA TLNQNCRRV*MHTFNAHAATD ITGFGVLGHSQNLAKQQRNEV SFVIHNLPIIAKMAAVSKRASGT VWGGFGGTS\A\ETSGGITGFCPLP R\EQGGLAFCSEIQILPKYGRGS PKAWIIVGIVEKGNRTAPDPLTS PRVIEVLPRGATAA\VLAP\SS NALLLSLAREIERTEVVWTLEP LSTITDGSQELIVKKFPKKAACI VVPAAALSR

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8343	38711	A	8400	30	2391	ARGRPLLAARSSRRCGPRLPFK RAGPAPAAPHRGDQEARWFSG AAPSRLLPPAPRFSGPAAIFLSAQ GPPSGAMQPTLLLSLLGAVGLA AVNSMPVDNRNHNEGMVTRCI IEVLSNALSKSSAPPITPECROV LKTSRKDVKDKETTENTKFE VRLLRDPADASEAHESSSRGEA GAPGEEDIQGPTKADTEKWAE GGGHSRERADEPQWSLYPSDS QVSEEVKTRHSEKSQLREDEEEE EGENYQKGERGEDSSEEKILEE PGETQNAFLNERKQASAIKKEE LVARSETHAAGHSQEKTHSRE KSS/QFSAA*EAGSQENRPQESK GQPRSQEKSEEGDEDATSEVDK RRTRPRHHHGRSRPDRSSQGG SFPSVEEKGHPQEESEESNVSM ASLGEKRDHSTHYRASEEEDPD YGEEIKGYPGVQAPEDLEWER YRGRGSEYRAPRPQSEESWDE EDKRNYPSELDDKMAHGYGEE SEEERGLEPGKGRHHRGRGGEP RAYFMSDTREKRFLGEGHHR VQENQMDKARRHPQGAWKEL DRNYLNYGEEGAPGKWQQQG VLQDTK/ENRVEARFQDKQYSS HHTAEKRKRLGELFNPPYDPL QWKSSHLERRDNMIDNLEGE EENELTLNEKNFFPEYNYDWW EKKPFSEEDVNWGYEKRNLARV PKLDLKRQYDRVAQLDQLLHY



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8344	38712	A	8401	73	1922	ILPVPHP/CRQVLKTSKCPTRQA DLGHCSDDPCSYSLHITFPADASE AHESSSRGEAGAPGEEDIQGPT KADTEKWAEGGGHSRERADEP QWSLYPSDSQVSEEVKTRHSEK SQREDEEEEEENYQKGERGE DSSEKHLEEPGETQNAFLNER KQASAIKKEELVARSETHAAGH SQEKTHSREKSSQESGEETGSQ ENHPQESKGGPRSQEESSEEGEE DATSEV/DKRRTRPRHHHP/RSR PDRSSQGGSLPSEKGLPQESEE ESNVSMASLGEKRDHHSSTHYR ASEEEPEYGEGRKRGYPGVQA PEDLEWERYRGRGSEERYRAPRP QSEESWDEEDKKNYPSLELDK MAHGYPEESEEERGLEPGKR HHRGRGGEPRAYFMS/DTREK RFFGEGHHRVQ/ENQMDKARR HPQGA/WKELDRNFLNYGEG APGKWQQQDGLQDT/KENREE A*VFKINHFS/SHHTAEKRRLGL ELFNPPYDPLQWKSSHFERRDN MNDNLFEGEEENELTLNEKNFF PEYNVDWWEKKPFSEVDVNWG YEKRNLAR/VPKMDLKRQYDR VAQLDQLLHYRKKS/A/EFPDFY DSEEPVSTHQEAENEKDRADQT
8345	38713	A	8402	1	381	
8346	38714	A	8403	1	444	MKLIVGIGGMTNGGKTLTNSL LRALPNCVHQDDFFKVPALA RGVLESMDMEAMLDTVQAWLS SPQKFARAHGVSVPQEAESDTHI LLEGLFLLYSYKPLVDLYSRRY FLTVPYEECKW/KEKYPQLHSP *SPRPLRWPRVAHVPEV
8347	38715	A	8404	3	421	
8348	38716	A	8405	3	4065	SAPPDVTITYTSEHSIQVERPQGS TGSRTAPKYGNAELMETGDGV PVSSRVSAKIQQLVNTLKRPKR PPLREFFVDDFEELLEVVQQDPD NQPKPEGAQMLAMRGEQLGV VTNWPPSLEAALQRWGTISPKA PCLTTMDTNGKPLYILTYGKL WTRSMKVAYSILHKLGTQEP MVRPGDRVALVFPNNDPAAFM AAFYGCLLAEVVPVPIEVPLTR KDAGSQQIGFLLGSCGVTVALT SDACHKGLPKSPTGEIPQ

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8349	38717	A	8406	10	580	KQCALLTFICSLPMSFGFAPAIT VTVVN/PRHPLIRDMRLRIKEDE DDKTVLDLAVVLFETATLRSG YLLPDTKAYGDRIERMLRLSLN IDPDAKVEEEPEEEPEETAEDTT EDTEQDEDEEMDVGTDEEET AKMS*ALLTFICSLPMSFGFAPA ITVTVVNHVFLCSKTGSQVFRS ENWKVWAESSRGDHDCLDL CSVLCWGRTATGAFSCPAQLIF AVSSSSSVPTSSSSSCSVSSV SSAVSSGSSGSSSTFASGSMFK LRSILSILSPYALVSGKRYPD SVAVSNKTTARSKTVLSSSSLI RRSMLSISGCRD
8350	38718	A	8407	1	1967	MTMAAAVVARAGARAATA AALRGCGTAARGPCAGPAR PLCTAPGTAPDMKRYLWERYR EAKRSTEGTKKYTTSLNARHY YTHFTEENEDEINSSSYASQKK TFEINPRHPLIRDMRLRIKEDED DKTVLDLAVVLFETATLRSGYL LPDTKAYGDRIERMLRLSLNID PDAKVEEEPEEEPEETAEDTTE DTEPDEDEEMDVGTDEEETG KESDDPMAYIHFTAEGEVTFKS ILFVPTSA PRGLFDEYGSKKSDY IKLYVRRVFITDDFHDMMPKYL NFVKGVVIRKKLVKTLDMIK KIADDKYNDTFWKEFGPTTKLA GVIEDHSNRTRLAKLLRIQSSH HPTDITSLDQYVEK\MKEQDK IYFMAGSS\KAEESPVERLLA KKGYEVYILTEPVD\EYCIQALP VEFD\GKRFQNVVQGECKFHE S*ENLRK**CKSVEQRISALCLN WMKDKALKDKI*K/ALWVSSA ALTESPVLLLVAQPVVDWVSWP TLGE/RSMKAQAYQTGGHLL QIYYAESERKHFEINPQTPRLIR DMLRRIKEDEDDKTVLDLAV VLV*NRQLGSGYLFQTTLKAY GDW/RLERMLRLSLNI*PLMPK VEEPR/EEPEETAEDTT\EDTE VQDEDEEMDVGTDEKGRTSKG
8351	38719	A	8408	181	462	GMAASDSSKGTGRGKQVVAG AVGDSAKESQGGPPGAPPRRA AGL/WRHHCSF*AD*TTNAPG GKNRPFGKGAGGEQGTAGDFT QMPRTQNTL

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8352	38720	A	8409	3	228	STGVVPSQQNLPLEKASVLFNT GALYTIQIGTRCDRQTQAGLESA IDAFQRAADMSPPGLTRRSLGP TRWHQGTTH
8353	38721	A	8410	129	311	RCFQDCSHSTPGTGPRRSGCL LSSAAPW*KPPAAPRTPHRSRSH NRGPRRQQHARHQDDP
8354	38722	B	8411	1	789	
8355	38723	A	8412	1	933	TVVLKDFILEHYSEDGYLYEDE IADLMDLRQARRTPSRDEAGVE LLMTYFIQLGFVESRFPPTRQ MGLLFTWYDSLTTGVVPSQQNL LLEKASVLFNTGALYTIQIGTRC DRQTQAGLESAIDAFQRAA/VGP TRGGRASTYEMTPAAS/PEIPGA SLQREE/QWTGAWTHQQIYPQP GTPP*SPPQAQPSRFLFAMDFA ATTSAIGSARPSTNQS*GYFHTG RSWQPVAA**ECHILRGNAENVL HDLSSH***RQN**NOENLQEA LPELGHQQEQTEVSQHLVPPIG RGCTASGGEEAALPFQPSQLRQ FLVL
8356	38724	A	8413	1	389	
8357	38725	A	8414	1	506	
8358	38726	B	8415	125	700	
8359	38727	B	8416	19	338	
8360	38728	A	8417	1	3335	MAALWNTCGAWKNMLIPECH SQLLRVAANPKVREQVRLELSF VNSDLQMLKEELEGLNISVGVY QNTDEDGYLYEDEITDLMDLR QACRTPSRDEARVELLMYFIQ LGFVENRLFPTWQMGLFTW YDSLTTGVVPSQQNLLEKASVL FNTGVLYTIQIGTRRRYRHTQAGL QSAIDAFQRAAGVNLNLTETFT HNPSYDMIPAMLSVLVKMMLA QTQESVFEKISLPGIWNFFMLV KVAQEAAGVGEVYQQLH
8361	38729	B	8418	1	1689	
8362	38730	A	8419	2	722	CPGSGSERGQRQPCGRSRGRTE PGFSPC*KSAAPRPAVSLKASAP RPSSSS/GPAGISSPGRESRSCGT QNILGPFLVSG*PL*GR*QCFP AAAEPPAVPL*AEDISA/GPPAV *AP/SGLAHLASG/PGPLPPLGG AGLV*QSI**GGHQGADEGP*G EMDAKEAGPAQNCDDLHVCPCG ARGAEGAPGEGCIS*QPHAPDA L*AASELPKDELLRQCSGG*RC SPAGSAAPRAGSSAVLEPQ

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8363	38731	C	8420	144	439	
8364	38732	B	8421	1	4747	
8365	38733	A	8422	1019	1880	YCCLPRGGNAGCQTRQDPSCRPGPGSQGLSLPPGR/PGAAVECGARSRGWQQDGGPPSPGKAQVPAEPAPPQTVPGPPEDFCLGPRNEVPDGG/GARQSHHPGPPRSPGPEGSPQAAARLVDRVSRPQNQLPNPGP* <sup>*</sup> DQPPRPAIPTATPSGCNGPGFPAPRPRLSSEEA <sup>*</sup> PSRAGPEEEA <sup>*</sup> PTYT <sup>*</sup> PKLRGRPARGPVCR/PPAGPPAV* <sup>*</sup> PEFRRFALPRASVSGFQSS/PVAAGGAPDPGPGRLLYTDAHGDLPLTNTTACTGPWPAGPRHCASGAEA
8366	38734	A	8423	240	763	VLVARRPQRPGEPAVLQQ/PAAGP/PVPRKPNPSPSPAGLRPPGRAGPLTSPRCPLPAFTGHRTP/VVGPVVRPKAAGPRRRTYQGRGMGPRPRRRPVVPVGGERSHSHPSGPPLRSPGEWGLTSSSCPARGLEGVSA/TQNQLPNPGP* <sup>*</sup> DQPPRTCHPHGYTQRI/PSGPPRLRSPGPEWGLTSSSCPARGLEGVSA <sup>*</sup> RISSRIQGRRTSLPEAIPATPNGYIGSGFPAG
8367	38735	A	8424	2	609	PYSISIVSTGPSADSVYTKVRLLGETLSVQCSYKGYKNRVEGKVWCKIRKKKCEPGFARVWVKGPYLLQDDAQAVVNITMVALLQDSGRYWCNRNTSGILYPLMGFQLDVSPAPQTERNIPFTHLDNILKSGTVTTGQAPTS <sup>*</sup> SGDPADFTTGVMVFTPLITLPRP* <sup>*</sup> PPDLPPRQATASLLPAPPARDPGPGWGRQ
8368	38736	A	8425	1	252	

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8369	38737	A	8426	3	1581	ALHCAIRHEDKWPTAVRANGH LLLNSEKMSKSTGNFLTITQAI DKFSADGMRALADAGDTVED ANFVEAMADAGILRLYTWVE WVKEMVANWDSLRS GPASTFN DRVFASLNAGIKTDQNYEKM MFKEALKTGFFEFQA AKDKYR ELAVGRDAQKL VRFIEVQTL LAPFCPLCEAHLGHSWGKPG LQLWNCFPWACGRVPV*WKFL IHSSQYLMEVTHDLRLRLKNY MMPAKGKKT DKQLQKPSHCT IYV\AKE\YPPWATLPPCLFLT V KHFEGLTGKTGLDNKAIASE LGSMPCLKKYMKKVMPFVAMI KENLEKMGRILDQLQEFDEKA VLMENIVYLTNSLEHIEVKF ASEAEDKIREDCCPGKPLNVFRI EPGVSRLLVN/RQPIPMAHFL NPKLEIRQGD\TVIPIRRLMKM NRGI*RPFPKVKPGWRI**SHCW GPRRSSCPWEKEYTREDPPFPE ACLFS/DV\DLMSKKIHLTENGIR VDIGDTINLSGSLNSCTLEIYPG FLGILL
8370	38738	A	8427	1	1052	MIKNIGPQYLTPSFLGEQEGDEE EEGHIVDAEAEEDGADADAK RKEKQEEVDYSEEEEEERE ENDDMDQEERNPHRRGARKT QEQDEEVGL/GH*GGPVSRPP DAAPETHPOPGAPGA\EAVER VQAVREIHPFIDDYQYD\TEES WGQVTVKLPLMKINFDMSLV VSLAHGA VIYATKGITRCLL\NE TTNNKNEKELVLNTEGINLPEL FKYAEVLDLRLRLYSNDIHAIA NYGIEAALRVIEKEIKDVFAVY GIAVDPRHLVLADYMCFEV YKPLNRFGRNSNSSLQQMTFE TSFQFLKQATMLGSHDELRS ACLVVGKVVRRGGTGFLKQKP
8371	38739	C	8428	154	219	
8372	38740	A	8429	1	1584	
8373	38741	A	8430	200	277	

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8374	38742	A	8431	3	877	LYLKVCYI*KELFFESNLYKQPS GEEVWERILRV*DNNGRNNKL YQAEFIDLGPVSRDSAFNVAAQ GVKKGSNRLFPWLAEIWIKKW PTVREVEIPDLPLFNVEEQIKL REIMG*WISHFRPTILHSWEGP EDIPLTRPSQNIIVRAAPASLKS PVIALLYMSDLMVRTAVTQLQ NLNTMGHGSQGGRRDRVAPLNH QRQSGHGYHNGQQRESGNQNS LTGVELWHWLNHNHVSRSSEVD RKPTTFLLNLKYKQKTSRSGRK TSLNYKNRESRPLNQFPDLSQF
8375	38743	A	8432	1	282	
8376	38744	A	8433	1	281	SVHTGHHHHYHRRHHHHHHHQ HQLHQHQHQGGGHHHHHHHH HHH/HYFQ*ATWEMLLWVGHS HL*RQP*KQHEHRDDVVSQAGS VPCASRGFHIR
8377	38745	A	8434	64	302	
8378	38746	C	8435	133	262	
8379	38747	A	8436	1	1962	MFSIPTGQLRAAASGARRHRGR GSIGGPFHAIQGPVETDITTAQH ETVAPPDLAHPSPASRGPRPY/G RHLALDEPFLHISGALF*DSLAV *EPPESRLDARPGARNSNSRCPI TA/RPPTDMDGTPSAQGAQSSA/ FAQLPPPHNSTRRAPAGDMPPS MPGATELLACSVPAQ*TSELRG GGFASSLSGSPCKFGSPASSDA WPRLQPRWPVTFPEAQPLEVPG GTEHGCSPWEPLSNSAAQTFF PPLHPTAPSCPLGLPGSPGPTSS TGDIPT*QDSGTSLKLYCPLQ GGAEAAHCV/PA/PEQPETNSKR KGETPTPN/DKEGETPTPNEKKE KHQQQTKRRNTNTKRKEGETP TPNEKKEKHQHTKRRRNTNT KRKEGETEPAQGGTNPGRVQQ SPAAL*CFSY*SECQAQCPDES AGARFTAGSAPDKGL/PPGPSS WAPSS*HLILATTVHLLVTRPC* PPSCTGPSGLVVGGRPSAHH HSDLLF*SSAGKPDSPWPCWTMS AMGILRPRGRASGAPGATPFP GEFQEAHAPPVQPSTAQSLPAP CLPLGASGGPRQHPPDVSRGG DRGLQQSVLSDAAP*PGVRGNP PRGARWGARAAPGAPGAPHS PCPQMPGRDPLVYPSPGTEAQ MSCLTPQFLQILLCDFE

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8380	38748	A	8437	438	699	LLEGKLTNRKDIHTKTPSVCHH HRGPKVDKTTKMGKKQSRKAE NYKNQASAPPPKDRSS\YQQRN KAGHRMTLMS*EKKASENQTS PS
8381	38749	A	8438	1	1334	MDGRLYSVTIQPSVSNLQLLL SGPKSAVLVVITLMCSETNLSF NEFSSEFKTTSPKMSIRKPQEK SADGKQFLQNDKRNPKLGNTQ TLRLNDVSGLLSRTKRNIVPPG WYSVYVTNNYVFKKSPKAKK VSESTTKNDPVKNIHIESHNID LNKIAMNSNLQVVVKRLDITIS IAKSSWNNQPLSEGYKASKKLI EIDGKDQHADRNMTLTLNRMT CKEQLSKSVVASGNIINSHCM PTVDLNNKRLENLKKSSILDMG RLISSVENVPKYEGETSSSVSN YSSPIKLMFLSEVKSEGVKYTL TSVGTSHSNVVLPSKPTTHHV TEETETNEDISNANSENYHSS HYDITDTFQRELNKFSAKETA GSSTMFIGDINSDBKQOEPKDNS SSATDPSE/NKKTR*TKKNRSPS CETD*ATNWKTTKA*N*SNKH
8382	38750	A	8439	115	523	QFFFSLSQALKLDQAIHISMDAF HSVSELFASQSRRLDPAAMDLL VLSQGHQTNILDIVHIIKALIT KVTENRQHVAAEGKTE/SAEADD VRIT/VNRNSFTTSLIEHHFHP*I RDMKSQMQLFLQQEILFFQKSS RN
8383	38751	A	8440	1	461	
8384	38752	A	8441	3	319	
8385	38753	A	8442	112	480	IFSSLNVAYPWPEKKVVDGSKC PIQQQLERKIKNFVLYLK/RLQL TKCEFKN*RLNFIRVKNKEKY VCT/SYHTKLLFNHLMALILIV FKYQSFFSLHSCNQPHAKVLE PALELQDEDMVH
8386	38754	A	8443	1	528	

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8387	38755	A	8444	2	811	GIHTRLNSELLKEEESNKRLEAE IEYQSRLTAAISKHSESVKTER NVKLALE*TDVSVQVKMSSDI SEVEDKNÉFLTEQLSKKQIKFN TLKDKFRKKRDTLRKKSLALET VHNNLSQTQQQIKEMKEMYEN AEAKENNSTGKWSCVEERICQL QHENPCIEQLDDVHQECLPS RKEKFKSEPPAFLSGNQVKSSS CSLQTLFPPDDLILYLENPKDST KKLLELNLNKFRTGYKIKLQKS VAFLNDKNEQSKENQECNPIY
8388	38756	B	8445	1	1581	
8389	38757	A	8446	617	2972	EQNKPYQWLQRKNSKRERSE KKQPQVKEGNNNTNKKSEIQLSE NICDSTSSAAAGRLTQQRKIGK TYPQQFPKKLKEEHDRCTLKQE NEEKTNNVNLKYKKNREELERK EKQYKKEVEAKLEPTLQSL MKSKTARNTPNRDFHNHEEMK GLMDENCILKADAILRQEICTM KNDNLEKENKYLKDIKIVKETN AALEKYIKLNEEMITETAFRYQ QELNDLKAENTRLNAELLKEK ESKKRLEADIESYQSRLAAAIK HSESVKTERNLKLALERTDVS VQVEMSSAISKVKAEFLTEQ LSETQIKFNTLKD KFRKTRDSL RKKSLALETVQNDLTQTQQQT QEMKEMYQNAEAKVNNSTGK WNCVEERICHLQRENPWLVQQ \LDDVHQKEDHKEK*\LISQGRG IESGKDDLVLEEKSKLITNECD HLKESLFQYEREKTEGVPKKEN EELRKL FELISSLYNVNRIRKK NDELEEEATGYKKLEMTINM LNVFGNEFDCHGDLKTDQLK MDILIKKLKQKFDLTAKEAL SSKCVNLAKDNQVLQOEFLSM KKVQQQCEKLEEDKKMLKEEI LNLKTHMENNRLVELSKLQYK LELDEKAMQAVEKLEEIHLQEQ AQYEKQLEQ/FKQGYNTASLNK KELTLKDVECKFYKMKATAYEE VTTELEEYKEAFAAALKANSS



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8390	38758	A	8447	1	2794	AVYLSRGCVCCIRCISSLLKEPH EEGVMSCFRSVATQKNDIRPDF QLGKMDSKIKELEPQLTILYQN PKTLKFQGKKS VKFALSPSMAL RK*PFKMFSI*SIFIALQFLHGY KPILFEPNQTWPGHVAVWQD TSIVAI/SANITQKVHPVI/W/SSIP PYGVALSSLTTGTAAPLCTQL GV*IPLDCAQATFISHDKMVISL KGYLFLSSCLGNSLLKYTEKL QEPPASAIACEAADKEPPSQKK RVDTS
8391	38759	A	8448	184	427	WAIAIQRHVVYDQEWQIADPC NM**VENAETLPPGPFNLISLES SARRRATSRDDNRRFRPHRSRR SRRSRSDNALHLASE
8392	38760	A	8449	1	903	MAQKFMAPNRARTLRDICTDR EAYPVQESMSGTRGQRKEDM GGAALSTGEGGARDVKAPLPE ATLCSQMGPTRPSGLCDLAG STLAGRWMHQSDFDGGMEAS KLPQGEGVRIQPMSETRRRRAT SRDDNRRFRPHRSRRSRSD FSLHLASEREASRLKDRPPLRA REDYDQFMRQSFQESMGHGS RRDLYGQCPRTVSDALQNAF GDRWGPYFAEYDWCSTCSSSS ESDNEGYPFLGEPPIQPARLYV TSDIDCCTNTAPTASPNLPH*VA EDSCTAGKDQRAKTCIISLY
8393	38761	B	8450	1	322	

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8394	38762	A	8451	1	2460	MEEKSKRRGVLSLLILALKFG DEPLGSPNSCKYKLTTLKELG WREVFSSQLCLCTSVASQMLS QYFEYTPHPGDICHPETCALQ KVFLTSSGQSSSTSSSQQFVLQ INAIQTILEKTPTHISTPTPTLA NPTAVGLEEDREQDVGTSRRG GAWDTRIKRELEKMSKCGGQ INGGDIAFASRAGHGVCWHPP CFVCTVCNELLVDLIYFYQDGK IYCGRRHAECLKPRCAACDEIIF ADECTEAEGRHWMMKHFCCFE CETVLGGQRYIMKEGRPYCCH CFESLYAEYCDTCAQHIGEAIF GSQ/HWSFC/RCGHLCFGEWG* PQLLWMLC*LELTGKPRDAIMS SLHSWHLRKGVRRRRRKEDK SPEVLP*KSSSGTLSH*R*RPH* SLFLGSRVSLPSGECRGPYPYS HSLRLYSQALPTGRGPSSSQFP FCQFYCCYKSLLCDCLSKSPA LEKAMRGIDQGMQTYDQGHW HATETCFCCAHCCKSLGRPFL PKQGQIFCSRACSAAGEDPNQSD SSDSAFQNAKESRRSAKIGK NKGKTEEPMLNQHSQQLQVSSN RLSADVDPLSLQMDMLSLSSQT PSLNRDPIWRSREPPYHYGNKM EQNQTSPLQLLSQCNIRTSYSP GGQGAGAQPEMWGKHFSNPK RSSSLAMTGAGSFIKECREDY YPGLRSQESYSMDSSSQSFSET
8395	38763	A	8452	2	942	NKNPKNHYPESYVSLKNDFTK LTSRRHRGVEQALVQLCHVFV CEHGHVIVTLSSGFIVYRTRAN YSSSAQGVGIAAALDAVLIRA HQRTQGCHELSALLAFEKGSE KKEEEGGQVSRSSSLKVQAQE LSATEDKGHISPFWEAVYHYA SGECRGPYPYSLSLRLYSQQA LPTGRGPSSSQFFCQFYCCYK KSLLCDCLSKSPALEKAMRGID QGMQTYDQGHWHATETCFCC AHCKKSLGRPFLPKQGQIFCS RACSAAGEDPNQSDSSDSAFQNA RAKESRRSAKIGKNKGKTEEP C*TSTASCK

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8396	38764	A	8453	1	937	VHQYVYSCLPFEKVPYVNSPGEK LRKQLLHQLPPHDNEVRYCNS LDEEEKRELKLFSSQRKRENIG RGNVRPFPTMTGAICEQCGG QINGGDIASFASRAGHVCWII PPCFVCTVCNELLVDLIYFYQD GKIYCGRHHAECLKPRCAACD EIIFADECTEAEGRHWHMKHFC CFECETVLGGQRYIMKEGRPYC CHCFESLYAEYCDTCAQHIGID QGQMTYDQGHWHATETCFCC AHCKSLGRPLPKQGOIFCS RACSAGEDPNGSDSSDAFQNA RAKESRRSAKIGNKNGKTEEP
8397	38765	B	8454	214	551	
8398	38766	A	8455	1	1140	
8399	38767	A	8456	1	2525	MLNIQSVPGIGQGHSRYLHNS PMHSGDFISNIHMRKPKFREIIF ADECTEAEGRHWHMKHFCFE CETVLGGQRYIMKEGRPYCCH CFESLYAEYCDTCAQHIGEAIF GSQ/HWSPFC/CGHLFCFGEWG* PQLLWMLC*LELTGKPRDAIMS SLHSHWHLRKGVRRRRRKEDK SPEVLP*KSSSGTSLH*R*RPH* SLFLGSRVSL/PSGECRGPYPYS HSLRLYSQALPTGRGPSSQFP FCQFYCCYKSLLCDCLKSSPA LEKAMRGIDQGQMTYDQGHWH HATETCFCCAHCCKSLGRPL PKQGQIFCSRACSA GEDPNGSD SSDSAFQNAKESRRSAKIGK NKGKTEEPMLNQHSQQLQVSSN RLSADVDPLSLQMDMLSLSSQT PSLNRDPPIWRSREEPYHYGNKM EQNQTSPLQLLSQCNI RTSYSP GGQGAGAQPEMWGKHFSNPK RSSSLAMTGHAGSFIKECREDY YPGRLRSQESYSDMSSQS FSET RGSIQVPKYE EEEEEEGGLSTQ QCRTRHPISLKYTEDMTPT EQ TPRGSMEALSANATENQDDCS FVNRLKGSNNRPGRRQELMVT WNFIQERNSGMDQCDG GGG KILDPVYILTVELTGFAKGWK M FSVKDQSVNVLGFAGCLSDAG GAKRQEHLRSRMPDL SKDSG MNVSEKLSNMGTLSNMQFRS

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8400	38768	A	8457	7	302	PLPSSPEQPAGRKGTGLPCALT EIYFRVTIYFYVEIEKLLIIIVAK QEGLSGNHKPVVERKYMTYLS AQD/HELIQVVQNGHLQMGCK SETGNEASPVs
8401	38769	A	8458	1	241	MTYLSAQDHELIQVVQNGHLQ MCGKSETGNEASP/G*GRGVNP WP/RHARSRMALTRSSASCCR CSGASSICTGSLSTGG
8402	38770	A	8459	31	454	QRSAWRSQIWSASRSV*SVFVR RASSRCLNTGSGPGHPDR*DC RT/ARRCGWTRRRMASPSAAC GRSRCCSACVI/LNIVELKEVVV GNHLESIFLVMGYCEQDLASLL ENMPTPFSEAQVKCIVLQVLRG LQYLHRNFIHR
8403	38771	A	8460	1	914	SYHHLRHHHHHLPHHCF/HHN NHYYHHYHHYYHHHHCHHYH YHHLHHHHHHHHHHDHCYYH NNNNCHHHHHHHHHHHH*Y HHYHPHHHHHHHHHHHHYHH HHHHHHHRHHYYHHHHHQHH HYHHLHHHHYHHYYHNNY/HR HHRYSCNNNHYYHHHPHHY HHHHC*HHHYLYHHHHHNNH HHHYHHHHYHHYYHYH/HHH HHHHHHYHHYCHDHNHYHYH HHHHYH/AHFFHHYHHYHYHY HHHHRHHHHLHHHYCHRPHH YHYLSCCETSHTLPQNAISSFD CKYLDGQDDEDFVVYKCLTLY
8404	38772	A	8461	102	420	DTGPGEGAAGCGGGVGEV AAPAAPGHS*VG/GNQPYLSPV CSRGSPTGRAAARGLSGCWP WWSPRSGSAPSQCSSASWSAW SAGAPRFAPSAPGHPEGRRCPA
8405	38773	B	8462	121	215	

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8406	38774	A	8463	44	1584	AVLDRGPRVGSSTSPGGMSTC LSSPLFATAAELGGGLCSAGR GPRRKVYLSVDEKKLRCCQPKS GRSVAERAAGHSAEGWRPVH VGPGLLGLAL*GP*AWGFQGR KGGI*KGAYTAKCMMGSDKAQ ASGIATGGGHSAGEAVG/PQ/ QGTVLSFEGGGGLSFRMPGSL IGPSVPCCKGHPGRCPPHHA EGTDTVATVAAT/GPPLAPSHG TSWQSGSLQ*DTGPGEAA/AA AVVGVGEGAEAPAGHS*VG VISHICPFVAGGSPGTGRAAA RGLSGCWPPWSPRSGSAPSQC SSASWSA WSAGAPRSAPSAPH PEGRRCPA*GWN PQGSKSSLKS SELWTPIPYVPAVP*HTCGYA AGPAPVQTPCRGGWNGAQVGL DPIGGHGDGTPHGS/APRLPGRV GGAP*AAVAAISTDPPATASLG PAPGGPACCPSL*ACPASSASP APARSSWPPAPASCGSAAPWW HQTGHGSLWWPEHSCRLSHRS PSGAPCWPFPRASPDRGTA
8407	38775	A	8464	1	541	MKSLEEKIGCLLKFLGDLDDQT CKEDLHILFSNHGEIKWIDFIR AKEGILFKEKAKETLGKAKDA NNGNLQLRSKEVTWEVLEGE EKEALKKITEDQQESLNKWK KGCRRFGKRRKGSAAQPGSGK GKVQFQDKKTKFASDDAHDEN GSTGPIKRGREETDKE*PASKQ PKTENA

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8408	38776	A	8465	1	1326	PAALGGGVVAVAVCEPVARLL WAGTLKIAVMAENGDNKEMA ALEAKICHQIEYYFGDFNLPRD KFLKEQIKLDEGWVPLEIMIKF NRLNRLTTDFNVIVEALSKSKA ELMEISEDKTKIRRSSPKLPEV TDEYKNDVKNRSVYIKGFPTD ATLDDIKEWLEDKGQVLNIQM RRTLHKAFKGSIFVVFDSIESAK KFVETPGQKYKETDLILFKDD YFAKNNEERKQNKVEAKLRAK QEQAQKQKLEEDAEMKSLEEKI GCLLKFGDLDDQTCREDLHIL FSNHGEIKWIDFVRGAKEGILF KEKAKEALGAKDANNNGNLQ LVRNKEVITWVLEGEVEKEAL KKIIEDQQESLNKWKSGRRF KGKGKGNKSCPSGSGKGKVQ FQGGKTKFASDDEHDEHDENG ATGPVKRAREETDKEEPASKQ QKTENGAGDQ
8409	38777	A	8466	2	331	CSTSLMIREMQVKTMMRYHLTP ARMAIIKKSRPGVCGPQFTASY CSSWNRGLSRAMAQSLTPRPLS TLQ/PLLA VDRGS/PVLGASHRL PAQC/CMTDSSSSTLGSAAAGSW QQ
8410	38778	A	8467	1	209	MNSHFLKEDIQMANKHMEKCS VPLLMIREMQIKPTVRYHLTSAR MPIIKKSKNSRCWHGCGEGHT LLHC
8411	38779	A	8468	2	370	CSTSLIIREMQIETMMRYHLIPA RMAIIKK/SRCWQCGGEQETLL HSWKQPQ/LWRSSSGTARERQF LHPLLLKARIEITPPESLAVLKIP MEGTWMELEAVILSKLTQKQK TKH*MLSLTSGS
8412	38780	A	8469	2	194	CSTSLMIREMQIKTTVRYRLTS ARMAIIKKSKNSRCWHGCGEH RTLHCCLNWKERNVSYVSA
8413	38781	A	8470	341	496	

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8414	38782	A	8471	46	711	SLIHLELJFCIGLDVRLGKDFMT NNLKGNAIKTKINFWDLIKLN FCKAKRNSQ/RANR*QTEWEKT FIICTSDKGLTSRIYNKLLQISKK KTNNPIIKWAKDMNRQFSKEDI QMANKHMKKSTSLMIREMQI KTTVRYHLTSARMAIIKKSINS RCWHGCGEHGTLHLCWK/SKS LYEKDCTRMFIAAQLAIKWTW NQPKGPSINAWIKDWCQSKTN HNK
8415	38783	B	8472	36	1199	
8416	38784	A	8473	3	184	FFFFLRRSL/DSVAQAGVQWR DLSSLQAPPPGFTPFSCLSLLSS WDYRRLPPRANFLYF**RRGF TMLARMVVIS*PRDPLASASQS AGIQKNSFFLETRVSAFVAQA GVQWCDLGSPPPPPGFK*FSC LSSLSSWDYRRLPPRANFLYF
8417	38785	A	8474	3	295	AAAFFVFFETEFRSVAQAGVQ WRDLDSLQAPPPGFTPFSCLSLP CSWDYRRVPPCANFCIFSRDG VSPC*PGWRSRDLVIHPSRPPK VLGLQAMS
8418	38786	A	8475	1501	1879	IRNTHAKIIECLLPFLTEL*CNF FFFFLRRSL/DSVAQAGVQWR LGSLQAPPPGFTPFSCLSLLSSW GYRRLPPCANFFVFLVIERGFT VLARMVLM*PRDPPASASQSA GITGVSHHARPTLK
8419	38787	A	8476	1550	2469	FFPPFFLRRSSPLPRLQCSCGMI LAYCNLRLGSSNSVASASGVA GITGTCHHTQ*IFVFLVETGFHH VGQAGLEFLTSGDLPTSASQA/ RDYRRDDHTRPEKCF/C*KTHIL WHSPSWSS/EERGSQFFSQDS*K SSRYPKLLGMWVIAINIYGTR T*K*EKFKTREYIGTHSHRGNH GVNTYHVASEKLH*YTYRMK KAKNFFFFLRRRELASVAQAG VQWRDLG/SLSQSPPGFTPFSC/P ASLSWDYR/RVLPPLANFFL YFFS/MRRGFTVFSR/MVIS*PR DQ/PASASQ/SAGITGVSHRAR/L KIIFLFFFSETESRSVAQAGVQ WHDLGSRHRPPPGFTPFSCLSFP SSWDYRGPPRPPANFCVFSRD GVSPC*PGWRSRDLVIRPASAS QKCDWYRREPRPA
8420	38788	A	8477	1	2268	

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8421	38789	A	8478	1	2312	MAGPPSGPGRPEVCGAGRTRV AKARFRRRRAFASLGWSSGRE VVTFGDVAVHFSREEWQCLDP GQRALYREVMLENHSSVAGIG EDAPWGPFPCHSQHPPSQASIR GPCVYTVADVPVTGIAVIPPA VCF SRLKDCDTRTEDKEFLHKE DIHEDLESQAISENYAGDVSQ VPELGDLCDVSDRWGVPEG RRLPQSLSQEGDFTPAAMGLLR GPLGEKDLDCNGFDSRFLSPN LMACQEIPTTEERPHPYDMGGQS FQHSVDLTGHEGVPTAESPLJC NECGKTFQGNPTLFSVKQSHST GEA/SFMCDDCGKTF SQNSVLK NRHRSHMSEKAYQCSECGKAF RGHSDFSRHQSHSSERP YMCN ECGKAFSQNSSLKKHKV/HMS EKP YECNECGKAFRA/SSNLIQH QRIHSGEK/PYVCSECGKAFRRS SNLIKHHRTHTGEKPFECG*CG KAFSQSAHLRKHQRVHTGEKP YECNDCGKPF SRVSNLIKHHRV HTGEKP* KSSACGKAFSQSSSLI QHRRJHTG\ EKP HVCNVCGK\AF SY* LQCESTRFIHTGRGRPYRC SVCGKA FSHS SALLI HQGVHTG DKPYACHECGKTFGRSSNLILH QRVHTGEKPYECTECGKTF SQS STLIHQHQRHNGAEAP/YKCNQC GKA FNQSSKFSIHPQKVHIGEK\ PSPC VECGKGFSQSSSHFFQHRY
8422	38790	C	8479	194	458	
8423	38791	C	8480	214	378	
8424	38792	A	8481	107	345	GPLTCRYWEIHSQEPGPPRSLE MVLFSFSQN*SPVWSKEKNL*P *RDMR*/YAKPPGRCK*K*IQQ MTQMRGRNIQEKASP



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8425	38793	A	8482	1	1454	MHEEEGESGDSRVYMSTQCTH VTLNKFLGFVSESVSGLNIQES MKEVLRGQSLKHNPIREAGLET LQSGRQLERRGRLSGMARPLSL AAAGAPDLLFTALCSLLIEAQP LRPFDLQTTLTAAECHYTGKKF SLNEGKPVLRKNSQNTNTWEPG TIITWGRGYACVSPGDQSPVWV PTERLKL RVNSDKESHREKTSK SETAFIPAQDLAYNRFYLIILLT LSVSPVSPQTDLPAT*NYSYWA YVPFPPLIRPLTWMDAPAEIYT NDSVYMPGATDDHCPTRPREE GTA FNVTMGYKY PPLCLGHAH VDGCIHLQAQIWAAYLPERLAT REQGHLISLSLSPLRQMKGGVI GDTPNFQYKPVGKPCPKNFEGP SKILIWEDCVNSHVVLKND A YGLVIGWAPKGYFK/NNCSSGG RECLEATYFISHWEDKDHHTL HRRVSSFFPL*WEDKGITPPRPH MIFPILSLEHSELWKLAIAMSGL
8426	38794	A	8483	49	1393	AEPAPTHLPPPPSTAPQPERNSC CISQQSFSVP*/SPDSDRPRGRH /SPPPP/SPCPPPCLPPPKSTTAM PTRCQCPCPPPIPTVAAFPLPPSHF LRTLPA PRPPTQPPPLSH/TTHPP EQRTLGPKFRLFSTPSPKNLEYL MNKSGRSPGCLLREATGTADL ARSIASLTAPQTDASGISGGRST LRQTRCSSGRLRTHPRLSMRAS LPLRPRRACL PQCRDKELLITK RK YRKKKDFAA GLEDVTEFGQ REENPRHTFIYSLPLGLQKHQV LTVDIGFGGTAIMTGIA RVPLA GAAGGPGVGRAAGRGVPAGVP IPQAPAGLAGPVRGVGGSQGV MTPQGRGTVA AAAVAATASIM APPPGMRPPMPPIGLPPARGTP IGMPPPGMRPPPPGIRDCGGLT PLGDCVCLKGSLARVLCRAIVQI YSICVLLTTSEQQLSIRIHPQNA V

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8427	38795	A	8484	49	752	AEPAPTHLPPPPSTAPQPERNSC CISQQSFVSP*/S/SPDSDRPRGRH /SPPPP/SPCPPCLPPPKSTTAM PTRCQCPPPPIPTVA AFPLPPSHF LRTLPA RPPTQPPLSH/TTHPP EORTLGPKEFLFSTPSKNLEYL MNKSGRSPGCLLREATGTADL ARSIASLTAPQTDASGISGGRST LRQTRCSSGRLRTHPRLSMRAS LPLRP RRACLPQCRDKELLITK KKYRKKKD
8428	38796	B	8485	511	1349	
8429	38797	A	8486	3	431	ADAVGGPGGPGMAGCDGLPG GFGSDIRPRLWLWLGPRLWSS* RGTNII LASVPKLLLM/DCYA LARDRTATLG/TFDAISK TASN WIPDLWKETVTFKFPYQFTDHL L/VKTHTRVSKQKTQVPAVATT AARQTM EGQA PVEYI
8430	38798	A	8487	1	470	
8431	38799	A	8488	3	314	
8432	38800	A	8489	1	458	
8433	38801	A	8490	1	855	PTRPLVL RVGATARALPRPSRS CSPSAVVPSAPSSCPPQPRVTPK PEPEPEQVIKNYTEELKVPPDED CIISMEKLSTAGYSVDVDSKAI GSLAVGHLLTKCSHAFHLLCLLA MYCNGNKDGS LQCPSCKTIYG EKTGTQPQGMFVLR FQMSLP GHEDCGTILIVYSIPP/GIQGP.EH PNPGKAVSLPEGFPAQCYLPEQ RPGPAKSLRAP**R WAWK/RRLI FTVGHVPAPTGETDTVVWNEI\ HHKTEM DRNITGHGYPDPNYL QNVLAELAAQGVTEDCLEQQ
8434	38802	A	8491	1	3797	MEYYAAIENDEFMSFVGTWMK LEIIILSKLSQEQKTKHRMFSLID FGFSNLFTPGQLLKTWCGSPPY AAPELFEGKEYDGP KVDIWSLG VVLYVLVCGALPFDGSTLQNL RARVLSGKFRIPFMSGTGLVPEL DKRLKAGCLSAIECEHLIRHML VLDPNKRLSMEQICKHKWMKL GDADPNFDRLIAECQQLKEERQ VDPLNEDVLLAMEDMGLDKEQ TLQSLRSDAYDHYSAIYSLLCD RHKRHKTLRLGALP

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8435	38803	A	8492	1	2563	MGDFNTPLSTVDRSMRQKV DTQELNSALHQADLIDYRTLH PKSTEYTFSSAPHHTYSKIDNIG SKALLSKCKGTEIITNSLSDHSA IKLELRKKLTQNHSTTEKLN LLNDYVWHNEMKAEIKMFSET NENKDTTYQNLWDTFKAVCRG KFIALNAHKKRQERSKIDTLTS QLKELEKNQEEVESLNRPTG AEIVAINSLPTKKSPGPDGFTA KFYWRYYKEELVPFLKLQFSIE KEGILPNSCYEASIIIPKGRDT TKKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFIPG MQGWFNICKSINVIQHINRTKD KNHMIISDAEKAFDKIQPFML KTLNKLALQNLKLISN/SQQSLR IQNQCTKITSILIHQ*QTNREP NH E*TPIHNCFKENKIPRNP TYKGC EGPLQGELQTTAQGNKRGYKQ MEEHSMMLMGRKNQYLENGHT AQGNL*/IQMPSPSSY**LSSQN WKLL*SSYGTKKIGPHSQVNP KPKEQSWRHHTT*LQTILQGY S NQNSMVLAPKQR*RPMEQNRA LRNNAAYLQLSDL*QT*QKQA MGNGFPI**MVLGKLASHMEK AETGSLPYTYLKN*FKMD*RLT H*S*NHKNPRRKPRQYHSHVIRH GQGLHV*NTKSNNGKSN*RM GSN*TKELLHSERNYHQEQAT HKMGENFRNLLI*QRANIQLQ

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8436	38804	A	8493	1	1839	MPRALAFQAPVNIQAEQAGTA MNISVPQVQLINPENQIVEASSN LWELSAETTFFAISLLPFLISNS MPDGTNLNLSDEGEEPSPEALV RYLSMRRTVGVADPRTEVME DLQKLLPGFPGVNPQAPFLQVA PNVNFMHNLPMQNLQPTGQL EYKMSGLPLSPRLPLISWSVLPT LFLAEQSLLOPPTLQLLNGMGP LGRRASDGGANILHAQQLLK/ RPRGPSPLVTMTPAVPAVTPVD EESDGEPDQEAQVQRYLANRSK RHTLAMTNPTAEIPDLQRQLG QQPFRSRVWPPHLPDQHRSTY KDSNTLHLPTERFSPVRRFSDG AASIQAFKAHLEKMGNNSSIKQ LQCECEQLQKMYGGQIDERTL EKTQQQHMLYQQEQHHQILQQ QIQQPAQSQQVTIQVQEPVDML SNMPGTAAGSSGRGISISPSAGQ MQMQHRTNLMATLSYGHRPLS KQLSADSAEAHRLKWETREKQ LEDSSVSSNTGGDVTNEGKST ESADFGFSNLFPPGQLLKTWCG SPPYAAPELFEGKEYDGPVKDI WSLGVVLYVLVCGALPFDGST LQNLARVLGKFRIPFFMSTG YFHLGSHCNVVLNAKDKVGF
8437	38805	B	8494	1	3879	
8438	38806	A	8495	1	4065	MGKKQSRKTGNSKKQSASPPP KKRSSSPATEQSWTENDFDEL EEGFRRSNYSELREEIQTKGKE VENYEKSLKECITRITNTENCLK ELMEPKTKARELRKECRSLRSR CYQLVERVSAMEDEVNEMKDT HRLKVKGWRKIYQGNKGQKK AGVAILVSDKTDKPTKIKRDK EGHYMMVKGSIQQEELTILNIY APNTGAPRFIKVLSDLQRDL SHTLIMGDFNTPLSLDRSTRQ KVNNNTQELNSALHQA
8439	38807	A	8496	1490	1813	TGNLQNGRKLFPHTLTKG*YP ESMMNSNKFTRKKQTTPSKSG RRT*TDTSQKKTQMPPKNT*KN AHHHWPSEKSKSL*DTISHQ LEWQSLKSQETTGAAGEDVDK

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8440	38808	A	8497	1614	3085	AGEKNKADKQLQQSLRIQNQC TKITSILIHQQQTNRPNHSTPI HNCFKENKIPRNPTYKGCCEPL QGELQTTAQGNKRGYQMEE HSMLMGRKNQYHENGHTAQG NLQI/QMPSPSSYQ*LSSQNWKK LLSSSYGTTKIGLIHQVNPCKPK EQSWRHAT*LQTLQGSYNQN SMVLVPKQRYRSMEQNRALRN NAAYLQLSDL*QT*EKQAMGK GFPI**MVLGKLASHM*KAETG SLPYTLYKNQFKMD*RFKR*T* NHKNPRRKPRHYHSGHRHQGG L/LCPKHQKQW/HTKAKIDKWD LIKL/IELLHSCRNYHQSEQATY KMGENFRNLLI*QRANIQLQ* TQTNLQEKNKQPHQKVGEHGE QTLKRRRLCSQETHEKMLIIT GHQRNANQNHNEIPSHTS*NGN /QLKSQETTGADEDVEK*EHFY TVGGTVN*FNHCGSQCGDSSGI *N*KYHLTQPSHYWVYQTQTIN HAAIKTHAVCLLRHYSQ

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8441	38809	A	8498	2	2013	LNQEEVESLNRPTGAIEIVAIINS LPTKKSPGPDGFTAKFYWRYK EELVPFLLKLFQSFKEGILPNSC YEASIIIPKPGRDITTKENFRPI SLMNIDAKILNKILANRIQQHIK KLIIHDQVGFIPGMQGWFNICK SINVIQHINKTKDKNHMIISIDAE KAFDKIQPFMLKTLNKLQAQ LLKLISN/SQQSLRIQNQCTKITS ILIHQ*QTNREPHE*TPIHNCFK ENKIPRNPTYKGCEGPLQGELQ TTAQGNKRGYKQMEEHSMMLM GRKNQYLENGHTAQGNL*/IQM PSPSSY**LSSQNWKLL*SSYG TKK/GPHSQVNPKEQSWRHH TT*LQTLQGYSNQNSMVLAPK QR*RPMEQNRALRNNAAYLQL SDL*QT*QKQAMGNQFPPI**MV LGKLASHMEKAETGSLPYTLY KN*FKMD*RLTH*S*NHKNPRR KPRQYHSVHRHGQGLHV*NTK SNGNKSQN*RMGSN*TKELLHS ERNYHQSEQATHKMGENFRNL LI*QRANIQLQ*QTQNLQEKN KQPHQKMGKGHEQTLLKRRHL CSQKTHEKMLIITGHQRNANQN HNEIPSHTSQNGD/QLKSQETT AGEDVEK*EHFYTVGGTVN*FN HCGSQCGDSSGI*N*KYHLTQP SHYVVYVYQRTINHAATKTHAH VCLLRHYSQ
8442	38810	B	8499	1	2860	

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8443	38811	A	8500	3	2202	EGRNKDVI* <sup>N</sup> QREQRHNIPESL GHIQSSV* <sup>REI</sup> *NTKCPQEKAGK IQN* <sup>HPN</sup> ITIKRTRKARANTFKS * <sup>QK</sup> ARNN* <sup>NQ</sup> SRIEGNRDTKNP SKN** <sup>IQT</sup> TIREYYKHLHANNLE NLEEMDKFLDTYTL <sup>PRLN</sup> QEEV ESLNRPTGSEIVAIINSLPTKKS PGPDGFTAKFYQRYKEELRIKY LGIQLTRDVKDLFKENYKPLLK EIKEDTNKWNIPCSWVGRINI VKMAILPKVIYRFNGIPIKLPTF FTELEKTTLKFIWNQKRARVAK SILSQKNKAGGIMLPDFKLYYK ATVTKTAWYWYQNRDIDQWN RTEPSEIMPHIYNYI.IFDKPEKN KQWGKDSL <sup>FNK</sup> WCWENWLA CRKLKMDPFLTPYTKINSRWIK DLNVRPKTIK <sup>LEEN</sup> LGN <sup>TIQ</sup> DI GMGKDFMSKTPKAMATKAKID KWDLIKLSFCTAKETTIGVNR QPTKWEKIFATYSSDKGLIFRIY NELKQIYKKKTNNPIKKWAKD MNRQFSKEDIYAAKRHMKKCS TSLAIREMQIKTTMR <sup>YHL</sup> TPVR TAIIKSGNNRCWRGCGEIGTL LHCCWDCKLVQPLWKS <sup>VWRF</sup> LRDLELEIPDP <sup>AIPL</sup> LGIYPKDY KSCCYKDTCTRMFTAALLTIK TWNQPKCPTMIDWIKMWHIY TMESYAAIKNDEFMSFVGTWM KLEIIILSKLSQGQKTQRIFSLI DGN

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8444	38812	A	8501	437	2163	KQKCNISHLWNAVKVERIKYL GIQLTRDVKDLFKENYKPLLKE IKEDTNKWNIPCSWVEESIP*K WPYCPR*FTDSMPSPSSYQ*LSS QNWKLL*SSYGTKKEPASPSQ S*AKRTKLEASHYLTSNYSTRL Q*PPGKRGPPEVQGHNADENN HTFDRQGNRRHEHSIDQLAVT DVHSTTAETFLSTRGGFSKID HMLGCKTNLKNYKEIEIQSIFS NHNEIKQEINSRRKTRKSTNLW ELSSALLMNGSEKKTQVNLN WKLMAKMQHITLMECSERK NKIPRNPTYKREGPLQGLQT TAQGNKRQYKQMEHPMLMG GRINTVKMAILPKVIYRFNAIPI KLPMTFFTELEKTTLRFIWNQK RARIASLSQKNKAGGLTLPD FKLFYKATVTKTAWYWYQNR DIDQWNRTEPSEIMPHIYNYVIF DKPEKNKQWGKDSLKNKWCW ENWLAIACRKLKLDPLTPYTKI NSRWIKDLTVRPKTIKLEENL GITIQDIGMGKDFMSKTPKAMA TKAKIDKWDLIKLSFCTGKET TIRVNRQPTKWKKIFATYSSDK GLISRIYNELKQIYKKKTNNPIK KWVKDMNRHFSKEDIYAACK HMKKCSPLAVREMQIKTTMR YHLTPVRMAIHKSGNRCWR GCGEIGTLLHCWWDCKLVQPL WKSVMQFLRDLLEIPDPAIPL
8445	38813	A	8502	1	2001	MPHIQVMLMQEMDSHSLGKLC PYGFAEYSPSSCFHGFVLSVC GSSRDKATQRVDALVRQVIVN GGIVLDQFAVHDVALADLIDL LVDSLAMMLCGVPTTGDPFVA FALGHPDDFDHLILPKHLVDRY LLEPLLPVQLLSHSAVHLD LHQFCSDFSQYGIQLTRDVKDLF KENYKPLLKEIKEDTNKWNIP CSWVGRINIMKAMRPR*FID SMPSPSSYQ*LSSQNWKLL*SS YGTKKEPVSPSQALA
8446	38814	B	8503	152	3166	



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8447	38815	A	8504	15	2745	HPTVNIRQINETESQQGYPGIEL SSAPSGPNRHLQNSP/PPNQQNI HFFQHHTTPIPKLTT*LTSLDRS TRQKVNKDTQELNSALHQADL IDIYRTLHPKSTEYTFFSAPHHT YSKIDHIVGSKALLSKCKRTEH TNYLSDHSAIKLELRINKLTQSH STTWKLNLLNDYVWHNEM KSEIKMFFETNENKDTTYQNL WDAFKA VCRGKFIALNAHKRK QERSKIDLTLSQLKELEKQEQT HSKASRRQEITK
8448	38816	A	8505	2853	3925	AVGPSVRTPRPYLCVRKDVHD VVPILRPSATSLFMPRAAGQGG QKAGGTEKSSGP*KDDV*RLQP PNGFRHH*VQ*TCRKGCPLHSK RNTFQFQN*R*NLLYPALPNIPH SSVEEGVGS*ARSEDLEGAQLP *LLARLFTCRSNTYRGLKFTEA* GGE*QSIQYSTRRANYPKY/HM HPIQEDPDS*SKS*VTYKET*TP TQ**WETLT/PPLSTLDRSTRQK VNKDTQELNSALHQADLID/TT ELSTPNQKNLHFFQHHTTPIPKL TTYLEVKL/PQQM*KNRNYNKL SLRPQCNQTRTQD*ETHSKLLN YMETEQPAPE*LLGT*RNESRN KDV L*NQREQRHNPESLGHQIS SV
8449	38817	A	8506	2	376	IPYLP*STYMETGMIVVVGQIY GYHHYMQDRIDDNGWCAYR SLQTICSWFKHQGYTERSIPTHR EIQQALVDAGDKPATFVGSRQ WIGSIEVQLVLNQLIGITSKILFV SNTRKNKKVGNIVS
8450	38818	A	8507	1	1008	
8451	38819	A	8508	218	343	
8452	38820	B	8509	306	1434	
8453	38821	A	8510	3	659	

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8454	38822	A	8511	3	1990	EPHRIASPRFQAFDSGDTDRTL *FLSDIEEELTRGDPEQRHVPL RRKSEWKWAADRAAIDSRWN WLQAHVSDLEYRIRQQTDIYK QIRANKGLIGLGEVPPPEHTTD LFLPLSSEVKTDHGTDKLIESVS QPLENHGAPIGHISESLSTKSC GALRPVNGVINLQPVADHIP GDCSDAEEQLHKKQRLNLVSSS SDGTCVAARTRPVLSCKKRLV RPNSIVPLSKKVHRNSTIRPGCD VNPSICALCGSGSINTMPPEIHYE APLLERLSQLDSCVHPVLAFPD DVPTSLHFQSMKLSQWQNKPF DKIKPPKKLSLKHRAPMPGSLP DSARKDRHKLVSFLLTAKLSH HQTRPDTRHQHLLDVGAVPM VERVTAPKAERLLNPPPPVHDP NHKSMRLRDHSSERSEVLKHH TDMSSSYLAATHPPHPSPLVR QLTSSSDSPAPASSSQVTASTS QQPVRRRRGESSFDINNIVIPMS VAATTRVEKLQYKEILTPSWRE VDLQSLKGSPEEENEPAAPDV SSSHSLSEYSHGQSPRSPISPELH SAPLTPVARDTPRHLASEDTRC STPELGLDEQSVQPWERTFPL AHSQPAECEDQLDAQERAARC TRRTSGSKTGRETEAAPTSPPIV PLKSRHLVAAAATAQRPTHR
8455	38823	A	8512	119	739	ADDRDHLHIQTWCAKAPVFLQ PGSSWLSTKGKKM/PETPASDE PPLRQPAVRFELQHAAPPDLSQP LGSFGHS*GPSSDTGQPAAGR PRRQP*AAVQDLGPQTRGSASP ESQTVLPAAPSPAGSARPHGSM SASAPSPASQMSKPPCAAAC LRGSGAGGGTVGPCLEPGGSAP PRARLPRCAAGSARPGAAAGPP PGAGTTTAVP
8456	38824	A	8513	1	343	MRMCLRIPTLMTKCTNWHVT GHLCRPT/MREPTPEP/WTGDDT TA*METRWPAEQPALAERLFR AAPRGAFAGIAAPSPAAPPQPG SLGILPEPTPAQAWAARNQLRG RIKERGS

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8457	38825	A	8514	3	405	KKFNPAGERVCTILVDPSIPSTA YPSYGVPHS*GPSLSLPHL/SSSS RPSSISCPLNGPWKGCs*PPCRA QCAQPQQT*ESCHS/SSNCIPP AWEGETPSKKNKINGNPWSKIR DKTSGGEVEVWGLVAVAPVM
8458	38826	A	8515	100	1397	PPASTYLMLERLKAPWSAALQ RKYFDLGIWTAPISPMALTMLN GLLIKDSSPPMLLHQVNKTAQL DTFNYQSCFCMFQSVFDHFPEILFI HRTYNPRGKV/CIYLPGGWTSQ AAGGSSCPSSLCHPC/ARRDT/ CRPVPDVPSIQEV*SSMGESLYH PGGSSFPSTAYPS/SWSSPQLRSF SQPSTFVSSSRPSSISCPLNGPW KGCs*PPCRAQCAQPQQT*ES CIHS*ATASLQSPCSFTHTGCS TTASGWLTAAGEAELRAATTSR ASRSPPTSSASSLVPPHLRNKV WLLCSVTCRSLQTRQTSTRAC VPRTIMLPQTPSKAPNWSSW* NPTSTSPMPSAQQQPNCWA ASLLWSRNPHTSLLAAQKR*TY RSWKIPIRCSPSPLAAAAATLTR PSTCPAATS*PCSVPAARCSSPT CCRLSGRQAVLPV
8459	38827	A	8516	1	326	CLTQMYFLIS/FANVDTFLLAIM ALD/RLLAICSALRYCSITPGIYS HFYCDAYLLMKIACSIHVNQH VFLGAVVFL/APCALILVSYIRI AAAILRIPSPTRRRKACISIC
8460	38828	A	8517	2	669	TISYPQCLTQMYFLISFANVDTF LLPIMALDHYVAICSALQ*CSII P/ELCQGLPVLA*AGSSLISPVHT VIMSRlafCSSAQISHFYRDAY LLMKIACSHT*INQHVFLGAVV LFLAPCALILVSYIRIAAILRIPS PTRRRKACISICSHLSLVTIFYG TVLGICI*PPDSFSAQDAIATIMY TVVTSMLNPFYSLMNKEVQEA VRRLFSRGSHSSWCW

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
8461	38829	A	8518	1	3594	MVAAAAAATFARLRRTAATAA LAGRSGGPHCVNGGRCNPGTG QCVCPAGWVGEGQQCHCGGRFR LTGSSGFVTDGPGNYKYKTKC TWLIEGQPNRIMRLRFNHFATE CSWDHLYVYDGDSTIYAPLVAA FSLGIVPERDGNETVPEVVAT GYALLHFFSDAAYNLTFGNITY SFDMPNPNCSGRGECISNSSD TVECESENWKGACDIPHCTD NCGFPHRGICNSSDVRGCSFCS DWQPGGCSVPVPANQSFV
8462	38830	A	8519	1	471	ALCAPQPGKCFCTTKGSSG/DE CQLCEV/ENRYQANPLRGTCYN TLLIDYQFTLSQEDDRYYTAI NFVATPDEQNRDLDMFINASK NFNLNITWAASFSAGTQAGEE MPVVSKTNIKEYKDSFSNEKFD FRNHNPITFFVYVSNFTWPIKQ VQTEQ
8463	38831	A	8520	1	4289	
8464	38832	A	8521	1	3488	MDYGVLTRLTGSSGFVTDGPG NYKYKTKCTWLEGGQPNRIMR LRFNHFA TECSWDHLYVYDGD STIYAPLVAAAFSLGIVPERDGN ETVPEVVATSGYALLHFFSDAAY NLTFGNITYSFDMPNPNCSGRG ECKISNSSDTVECESENWKG ACDIPHCTDNCGFPHRGICNSSD VRGCSFCSDWQPGGCSVPVPA NQSFWTREYSNFKA/LPRASH KAVVNGNIMWVVGGMFNHS DYNMVLAYDLASREWLP
8465	38833	A	8522	4794	5740	YICNWKMKDSSFPSLVQSPRS PGSCGLSGWGWGCPRVASAGS ACSCNSAVPARRTQACRRELI GGRSTIFTDVQGGWAGPGTVN EGNSACPPTLRVTVAAWLSLLF VLCRVCAASVPSLVRLRWGPQ CSGPWGAWAPPWAARVSQPG AGPGRGAEQQLPAASIQWPC HQAPHLLLVLALVTSQGPSRCR GFCLAGPCQGGPGGLJLIFCHW NVPLQFSSLFFF*DGVSLLPR LECSGSISGHCLNRLPGSSDRPA LGS*VAGDYRCLPACSANFFVF LVEKGFHHVGRAGLKLL/MVIH LPRPPRVLRLQA

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8466	38834	A	8523	594	2868	CWTSRNRPRIPGSCHPMELPRPF RGKAKVQNHQLVHHNKALIN RGLSTFWLDDGAIQAWHCPVK TYYQYTPVSSKAMY/DAFWNG/ KFRDC/AFHSLWNEDPFVCEYQ GQSSDLQPQPVNAGGSGGGGS GGGSEGGSGEGGSGEGGSE GGSEGGSGGGSGSGDFDYK MANANKGAMTENADENALQS DAKGLDSVATDYGAIDGFIG DVSGLANGNGATGDFAGSNSQ MAQVGDGDNPLMNNFRQYLP SLPQSVCECRPYVLSAGSEIGAA CASRSGYDNKGVRDIGYTDCK RSEDLPLRHQLGGKKA/QFTL QGFTLPEGAPAGNSGSLAVHK TAQSSYRHHALLILTPMSGTRF PPIPGPVNVNIRVFPAPSSECRC YWSWVPGSPVHCQSDGSPVPI SYAPLASQYSSSFLFFNRQPYA PYDYLVSVMTPSRTLREQIRIYA PSAPRLPPPEVYCSNSTIVYVRN NPSGPTPGFAGTLLLEGRSGGP FRFYAKRAKGDVLPFSLNLPL QTLIRFMVDIACGMEYLSRNFI HRDLAARKCMYEFWRTRGWE TAAAYVGGGTTFFRKESQKLQ QSAKKRDAELANGALGIIELNN DYTLKKVMKPLITSNTVTDEIE RANVFKMNGKWYLFDTDSRGSK MTIDGINSNDIYMLGYVSNLSLT GPYKPLNKTLGLVQ/MGLDPND
8467	38835	A	8524	302	409	
8468	38836	A	8525	199	359	ARRQQSVSVKSYRWEEEDQHCG ELQGSE*VSDGLFKPP*S*HG/W VEEERQKEQN
8469	38837	A	8526	1853	2032	VKQSTALLPHAVAC*PKVISSG ARGLSILVLIRIVMMVMSMLP QLALSGWGRFVLP
8470	38838	A	8527	118	445	AAGGEPGDAPWVPGVWEPPES VCRGPPPSSTFPHVPLSTFGASG PENSRDCSWLSPOH*AA*VASG NNGPQAAQGSLSGIPDAATLSG I*RASILHVSVEIISSPGFR

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8471	38839	A	8528	1	770	MRVLGIETSCDEGTGAIYDDEK GLLANQLYSQVKLHADYGGVV PELASRDHVRKTVPLIQAALKE SGLTAKDIDAVAYTAGPGLVG ALLVGATVGRSLAFALGRFGDP CTPYWRASVSARCWKIPAPNFR CALLGSAAYAVNHGTGLSKKP TTLGSDHJSKTPAQLAKRAGEA RRNGWQGA LFPWESARSGEEE TP/VICRH*HSHRAAAKSGLGA GGTSSGGRYRLGGYSILADHGG *KFHCA*RHGATSGDGKVL D
8472	38840	A	8529	3	834	VGRVEIADQYQDLAILWNCLG SDHASSRQRRPFRGKAKVQNH QLVHLQSSHQFWLPHFLAG* WGD SGLGGGS/EGGGSEGGGSE GGGSEGGGSGGGSGSGDFDYE KMANANKGAMTENADENALQ SDAKGKLD SVA TDYGA AIDGFI GDVSGLANGNGATGDFAGSNS QMAQVGDGDN SPLMNNFRQY LP SLPQSV ECRPYVFGAVRHDV RRIRVTGVTRVTPPEEVDTSVH SRGAHRIRSGFAPKRSVRVTTD TCIKRNSTCGVKLSLWDGGGF
8473	38841	B	8530	1	811	
8474	38842	A	8531	1	1044	
8475	38843	A	8532	3	1472	GVVGERAGMARPGRPREGGGS G/GYSRPVPPAGGPGP*RGRTRI/ SGLANGAGPVVFQFLTELTRLF QKCR TSGSVYITLKKCKQREGS RAMLP GPFPYTPVSSKAMYDAY WNGKFRDCAFHSGFNEDPFVC EYQGQSSDLQP PPNAGGGSG GGSGGGSEGGGSEGGGSEGGG SEG D GSEGGGSGGGSGSGDFD YEKMANANKGAMTENADENA LQSDAKGKLD SVA TDYGA AID GFGIDVSGLANGNGATGDFAG SNSQMAQVGDGDN SPLMNNFR QYLP SLPQSV ECRPYVFGAGKP YEFSDCDKIKILRGVFAFLLYV ATFMLPVIANIAIPQKRPFMQQT RCEVQCRE D IEVQKLKSYDKLL ASINKKPGVNGWQKRRTVNA GEAHDQQALDYALYHLRIMTP AHDERS SIAAKGLTGE GYKGH VFWDTEVFLLPFLHFS DPTVAR SLLR YRWHNLPGRARRKRDGN GWAGGAPISV GKARAAKK
8476	38844	A	8533	609	855	

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8477	38845	A	8534	369	1278	GHTACFWYSQGRHPGPELSPFL *GPG*NAGHVISMPAARPMPC LGTGGLDVLHHLRDLPPAAL PGSAWPGEGALPLPGVSGRG RSAACLQPGAWPGRGAAPVRR RPRAAAGSVREAELESPLHA AHRDC*LARKLNSGGYIPQAEY GKHAGLPLPGARALSCGCRAR APVPAALPHLLDHQDPGPAGR IYGTGAGTQTLDGSAPTSRAL GSTQMPPEARPLAGWGVAGV WSRG*SR*TRGSAS/SPRPRRCA LLALPGAASVGLDRLARNPRGSR PPKAPSGRGGPLPPHRSTPRR
8478	38846	A	8535	3	2494	YQRQSSPEDPAETASPTYALIA ACQSEIQLQTRQQPCDMPAGPL DCDPVKGSSRKRMLMNAPPV VALQPKWEASVPPGSFRPECF SEADKGVESMSPTMHKELPAL AACGLVADFPVGEETADFG PLVLDSDSDSVDRDIEEAIQEQ L/KGGGSRCKRELAHSS/APTAL CSPKLVPGGG/GPGGSQVGS KDQGSASPVMSRADSFQESIR AEIEQFLNEKRQHETQKCDGVS EKKPDTHENSASLSKSHQEP TKVVHRQGLMGVQKEFAFCRP PRLAKTNVQPRSLRSKVTITTT QEKEGSTKPA TP/TRPSEAVQN KSGIKRSASTARRGKRVTSVQ APEASDSSDDGIEEAIQLYVQ KTRKEADGDPQRVQLQEERA PAPPAHSTSSATKSALPETHRKT PSKKKPVPTKTDPGPDLDAD IISP KIPKETKAPPTSPASRSKF VEWSSCQADTSAELNAVLDIFK TILP/APMEGSDGSLASPLFYSP NVPSRSDGSSVSDSDSIEQEI WTF LALKVQSRLLARGAAGQ APERVEKQAPAGAEELPKSKRD SCEGSRKKPPSVFGSRAERTKP RPSCSSVSDSDSIELEIRKFLVE KAKESGVPGQAQPLWKPTLA GEEGLRSPAKQEGLTSAIVAGIS AALGPEHTWVPGATTPTPSVA PVLVPAVPTHWKKLAPACGGP

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8479	38847	A	8536	1	2463	MHKELPALAACGLVADFDPVG EETADFGPLVLDSDSDSVDR DIEEAIQEYL/KGGGSRCKRELA HSS/APTALCSPKLVPGSGG/GG PGSQVGSSKDQGSASPVMSRA DSFEQSIRAEIEQFLNEKRQHET QKCDGSVEKKPDTHENSAKSL KSHQEPATKVVRHQRGLMDVQ KEFAFCRPPRLAKTNVQPRSLR SKVTTTTTQKEGSKPA TP/TR PSEAVQNKSGIKRNASARRGK RVTSIAQAPESDSSDDGIEEA IQLYQVQKTHKEADGPPQRV QLQEERAPAPAHSTSSATKSA LPETHRKTPSKKKPVPTKTDDP GPGDLADHSPKIPKETKAPPP TSPASRSKFVEWSSCAQDTSAE LTA VLDIFKTLIP/AMEGSDGS LSASPLFYSPNVPSRSDGDSSSV DSDDSIEQEIWTFALKVQSRSL LARGESCPQAAQGPLSPPGLSS QTGSPKAPLSKTLDDL/LGCKRK HRGG/SKAQPARPRDGRAPLG WDL SIQGTASEAPGGEGAARVP GDTRTSQGQKTD EARHLDDK KSSDKSSSLDSKDLDTAID LLRESQGPAPSPGSLSDNSSSV SDDSIEIRKFLVEKAKESGVP GQAQPCLWKPTLAGEEGLRSP AKQEGLTSAIVAGISAALGPEH TWVPGATTPTPSVAPVLVPAV PTHWKKLAPACGGPGQSLDID
8480	38848	B	8537	1	3345	



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8481	38849	A	8538	1	1339	MTKKSPGPDSTFGHWCVISIPS GYERSRLKVTLP EEGRGALPFL VSVAISSGSCSDNNAAVPTVLE GATTVISAAVLRDPHDGAREII LEAMTISAVAIAAEISWTSQCG LCLHPGMFMPYRHGDGIRDLLP LVL SATICA EFFKGDSKKPSKK RVKRKPYSTTKVTSGSTFNENI RRYAVHTNQCRPHGSRVKKK RYPQEDDFHHTVFSNLERLDKL QPTLEAEESLVHKDRGDGERP VNARVVQVAPLRLESSYSGIT CQENNLDAKKA/TP/CRTPYMT SLTRTPHTTSLTRILSTA/SANEA ADKGANEDAAQGANEDAAH GMPARMPPRASPTRSPPRASPT RTPPRASPTRTPPRASPRTPPT GSPRRTPPRASPTRTPSTASPTR TPPMASPTRTLTALLTRMPCT ASLMRTPTYTSLMRVPYMTSL MTPYKAR
8482	38850	A	8539	1	3090	MHKELPALAACGLVADFDPVG EEETADFGPLVLDSDDSDVDR DIEEAIQEYLVKGSSKDQGSASP VMSRADSFEQSIRAEIEQFLNE KRQHETQKCDGSEKPKDTH NSAKSLSKSHQEPATKVVRHQ GLMGVQKEFAFCRPPRLAKTN VQPRSLRSKVTTTTTQKEGST KPATP/TRPSEAVQNKSGIKRSA STARRGKRVTS AVQAPEASDSS SDDGIEEAIQLYQVQKTHKEAD GDPPQRVQLQEER
8483	38851	A	8540	1	2919	MHKELPALAACGLVADFDPVG EEETADFGPLVLDSDDSDVDR DIEEAIQEYLVKGSSKDQGSASP VMSRADSFEQSIRAEIEQFLNE KRQHETQKCDGSEKPKDTH NSAKSLSKSHQEPATKVVRHQ GLMGVQKEFAFCRPPRLAKTN VQPRSLRSKVTTTTTQKEGST KPATP/TRPSEAVQNKSGIKRSA STARRGKRVTS AVQAPEASDSS SDDGIEEAIQLYQVQKTHKEAD GDPPQRVQLQEER
8484	38852	B	8541	1	1122	
8485	38853	A	8542	1	1074	
8486	38854	B	8543	1	1017	

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8487	38855	A	8544	1	1436	MNLPRALRSTPQRSLRSDG EDGKIDVLGEEDEDEVEDEEE EASQQFLEQSLQPGQVQARWG GVALPREHIEGGGGPSDPSEFG TEFRAPPRSAASSEDARQPAKP PYSYIALITMAILQSPHKRLTSL GICAFISGRFPYRRKFPWQWQ SIRHNLSLND CFVKIPREPRGPG KGNVWSLDPASQDMFDNGSFL RRKRKFQRHQLTPGAHLPHFPF LPAAHAAALHNPRGPLLGAAPAP PQVPVGAYPNTAPGRRPYALLH PHPPRYLLLSAPAYAGAPKKAE GADLATPA/ALPVLQPSLATVK PVGQFCNSSSGIRRRTGNGCAP TKGAVLGGHLSAASAAA VSG GGRGLWADIARALWAERDLTS FFSIAHAQFPGRVRRALLEPGSR QPHSPTGVQKRPLLAPAGLGQ SKSSETTENRG/CPMSCQLLAGL RSNSPLSVVRKRLRADLPSFIAN KRPGRAATAAEPRRDFL
8488	38856	A	8545	1	1287	MNLPRALRSTPQRSLRSDG EDGKIDVLGEEDEDEVEDEEE EASQKFEQSLQPGQVQARWG GVALPREHIEGGGGPSDPSEFG TKFRAPPRSAASSEDARQPAKP PYSYIALITMAILQNP HKRLTSL GICAFISGRFPYRRKFPWQWQ SIRHNLSLNE*FVKIPREPGHPG KGNVWSLDPASQDMFDNGSFL RRKRKFQRHQLTPGAHLPHFPF LPAAHAAALHNPRGPLLGAAPAL PQVPVGAYPNTAPGRRPYALLH PHPPRYLLLSAPAYAGAPKKAE GADLATPGTLPVLQPSLGPPW E/RGQGGGVATGR/GCISFSIESI MQGVRGAGTGAAQSLPTVAW SYCPQLQRPSLARTILQQQQQH QEEDCANGCAPTKGAVLGGHL SAASALLRYQPVAKGLWADIA AAPLGEGTSPVFL

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8489	38857	A	8546	202	823	AQNPTAFGVKHTSSGGEETFPN IRGIKSPPOLSSSIRL.SKNILST TGKTVHQTRDDQPRDFFKKR NRVNESHQKSSNMNAGPSWVK VQHSKNSSGKRQSKSQVPHASS QPRSSLTAVTQPTEEKLIESISPE ARRKRNPGLGFRCCGASRNKLF DFQSMKIIKENADEDSASDLS SGKNSSHSSPHTSRSSQSS*RN RVNESHQKSSNMNAGPSWVKV QHSKNSSGKRQSKSQVPHASSQ PRSSLTAVTQPTEEKLIESISPEA RRKRNPGLGFRCCGASRNKFLD FQSMKIIKENADEDSASDLSDE RIPPPSPLTPPDLNLRAEEIGSSL L
8490	38858	C	8547	219	1013	
8491	38859	C	8548	252	452	
8492	38860	A	8549	25	443	
8493	38861	A	8550	20	1371	RLRGPALGAGGGSVTLRL/PRS EQAARKEAGLNTMIPLEKPGSG GSVPRRHLRLPGGSSGS*AGRA RTPPPQARGLLTEIRAVVRTEP FQERLQPVPRAGSWAGGKFSSG EKMYKEKILGKNLLQSS*EKRR KISQDCRMIIHEIAVLELAQDN PWVINLHEVYETASEMILVLEY AAGGEIFDQCVDREAEAFKEK DVQRLMRQILEGVHFLHTRDV VHLDLKPQNILLTSESPLGDIKI VDFGLSRILKNEELREIMGTPE YVAPEILSYDPISMATDMWSIG VLTYVMLTGISPLGNDKQETF LNISQMNLSYSEEFVLSA VDFIRTLVKKPEDRATAEECL KHPWLTQSSIQEPSFRMEKALE EANAQEGHVSVPINSDTDKSE TEESIVTEELIVVTSYTLGQCRQ SEKEKMEQKAISKRFKEEPLL
8494	38862	A	8551	1	1275	
8495	38863	A	8552	1	4173	

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8496	38864	A	8553	2	5115	PDQFHNMDLRGGPHDGVITPRS TSDTDLVTSDSRSLTMVSSYY SIGHSQDLVIHWDIKEEV DAGD WIGMYLIDEVLSENFLDYKNRG VNGSHRGQIIWKIDASSYFVEPE TKICFKYYHGVSGALRATTPSV TVKNSAAPFKSIGADETVQGG GSRRLISFSL.SDFQAMGLKKGM FFNPDPYLKISIQPGKHSIFPALP HHGQERRSKIIGNTVNPWQAE QFSFVSLPTDVLIEVVKDKFAKS RPIIKRFLG
8497	38865	A	8554	202	260	ARVHQPVSLKQRFPLELRHH QDSEAHAPPPGAAASRGGI*V AWPAPRAGVVSLGCRSSWTA AMELSAEYLREKLQRDLAEH VLPSPGGVGQVRGETAASETQ AGERVPSRRAPAHPL
8498	38866	A	8555	72	578	GSKGSVAGARAWVVSLGCRS RWTAAAMELQRRIPPREAAGP WRRSMWRWRTRPSTVAPVASE SWWCRPSSRGNRCFQRHSLDPS MTHCDMVITYGLDQLENCQT CGTNYIISVLLNLT LIVEQINTKL PSSFVEKLFIPSSKLLFLRYHKE KEVVAVAHAVYQAML
8499	38867	A	8556	299	939	LPSPGGVGQVRGETAASETQVL YRAMRRVTAANQAFFSEAEVT AAKERGIVLPLRC/DPS/QTHCD MGITYGLDQLENCQT CGTNYII SVL/NLLTLIVEQINTKLPSFVE KLVIPSSKLLFWRYHKEKEVVA VA/HAVLSRPMQLGRNIPCFG RTAY*V*YWGKWTGCPNLNL PGTVCNFPEACSEIKHAEAFKNH VFVNDNAKFVVKFDLN

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8500	38868	A	8557	1407	2783	SSAASHSSSPGAASRARATAGS RRRSSPIQSCHPASACGQSQGS ETHRLAMRNRTPPS*GFSSK/H MRRSSSLASS*RG*KSVAVIL*IS ASGILPTDVILSPTPGSSETCHR PHPGH*EPDCLQKLPAALG*S *QFQLSHNSPRSA*AQYA/ESSG NSFFSSKVG*D*RFITTTVA/PGGP GRRTLPGKPSPEHPHRLPELPPP RSPAQVCDQTLVAPHDHNTAG/ TPGDQVCLTLVTSRSLVLSK GCFFLHIIISTLSVQAGVRHLSLV S*AAEPTSYL*VGPKLMAPS*K LKIRTRKPRADDSPGTSRYSSA HTRTRKPRADDSPGTSRYSAH TRMWKPRADDSRH/SRYSTGCR SPGQMTLHAPADTALHTPG/PR KPRADDSPGTSRYSTAHTRTRK PRADDSPGTSRYSTAHTRTQKP RADDSGTGTSRYSTPLASRRHRI AASASWALVVLICLTL
8501	38869	A	8558	92	1817	PLRNTGLCRGKGHPGLESSGR RRRDGRASERRQTQREGKTL CSSHSPWWLKANASAPAVWSQ AHTRTQKPRADDSPGTSRYSTA HTRTRKPRADDSPGT/PD TALQTP GRRSPGQMTPGTSRYSTGRGSP GQMTPGTSRYSTERRSPGQMTL QTPADTAQDAEAQGR*LQAPA DTALHTPGRRSPGQMTLQAPA DTALHTPGHRSRGKMTLQAPA DTALHTPGRGSPGQMTLQAPA DTALHTPERSEPGQMT/PRRPA DTALHTPGRGSPAQMTLQAPA DTALHTPGRRSPGKMTPGTSRY SAHTRTRKPRADDSPGTSRYST AHTRTQKPRADDSPGTSRYSTA HTRMRKPRADDSRH/SRYSTGC RSPGQMTLQAPADTALHTPG/P RKPRADDSPGTSRYSTAHTRTR KPRADDSPGTSRYSTAHTRIRK PRADDSPGTSRYSTAHTRTQKP RADDSRHQIQHRMQKPRADD SPGTRRYSIAHTRTRKPRADDS PGTSRYSTAHTRTRKPRADDS TSRYSTAHTRTQKPRADDS TSRYSTRAGCCPPGLASSAWAGL RLKTRKGWTW

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8502	38870	A	8559	13	299	EKGQDILQNLFWQLRHGPMSS APSASNTGWGSSS*SIIPSSTVSS WSTAMKLSLSEELAMTFHST ENIVVLGWVQWLTVPVVPALWD SEAGRSP
8503	38871	A	8560	337	1879	VHVGAAARRGFGVYPVLSLTVS GTQNCGPCLQTVVSTYQRV*PI SVIMVS*RLSRKETFSGRAVPILI LEPQSLASRTVHAIMM/HNQS MYVFGGCTQSSCNAAFNDLWR LDLNSKEWIRPLASGSYPSPKA GATLVVYKDLLVLFGGWTRPS PYPLHQPERFFDEIHTYSPSKN WWNCIVTTHGPPPMAGHSSCVI DDKMIVFGGSLGSRQMSNDVW VLDLEQAWSKPNISGPSHPHR GGQSQLFKDAWLLHMHSGPW AWQPLKVENEEHGAPELWCHP ACRVGQC VVFSQAPSGRAPLS PSLNSRPSISATPPALVPETREY RSQSPVRSMDEAPCVNGRWGT LRPRAQRQTPSGSREGSLSPAR GDGSPILNGGSLSPGTAAVGGS SLDSPVQAISPTPSAPEGYDLK IGLSLAPRRGSLPDQKDLRLGSI DLNWDLKPASSSNPMDGMDN RTVGGSMRHPPEQTNGVHTPP HVASALAGAVSPGALRRSLEAI KAMSSKGPSASGRH
8504	38872	A	8561	25	313	

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8505	38873	A	8562	1	1409	MIERVLGKQWALSRAEGLRRH QCLEFLIHLVFQLMKVVNEMCP NITRIYNIGKSHQGLKLYAVEIS DHPGEHEVGEPEFHYYAGAHGN EVLGRELLLLLVQFVCQEYLAR NARIVHLVEETRIHVLPSPNDG YEKAYEGGSELGGWSLGRWTH DGIDINNNFPLDNTLLWEAEDR QNVPRKVPNHYYAIPWFLEN ATVAAETRAVIAMWMEKIPFVLG GNLQGGELVVAYPYDLVRSPW KTQEHPTPTDDHVFRLAYS ASTHRLMTDARRRVCHTEDFQ KEEGTVNGASWHTVAGSLNDF SYLHTNCFELSIYVGCDKYPHE SQLPEEWENNRESLIVFMEQVH RGIKGLVRDSHGKIPNAISVE GINHDIRTA/TDGDYWRLLNP/G EYVVTAKAGRFHCIPRTCMV GYDMGAHK/CLNFTLSKTN/LA RIRRDHWRSGKAAPSALPSPG G*KLGR/KRRQRG
8506	38874	A	8563	3	749	KTDHILGHKTCCLKTRFKIEIISGI LSDHSGIKLQINNKGNGFNHTS TWKLNNMLLNDQ*VNEEIKKEI *NHPEPTNDNGNATYQNL*DTG KEVLRGKL/IPISTYIK*VEKLQI NNLTMHLKELEKPEQTKRKITR RKEIIRAEINEIEAKKTIPKFN ETNSWFLENIHKTNEHLARLRK KDPNKIRFEKEDIITDTVEIQRRI RSYYAKKWENLEETDKFLDTY NLPRLNNEEVQNLSPITTTVPI
8507	38875	A	8564	1	842	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, ▽possible nucleotide insertion)
8508	38876	A	8565	1	1203	VPELFNGCRQLLEEVEVAT*PR RFRDSPGGSVQGLWTSRLRAAE MLFPVHLVPRPM*ILERFVPHA LDYLLGSRLFKPEPLPKQVNP RSLDHLQVAREHFNYLTQCH CYHVAEFELPKTMNNSAENHT ANSSMAYPSLVAMASQRQAKI QRYKQKKEHRLSAMKSAVE SGQADDERVGRGYLLHLQRW VDISLEEIESIDQEKILRERDSSR EASTSNSSRQERPPVKPFHSHF GTWLHSQSTFGAGYSKGWPTY RTVSDWYEQHRKLWSTYPDQ GIAKAAPEEFKRAAQQQEDQ KKRRKRMRTKQLPQSPGVGM TGS DTHP*GPMGTDRTWADLP TTPQDSGVHTPLPRKTMQSSP PPVSWLQLCTTEGDKAKSCFAF SKVSSDLSVYLYP
8509	38877	A	8566	1	995	GTKELLT*LGGSPLLLT*TKPL GVDPL/LKGGVTQGFNEKAVFA ALRPSYGGQPAKPAFAGAMSL AGAQQSLWSVEGKNLVCGL LKLTKANVIHATVTSVTLHSTE GKALYQVA YENEVGNSSDFYD IVVIATPLHLDNSSSNLTFAGFH PPIDDVQGSFOPTVSVLHGYL NSSYFRFRP*AFPLSNILTTDF PSFFCTLDNICPVNISASFRRKQP QDAAVWRVQSTKPLFRTQLKT LFRSYYSVQTAGVGRANPLYG FRPHGFPRFALHDQLFYLNAL WAASSVEVMVAANKVAFW LYNRWYQDLKDIDQKDLMIH
8510	38878	A	8567	1	372	



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8511	38879	A	8568	1	1699	MHAKSIKTQALADMEKIKVVV RDKNWVARIIPQMTSGKHVGV TTTSSAKLSQGGKDSVAVKRV RSGLMIGFRFMVIPPYSFGPQVL MEIPKADADKLLCPSCAAVVLG QKKHETQTLSELKELPVQDNVV PKEDPGTWEWRTVKEGILEEV MCWLQSRVEGDWAKEERKIFH EGELAEAKAGRGGLASCTCCPL TPGKMAGPWTFTLLCGLLAAT LIQATLSPTAVLILGPKVKEKL TQELKDHNATSLQQLPLLIAM REKPAGGIPVLGSLVNTVLKIH WLKVITANILQVVKPSANDQE LLVKIPLDMVAGFNTPLVKTIV EFHMTTEAQATIRMDTASGPT RLVLSDCATSHGSLRIQLLHKL SFLVNALAKQVMNLLVPSLPNL VKNQLCPVIEASFNGMYADLL QLVKVPISLSIDRLF/*PSVSC QG*HHSALPGGQVVGLTGKGD QVVHNSAASLTMPITLONIPFSL IVSQDVVKAAVAALVSPSEFM VLLDSVLPESAHLKSSIGLINE KAADKLGSTQIVKILTQDTPEFF YRPRPCQGGPTDRAGSVSLQ
8512	38880	A	8569	1	1060	MGLPAQGVGGNTLAKLLASDD IAKGGKRNKSEASVVRNAADA PKVLQDLSARLMGDFELRNCN SPCTLLIGIVVLINAAETLVFLS DHMEDQGSQNLNVAVLSYFQQ QDPEGQKEETAGIDLMDMASDI LQPKGDDVARISWYLRDIITRY QETFNVIERCPKVIAAVHGGCI GGGGAAAPMPRPLASSLSSVM GQTVSQEAAAPPQSQQWFWWS FSIPGLYLLGVDLVTACDIRYC AQDAFFQVKEVDVGLAADVGT LQRLPKVIGNQSLVNELAFAR KMMADEISSKSPVALQ/S/KVN LLYSRDHSVAESLNYVASWNM SMLQTQDLVKSVAATTENKEL KTVTFSKL
8513	38881	B	8570	331	1200	
8514	38882	A	8571	3	379	TSLTFHSPÉVPSS*PPSCTR*AGA ARGPRPPGAAGRPR*SC*GPGT RRWQS*GGTSPGLPVPGGRSGA ASCGLPDCEL*PLKRSQAQGRNQ CPV*SSPRWSRSRSEPCAARG WPPSACRHGNNR

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8515	38883	A	8572	384	1718	SLQLPRGLLPESCAADPGA*PPS CTR*AGAARGPRPPGAAGRPR* SC*GPPGT/PALAKPPSCPVVTS AAPTQARPMIKPQGAAWSTQK LPIPTASPTQKSPIPTASSTQK LPIPTAAWSTQKLPPTAAWST QKLPPTAAWSTQKLPPTAAW STQKLPPTAAWSTQKLPMTAA SSTQKSPIPTAAWSTQKLPPTAA WST*KLPIPTAAWSTQKLPPTA ASSTQKYTIATAASYHAKATDA WST*KLPIPTAAWST*KLPIPTA AWSTQKLPPTAAWSTQKSPIPT AAWSTQKLPMTAAWSTQKLP PTAAWSTQKLPPTAAWSTQKLP PMPTAAWSTQKLPMTAAWSTI TTMGATTHGPSTDTQNVVFLH PRCPEQASSQKSGAGAD*GLSN PKVSSAEAPSCAKDEPEVEKGR GPAPWTSQRWRAVGRPRG
8516	38884	A	8573	302	543	KLHLGWGKTPG*HWGLY*NLP RLNGPNSLMPSLRRVRRNKAR QVTSIAGCALQMEQWMHGMT RHPTRISTPITAAREVRI
8517	38885	C	8574	253	396	
8518	38886	A	8575	1107	1751	LQDLSQYFGGSQLIK*IG*TTSI ITNSNL*TTLEM/SVKGIAEQLG TNCQMAWENRIALDMILAERG GVCIMIKTECCAFIPNNTAPNGS ITKALQGLTALSNEALSSGVN DPFTGWLEKWFQKWKGITASIL TSLTAVMGVILVGCVPICIG LVQRHRGPPLVVIETKPLGLER LAGLPVGHALKLGSQIATPQN GENADRRREAFPAAS
8519	38887	A	8576	1	1365	
8520	38888	A	8577	3	263	QLILKDKFITQSAADIKEKLQKS TLGPERNLKTLNLAT/CCFL** RSGGAGGTGQTR*EGGHFHS GPRASGLWRLWNAESLGKSNA
8521	38889	A	8578	365	470	
8522	38890	A	8579	1	1278	
8523	38891	A	8580	23	257	
8524	38892	A	8581	1	1812	

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8525	38893	A	8582	265	699	LLGSTVLFHDPQLLIELYHSSHG PKVPFLGIREAKNSRSENTRLAT ILGAGLLPSWKVFTTILGAL*A RTPR*HFGNH/VTDIQS/RIEAVK LQMEPKMQSKTKIYRRPLDRPA SPRSDVNDIKGTPREEISAAK/PL LRPNSAGSS
8526	38894	A	8583	2	181	
8527	38895	A	8584	1	69	
8528	38896	A	8585	1	674	MDLNYLTLEQMDLTDIYRTHFPT TTEYTFYSTGHGTFSKTDDVIG HKMSLDKFKKIEIMISNTVSDHS GIKLEINSERNLENHANTWKLN NLLLNECWVKNKMKMEIKKLF ELNDNNDDTYHNLWDRAKVVI RGKCIALNTYIKKSERAQTDNL RIKKNKMHIIISIDA EKA FDKIQH PFMIKTLISKISIRGTLYNLIKDI/S *QTHSQHNAEWGKIESIHSENW NRG
8529	38897	B	8586	1	415	
8530	38898	A	8587	1	516	
8531	38899	B	8588	110	382	
8532	38900	A	8589	140	253	QNKACQHPPKITRVHQWQIQT KKKSSYLLKKEFRRLVIKLIREA PEEGKAQCKEVQKLIQVQGEI IDEIDTINKQPKLQETMDTLTK MQNAQESLSNRIEQEEHKSLS ENIFGSIMEENFPLARDLDSQI QEAQRTPGKFITKRSSPRHIVIR LSKVTKERJLRVVRQKRKIVL KS*PGNMTKQGLSTSPKNHTSS PTMDPNQEEILDLEKRIQEVSY
8533	38901	A	8590	89	194	
8534	38902	A	8591	2	633	

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8535	38903	A	8592	298	2648	GSSKILLFNQNEDDKINFELFFF FVASALVLVQKAFSRSSWSSMA LADKRLENLQIYKVLQCVRNK DKKQIEKLTKLGYPELINYTEPI NGLSALHLASVSNDIDMVSFLL DLGAHPDVQDRMGCTPTMRA AELGHELSMEILAKAKADMTIV DNEGKVLGETGGLTSSPLAHIA VALHIPRDTQGVLFYCIPTKR HYRCALIALEHGADVNNSTYE GKPIFLRACEDAHVDKDVCLTF LEKGANPNAINSILKLLFAYNG DVGLISINGNTPLHYAAMGGGFA DCCKYIAQRGCDLKWKNLCHK TPRAVAKEGGFKAAASKEIRRC RENRR**TSQARSQKSQIPLWAL RLHDWSVEREAFLEAFVLD RGDGSISKNDFMVLEE*SRIM QAQNSWLPFAHLHEKTRGGGV NIN*ILLKEPDILNKSFVLGSYGP KKKEKGMGKKGKKGFVLP ICVPEIYAFRRQDGGPPYIMIE TYKNVTDSSRFNRDHPPEHIQ DDSVWYIDDSEKVFSPNINIITKA GDLASLKKAFESGIPVDMKDN YYKTPLMTACASGNIDVVKFLL EKGYASPSGQDQDVELLVESGA LIDAASJNNSTPLNRAIESCRLD TVKYLLDIGAKFQLENRKGHSA MDVAKAYADYRIIDLIKEKLDN LPKPAENQKLKGKTPILKTEG PEIKKEEELSSIYGVPTTSEK
8536	38904	A	8593	3	838	MGRGWTQAVGPRWSGGSSCTL YSVGADGRGQGHQSRGCRPPG PPSASSAPCLAWGAAGRARE GLRQNAERSPLTAPAGR*PC GAGPCR*SR*RLVGLRPW ASPGTGAACGRCCCP*P/P*P NPWHFTVSKAFSYMPSTTA/RL VRGPRLLVGPVPVAPYIPP/PGS PASRRGSRGRSRPSRPRPSV LSCHGVSL*TGPSLPGWLLQIW QRSQMS/P/PPKGPP*GREGPP PP/GPALLPAAAPGGQGHRAPA AGSCGRRRAARRMEWVRNSPP
8537	38905	B	8594	1	2700	

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8538	38906	A	8595	1	1240	FPPYATNEIGKVTGLNRRELGH GALAEKALYPVIPRDFPFRTIRVT SEVLESNGMRRIGQPPASSRPV RRVRAPLPPPLLEVRAPLPASRP SGEVLCTVTFDSLESIGKSDQVI TAINGIKDKNFMLHYEFPPYAT NEIGKVTGLNRRELGHGALAE KALYPVIPRDFPFRTIRVTSEVLE SNGMRRIGQPPASSRPVRRVRA PLPPPLLEVRAPLPASRPSGEVL CTVTFDSLESIGKSDQVITAINGI KDKNFMLHYEFPPYATNEIGKV TGLNRRELGHGALAEKALYPVI PRDFPFRTIRVTSEVLESNGSSSM ASACGGSLALMDSGVPISAV AGRTN*DWSPKPDPEKGEIRKII VC*QIFLGIEDYNGDMDFKIAG TNKGITALQADIKLPGIPIKIVM EAIQQASVAKKEILQIMNKTISK PRASRKENGVPVETVQVPLSKR AKFVGPGGYNLKKLQAETGVT ISQVDEETVFCNLHQHPVLMLE GKRLSFTEICKDDQEQAIRNLG AVILPAHNWVKSEILVGMGKII
8539	38907	A	8596	152	305	DNQNGKLIKCS*PCNFVHRAPY AVEITVLRFCNWTQVQAQRE RTFLILIK
8540	38908	C	8597	414	611	
8541	38909	B	8598	1	403	

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8542	38910	A	8599	1	1702	MDSDEGYNIEFDEDEECSEEDS GAEEDDEDDDEDDTLDLG EVELVEPLGVGGGERDGLLCG ETGGGGGSALGPGGGGGGGGG GGGGGPGHEQEEDYRYEVLTS EMILQHMVEICREVNEVIQNPA TITRILLSHFNWDKEKLMERYF DGNLEKLFACHVINPSKKSRT RQMINTRSSAQDMPQCICYLNY PNSYFTGLECGHKFCMQCWE YLTTKIMEEGMGQTISCPAHGC DILVDDNTVMRLITDSKVLLKY QHLLITNSFVECNRLKWCAPD CHHVVKVQYPAKPVRCCKGR QFCFCNGENWHDPVQCKWLK KWIKKCDDSETSNIWIAANTK ECPKCHVTIEKGGCNHMCVR NQNKAEFCWVCLGPWEPHG\ SAWDTVPV*NEDDAKAARDAQ ERSRAALQSYLFYCNRMYNH MQLRFIEHRLYAQVTQTMEE MQQHNMSWIEVQFLKKAADV LCQCRATLMYTYVFAFYLLK NKPSFHIFENPNKARFDENATE GLSGYLGTRKFPKDS/LQDIKQ KVP RPSTRYCESRRKGFVTSMC HEGYEKDLWEYIED
8543	38911	C	8600	118	219	
8544	38912	C	8601	16	408	
8545	38913	B	8602	1	996	
8546	38914	B	8603	1	1302	

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8547	38915	A	8604	983	2127	DNWKSIRGSCWQDPRELLTFM APCIGVVVMQTTTR*K*NTLAGH PSAGVCWCVTSAACIGAWD ATSPLSSTFATAPGLPRCCSQAS PAPRAEPLHGQPGAPPHALKRP PGLPWP*PQEARQYRHNQAY YSIQGDGAEDDDERIVRFHTRV INHHKKRKNSPRIVQSNDLTEAA YSLSRDQKRMLYLFVDQIRKSD GTLQEHDGICEIHVAKYAEIFGL TSAEASKDIRQALKSFAGKEVV FYRPEEDAGDEKGYESFPWFIK RAHSPSRGLYSVHINPYLIPFFIG LQNRFTQRLSETKEITNPYAM RLYESLCQYRKPDGSGIVSLKID WJIERVQLPQSYQRMDFRRRF LQHIFVLRERPETVLIDLIQRTK DAVRELDNLQYRKMKKLLFQE AHNGPAVEAQEEEEEGWNLD RAYDYVKERRTVTKPNPFSMR QLEEQGILLARPKRTAYIYGS VYRRCGYADHKVEIKHPGWAS ISRGVLVCDECCSVHRS.LGRHIS IVKHLRHSAPWPTLLQSGFPGP SRRAAPRAARGPTPRTEEA AAMALTFLLVLLTLATLCTRLH RNFRRGESIYWGPTADSQDTVA GSPDHGLLAFAHYHRLVRFLLW VLCPGWAFFLVNSRGGVFNPI LHPCPRHGQARFAGVGAEDY TFLYHPCAHWPWLKQLALLAY ACMANPSLTPDFSLTQDRVDIE
8548	38916	A	8605	1	224	RKQEWLSKQKENIQHFQAE ANLLRRQRQYLEECRRFKRR MLLGRHNLEQDLVREELNKRQ TQKDL EHAMLLRQHESMQUELE FRHLNTIQKMRCELIRLQHQTE LTNQLEYNKRRELRKHKVM EVRRQPKGLKSKELPNKSSSQ GYLQNSQTRQYKALRNHLLT TPKSEHKAVLKRLKEEQTRKLA ILAEQYDHSINEMLSQTAVSLFF LGQNKFSAPFLPPP*AVSEQLCA HSLV

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8549	38917	A	8606	1051	1875	SDQLTAHLNLCVEVAELQFLHR FMLSFPIHHLRLFTAPAQDASL VPLKGDILGVKLSGDDGRGKP AQHLFLSGLSSQQLPVLPSQ CQSLCVHHFPAVVVNLHDIIGAC VSCLPDLGP*QSCGSLAARSC GQSPGVWCLPSGSGRSSITLCRC H*GRSWTPGAPS**TPISSPRRSP GPCAASPGARGCPPAASPPAGS PGTEAAPAPGPGYSQPPGAL SSRCDSPCPLRRAPGAHGHTP RCPSVVARCRGVPRRGSSCSMS TSLTRSCSKL
8550	38918	A	8607	714	2148	MPAVAKSKPINRKRRCMPQV LRSASPIQEGEKISANENSLAVR STPAEDDSPGDSQVKSEVQQPV HPKPLSPDRASSI.SESSPPKAM KKFQAPARETCVECKTVYPM ERLLANQQVFHISCFRCSCYCN KLSLGTYYASLHGRIYCKPHFNQ LFKSKGNYDEGFGHRPHKDLI GQAKMKTEEILER/QPQLANAR ETPHSPGVEDAPIAKVGVLAAS MEAKASSQKEKEDKPAETKKL RIA WPPPTLGGSGSALEEGIKM SKPKWPPEDEISKPEVPEDVDL DLKKLRRSSSLKERSRPFTVAA SFQSTSVKSPKTVSPILIRKGWS MSEQSEESVGGRAERKQVEN AKASKKNGNVGKTTWQNKES KGETGKR/R*GKVHSLMENEN VFVINGARLPEDDNQLPPKQQ SSTKNPSLLEFGPSFVDNHLKK EFTTQNKQSQDVELWEGEVVK ELSVEEQIKRNRYYDEDEDEE
8551	38919	A	8608	I	4479	MCFSPPKLYKHEIHLKDLTCL KPSIESPLRQNRSSIEEEQKQE ENGDSQLILEKIQLQOWSISLNM TDEHGNLNLVCDIKKPMDEVY KIHLNQTDPPDIDINAMVALDF EYPMQTQENYENLWKLIAYYSE VPMKLHRELMLSKHPRVSQYQ RQDADEEALYYTGVRQAQILAE EWIMQPSIDIQLNRQSTAKKV LLSYYNQYSQTIATKDRQARG RSWVMIEPSRAVQKDQIVLEG GRCQLSCNVKASEP



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8552	38920	A	8609	1	9009	MDEFAPGKHLATSGDLFGDHN YGRRTYHTLEVKCAEEHPAVS DPFQRQSLRALSPLEDLPPSSG LRSGLTLELLMIHGNIPSPD GALRDLSSLQVFKFSYNKLRVI TGQTLQGLSNLMRLHIDHNKIE FIHPQAFNGLTSLRLHLLEGNLL HQLHPSTFTSTFTFLDYFRLSTIR HLYLAENMVRTLPASMLRNMP LLENLYLQGNPWTCDCMRWF LEWDAKSRGHSCRGCAIISLSH EIQLAGFCCEMLLL
8553	38921	A	8610	1	4971	MKASGILKCKDKAYEGGQLC AMCFSPKKLYKHEIHKLDLTC LKPSIESPLRQNRSRSEIEEQKQ EENGDSQLILEKIQLPQWSISLN MTDEHGNLVNLVCDIKKPMDV YKIHNLQTDPPDIDINAMVALD FEYPMTQENYENLWKLIAYYS EVPMLHRELMLSKHPRVSYQ YRQDADEEALYYTGVRQAIIA EPEWIMQPSIDIQLNRPQSTAKK VLLSYYNQYSQTATKDTQRAR GRSWVMIEPSRAVQK
8554	38922	A	8611	1	1283	LSFTTCSTFTSNYRSLGPAQAPS YG/SRPVSSVASVYAGTGNSSGS RISVSCSTFRGSMESGGLAAG MT/GGLAGMGGIQNEETMQSL ND/*LASYPDRVRHLETKNRKL ESKIWEHLEKKGPQVRDWSHY FKTIRNQRAQSLAITVDNACIVL QINNTHLAADDFRVKYETELA MCQSVESNIHGLCKVNDNTNV TRLQLETEIKALKEELLFMKKN HEEEVKGLQAQIASSGLTMEVD PKSQHLAKIMAAIRAQYDELA WKNGEELDKYLSQQIEESTTVV TTQSAKAGAAEMTLTELRCITV QSLINLNSMRNLKASLENSVR EVKACYTLQMEQLNGILLHLGS ELAQTQAKGQCAQYEAALLN IKVKLEAFIATYCHLLEDGKDF NLGDALDSSNSMQTIPKTTTHQ RVDGKVVSETNDTKVLRH

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8555	38923	A	8612	2	1365	RPQSLSPVLSLSPDSMSFTTRST FSTNYRSLGSVQAPSYGARPV SAASVYAGAGGSGSRISVSRST SFRGGMGSGGLATGIAGGLAG MGGIQNEKETMQSLNDGVASY LDRVRSLETENRRLESKIREHLE KKGPPQVRDWSHYFKIIEDLRAQ IFANTVDNARIVLQIDNARLAA DDFRVKYETELAMRQSVENDI HGLRKVIDDTNITRLQLETEIEA LKEELLFMKKNHHEEVKGLQA QIASSGLTVEVDAPKSQLAKV IMADIRAQY*RAGLGKNREEEL DKYWISQQIEVSTTVVTTQSAE V/GAAIETTLTELRRTVQSL LDSMRNLKASLENSLREVEA/R RTPLQMEQLQRGSLHLESELA QTRAEQQRQA/QEYEALEHQ GSSLEAEIATYRRLLEDGEDFN L/GDALDSSNSMQTIQKTTTTRI VDGKVVSJETNDTKVLRH
8556	38924	A	8613	170	399	
8557	38925	A	8614	141	287	LPSRRAGLGTCSPPCLSLPPASR APVRPEPLR*APPPAPRRVPVST TQG
8558	38926	A	8615	356	574	
8559	38927	A	8616	552	770	
8560	38928	A	8617	158	368	
8561	38929	A	8618	1136	1410	
8562	38930	B	8619	1	631	
8563	38931	B	8620	321	2234	
8564	38932	A	8621	170	444	
8565	38933	A	8622	325	722	LIELRHLVFFVLLFRDLQHIMA CNMRDAVRFFVCFVFFREGL SRSSGA/DDRFLAGP*LLSRGAG LGTCSPPCLSLPTPWAP/AAAP ASLT/TPPPAPRRVPVSTTQGLRS ASARHGTGRQLHLQPRCGIH
8566	38934	C	8623	1	1449	
8567	38935	A	8624	326	626	LPSHGAGLGTCSPPCLSLPPPLW AP/AAAEPPRQAPPPAPWCPVPS TTQGLRNASTRRRTGRQLHMI WPPASLKSPPATLPCHECAPIT LTFSCSSNMQT
8568	38936	A	8625	2009	2227	
8569	38937	B	8626	182	1513	
8570	38938	A	8627	497	761	NHTSCLPLGPGTTAAEELPSLVA GFGTCSPPCLSLPPTPWAPVRPE PPR*APPPAPQRPVPSSTTQGLRN ASTRHRTGRQLHLQPRCGIH

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8571	38939	A	8628	218	855	GAGLGTCSPPCLSLPPTQRA PV RPEPPRRAPPAPRRPVSTTQ G LRSASTRHRTGRQLHLQPQCG V H*VKPAGLLSLALETRTNPAA/ DKHLWQSIIQLKSDLLKEM L GSQTGNNGNVQDVLRYLVKSE T QKAIKVSLDCVRKRYRSSL SL QLKLCDCWGQALFSSALTLD P KEVVVRDLEELSNYKTTLEGS G IFDSVARVREESEAGT
8572	38940	A	8629	350	615	
8573	38941	A	8630	186	566	RLLSPAACRSGMTMIFPSIHPS QC RMIGLGWKK*SSVHNATPWAP VPPEPPGRAPPPAGRPVPLTT Q GLRSASARRRTGRQLHLQPQCG IHVVVKPAGLLSHEGPRLRSS SQ SDQPTNSGHS GMCL
8574	38942	A	8631	656	874	
8575	38943	A	8632	415	634	LPSRGAGLGNCSPCLSLPPTPW APVQHKPPRRAPPPTPRHPVPS TTQGLRNASAWRRSGRHLHLQ PQCGIH
8576	38944	A	8633	2	264	NKQPIWIPSRHLKPYHEPDAKE EIPGGS*GPTSCSHVETDAEEDP NCHEQHLSNTATHLGTDOEAVI DGRRKPEESRTTSHICRCS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
8577	38945	A	8634	1	1743	MGQVWALVHSTLETFTTDEEE GEYNEVTEQVCLPAKAGSAAV DLCTKAVSLLPGESPQKVPTG AGGPLPAGMTGLLLGRSSLNIK AVQVQTGVTDSYNGEIQVTS TSVPWKAKPGDHIAQLLIVPKK FARFEGTASSGKTKFLPRFRISF LMAAIVKPPEPIPLKWLTDKPI WTEQWPLSKEKLEALEDLITQQ LKKGHIAPIFSPWNSPVFIKKK SAEQDCEWFVFTILAVNNLQLK PAKRFIHWKVLPGQPNQQPIWIP SRYLKPYHKPDAKEEIPESGSG FPVAAMSRLTLRRTPVT/TSNTH RTQPPTWGQIEKLPQMAEENLR KAGQPVTISNWILPRITKFKPIE GAENVFTDGSSNGKASYSGSK GPLTEGNQMADRLVAKVISNA RHFHNLTHVNASGLKRRYSIT WKEAKAIQRCPTCQVMLSAAE QHLQKSAKTEAEKLVWWRD PITKSREIGKIITWGRGYACVSP GPNQQPIWIPSKHLKPYHKPDA GEKIPGESR/ETPGCSHVKTDAE EDANCHEQHPSNTATHLGTQD EAVTDGGRKPEESGTTSHNE*F NDSGDHHCLQOQGL
8578	38946	A	8635	820	1344	PDGTTDRADGRDLRSVSWETL RGCPAVRKDSIGWIRLRTLKK NVHLCLPLRQGGLFVCPVTSSS PQHISSHRGFWNISKDAPMSWP GSYSCHNVVAVPGQGQ*SRRA RMLRGLLSKAGHHSFCTDQAI LEITKFTFTWD*VTLGQ*FMLS ES*SSCKPNSCCPVQCLVHSGG
8579	38947	A	8636	3	760	

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8580	38948	A	8637	1	1354	MGISCPGSSKMLNSRALPVLKL TQGA LR DCKERANYTNFN IYK AVESQKGFVCVLYNGQSP EY VMIPCTSVSPITGQEVPE DRGMR MVMKNKPNKPSKM QSLKSSKH LTNSVIVIAVGIFFSVTLQARDP QLDDAIEQLRGVCIRA WEKITS GGEQYPSFSAIKQGPKEPYIDFI ARLQESLKKMIADSA AQDIVLQ LLAFDNANPDCQAALRPIRGKA HLVDCIKACDDIGDSSNGKAS YFGSKSVFQTSYTSQAQAE LV AVIEVLTA FDMPINVIDSSYM VYSTQLIEN AQLRFHTDEQLMT LFTQLQTA FRSTMHPFYITHIRA RHTPLPGPLTEGNQMA DCLVA TAVSNARHFHNLTHVNASGLK CRYSNTWKA AKAIHQRRPTCQ MVHSSSFTGGVNPQGLEPNSL WQMDVTHVPSFGR LAYVHV C VDTFSHFVWATCQSGES
8581	38949	A	8638	596	1820	
8582	38950	A	8639	275	1495	RLGSSLL EYTLPDQGNIIATFE PPFFKFGKAHSV DYIKACDGIG GPLTEGNQMA DCLVAN AISNA RHFHNLTHVNASGLKRRYSIT WKEAKAIQ CPTCQMVHSSSF TGGVNP RGLEPNSLWQMDVTH VPSFGR LAYVHV CVDTFSHFV WATYQSGESSACVS KHP LLQC FVVVGIPAFIKTDNAPGYTSQA LATFFSVWN IKHITGIPYNSQGG AIVERMNL SLKQQLQKQGGN RDYR/TP* MQLNLALL TLNLS LPKGQMFSAAEQHLQKPA AKT KTEQLIWW RDLITKSWEIGKIIT WGRGYA YISPGQNQQPIWIPSR HLKPYHEPDA RKRLQEDPEDP PSCSHVKTDAEEDPN CHEQHPS NTAIHLRSDQEA VTDGRRKPEE WSGTRTWWRPWSCRT
8583	38951	A	8640	232	789	ERPWGPEGNSEGSFCPKGLEPR TCLRGPAASAAAGAEGRQDDP GGPWCSPAAGDLGSPGVQSPG GGSPRGAQVAMSGSRRRRAEP GVWGALQ*HRR*ARRMHSFPP SL/PLL*NG*SPLFLVSKCLTGSP LRSASPCPPAARSC*KHPDSSPG RGPGARQSPALHPALPSLARRA APGRSFPLTSRK
8584	38952	A	8641	1	149	

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8585	38953	A	8642	1	2541	
8586	38954	A	8643	1	989	MQRGQQATGSSANAWGILQPK WVQTGPDNKRMARNVLYKER LLAESPNHVVAEAVIQRPNPHL QTRDITYEGLCQTLGSQPTLYQI PSLYCSYETNSNAYLLQLPIRKE VIHLEPYIALYHDFVSDSEAQKI RELAEFWLQSRVVASGEKQLQ VEYRISKSAWLKDTVDPKLVT NHRIAALTGLDVRPPYAEYLQV VNYGIGGHYEPHFDHATSPSSP LYRMKSGNRVATFMIYLSVVE AGGATAFIYANLSVPVVRVQ/ WPGTS*AFDNQCQNAALFWW NLHRSRGEGSDTLHAGCPVLV GDKWVANKWIHEYGQEFRRPC
8587	38955	A	8644	2	505	AWLKDTVDPKLVTNLNHRIAAL TGLDVRPPYAEYLQVNVYIG GHYEPHFDHATSPSSPLYRMKS GNRVATFMIYLSVVEAGGATAF IYANLSVPVVRVQ/WPGTS*A FDNQCQNAALFWWNLHRSRG GSDTLHAGCPVLVGDKWVA NKWIHEYGQEFRRPCSSPED
8588	38956	A	8645	298	401	KKSLLVRRSWRMKELKKKIGQ Y*KKLGRLLGKAI
8589	38957	A	8646	1	417	FRAAPAPESGGESVFGETHRAL QGAMEKLQR/RLWKEKVDLKE RVEKLELQFIHLSGQTDITGRK YISQGVASETQHWKEDIVRL AQDQEEMKVNQLQELR/EQVLQ LVGDHKEGHGK/FLTIAQNPAD EPTLGAPIAQELGC
8590	38958	A	8647	2	430	AAVKPLGSAETAVPARLGCRR FSRRCRRRRGRGSLLSFSAK VAFFNSAGANAQEEQRVCQP LAHPVASSQKKPEVAAPAPESG GESVFGETHRALQGAMEKLQR/ RLWKEKVDLKERVEKLELQFIH LSGQTDTHNKISY
8591	38959	A	8648	1	2769	
8592	38960	A	8649	1	314	FVNLFEIPVRVVEFGATCRAVA EPEQQR*SPSARPRPCCPLASV AAAAAAGGAAAYCL SPRRR*GAVSARPAGEPREPHE WDRNRSDFKRRRRGRDG
8593	38961	B	8650	46	307	
8594	38962	C	8651	1	4584	
8595	38963	B	8652	438	532	
8596	38964	B	8653	832	927	

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8597	38965	A	8654	320	1136	RIMETIANI.SSQSPVSLPLRVGL AEYLEMEED/DL.DSEQEAPRPM PNIPGDLSEREP/QVAFNSAGA SAQEEQRVCCQPLAHPVASSQK KPEVAAPAPESGGESVFGETHR ALQGAMEKLQVTTLWKEKVD LKERVEKLELQFIHL.SGQTDITV SERI.GHRWGELPGHPRGSI*A MSSCRKVHQPGGSVRDAAALGE EDIVRLAQDQEEMKYNLQELR/ EQVLQLVGDHKEGHGK/FLTIA QNPADPTLGAPVAQELGCAD EQGGFYPRSPDC
8598	38966	B	8655	97	235	
8599	38967	A	8656	1	2104	
8600	38968	A	8657	3	1107	FMTTDERKLFNHLKSPHLKYW VPFIWFGNLATKARNEGRIRDS VDLQSLMTEMNRYRSWCSLLF GYDWVGIPLVYTQVVTALAVYT FFFACLIGRQFLDPTKGYAGHD LDLYIPIFTLLQFFFYAGWLKVA EQLINPFGEDDDDFETNWCIDR NLQVSLLA.VDEMHMSLPKMK KDIYWDDSAARPPYTAAADY CIPSFGLSTVQMGLSGSDFPDEE WL.WDYEKHGHHRSMIRRVKRF LSAHEHPSSPRRSYRRQTSDDS MFLPRDDL/HSQGP TGCAKK PPQGLTHLE/DNPA SQKEAPRCT SAWESCPPSGRPARQALYRA*P HSPV*ELPPSKCHGT*GIDHSSR STSAHIRGLPP*FRYLHLEL
8601	38969	A	8658	3	397	
8602	38970	A	8659	346	474	

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8603	38971	A	8660	1	1344	MHSTWLFCFPARLLKLEPFPGQL PRLTIRASASRTTPAALERVTRD PCAATCLDRGSLKGLGHSPFQ SPPVTSCHCAENPTLKAPPYV GATSALVLSLGGPVPWLSVEL SIRTFASSGLIYYMAHQNQADY AVLQLHGGRLHFMFDLGKGR KVSHALLSDGKWHVTVDYV KRKGFTVDGRESPMVTVVGD GTMLDVEGLFYLGGLPSSQYQA RKIGNITHSIPACIGDVTVNSKQ LDKDSVSAFTVNRQYVAQAE GTYFDGSGYAALVKEGYKVQS DVNITLFRFTSSQNGVLLGIST AKVDAIGLELVDGKVLHFVNN GAGRITAAEYEPKATVLCDEGK WHTLQANKSKHRITLIVDQNA GWR*KSHTPQSTPVDNINPIYV GGVYAGVKQKCLRSQTSFRGC LRKLALFRGPQVQSDFDSRAFE LHGVFLHSCPGTES
8604	38972	A	8661	3	92	
8605	38973	A	8662	2	158	HTFPTFSSPHLVMMIQPSSSP PPPLPPPPSSPPLPLPPSPPLLL FFL
8606	38974	A	8663	21	471	DGPQDQPPHQSSSSPPPLPPPP PFPPPLPLPPSPPLLLFFCDEA LLCCHTGVELFFVIFAYCSG/PE TEPAISPRYASSGLNGFPLPRT PPAYAA*IPSSGIHFNPSLAIPST TTTLVTRPTTHHSRRPTTTQS STTAPSLRHP
8607	38975	A	8664	2	105	
8608	38976	A	8665	3	265	RKDLVANTALSGGTTMYPGIA DRMQKEITALAPSTMKIKIAPP ERKYSVWIGGSILASLTFQOM WISKQEYVDESGPSIVHRKCF
8609	38977	A	8666	3	757	NTPAMYMAIQAVLSLYTSGR TGIAMSDGDGVAHTVPIYEGYT LPHAILHLDLAGWDLTDYFMKI LMECSYRFTTMAEQEIVCDIKE KLCNIALDFEHKMATGASSSSL EKSYEVDPGQVITIGNEWF/*VP EALFQPS/MGMESCGIQTTFNS IMKCDVDICKELYAKMVLSSGT TMYLGIADRMQKEITALGRPST LRFRFIAPP/ERRKYSVWIGGSI LASLSTFQOMWISKQEYDES GPLHPSTANCF



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8610	38978	A	8667	3	171	CPLCRGNHWK VHCPSGR/MVP* VRSPQDDPTTGQRVP GASASS CHHPH*APGTFNH
8611	38979	A	8668	1	325	SPSRTCYQCGLQGHHF*KDC/TSE KPPPRPCLLCQGNHWK VHCPR/ VTKVLWVRSPQDDPATGLRV PDD*EHTIRRAYALGKSAVTSK PPPPYPARSRLNVRRLCSLATN
8612	38980	A	8669	3	377	
8613	38981	A	8670	1	423	
8614	38982	A	8671	1	1659	
8615	38983	A	8672	1	1449	MVNDTRPKVQVEYKGKTKIF YPEEVSSMVLTKMKEIAEAYLG KTVTNAAVTVPA YFNNSQHQA TKDAGTIAGLNVLRIINEPSAAD IAYGLDKK VGAERNVFIDLRG GTFDVSILIIQDGIFEVKSGDTHL GEEDFDNRIVSHFIAEFKHKYK KDTIRDVKLDKSIQHDIVSIGG YTHIPKIQKLLQDIFNRKELNKS INLDEAVAYGA AVQAAILSGD KSENVQDLLLLDVNPLSFGIEL AGGVMTV/LPVLIKHSTTIPTKQ TETF*QPIYSDNQPGVEGECAM TKDDNLLDKFELTGIPSAPHGV PQIEVTFDIDANGILNVS AVDKS VGKENTITTTNDKHRLSKEDM NIWSAEKYKAEDKRQRDKVSS KNSLESYAFHMKATYKDEKLQ GKINGEDKQKILDKFNEVIKWL DKNQAAKKEFEHQQTLEKV CNLIISKRYQSAGGMPGGMPGG FPGGGAPPSSGASSRPITEVD

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8616	38984	A	8673	18	1388	TRLQLLGFLWLPSSLLEPGLHPS NHGPRGPAVGIDLTGTTYSVGV FQHGKVEIIANQDQGNRTTPSY VAFTDTERLIGDAAKNQVAMN PTNTSF*LPNGLIGR/RFD/DAVV IQSDMKHWPFMVVNDAGRPK APS*NTKGETKSLYPEEGVFLW V*PKMK/EICRSLTLGKTVTNA\ VVTVPVSIFYNDSQRQATKDAG TIAGLNVLRLNNEPTAAAIAYG LDKKGLEQKRNRAHLLTWGG GTFDVSILTIEDIGIFEVKSTAG DTHLG/GEEDFDNRMVNFHIAE FKRKHKKDISENKRVRRLRTA CERAKRTLSSSTQASIEDSLYE GIDFYTSTIRARFEELNADLFRG TLDPVKEALRDAKLDKSQIHDI VLVGGSTRIPKIQKLLQDFFNG KELNKSINPDEAVAYGA AVQA AILSGDKSENVQDLLLLDVTP SLGIETAGGVMTVLKRNRTTI
8617	38985	A	8674	2	1559	RYLNLWIGTPTKGMSLKAFVQ PHKSYWLKTL.PDNMEALQIR K*VPNIGTCAVSWLKGPCSDV AVKKFFIFSLGNYWEGN*LI*EH GYKVV*HSNSYLEPISPAQTPK KRTTSYFSTLLCLRSLCSFLK RIECYEVNYQLDEELDR*EPAP QSQGLDLSPSFDIL*DHQSRTV YYLMNIHVTPRSIYLCRHGESE LNIRGRIGGDSGLSVRGKQVG WATHQMGWLGCPRWAAGFP ILPSRPYPNAGVTLAAPVPTHDS VLPALPTRAGGQDETEPLKAG PTGLPSAPPLEMGGGAPGKALS WMATPWCLPFCYVEVALTCAA PTVYQAVVWVLPPIHYLKCSPT AGQMRQCSDMRPERGRDVSE GTRDHYRELREFNLWLIPPCQG LLPTSHMKRTIQTAEALGPYE QWKALNEIDAVRCMG*ISC/VW G*LESGLPLRDQDKYRYRYPK GEVRFAGWPNA*DYSVSSQL NVLLCHQASMRCLLAYFLIKS SGTTLISALGMFDGI
8618	38986	C	8675	16	206	
8619	38987	A	8676	157	413	ALVCS/SSLAIREMQIKTTMYRH LTPVRMAIKKSGNNRCWRGC GEIGTLLHCWLDCKLVLQPLWK SVW*FLRNLELEIPFDPAIPLL
8620	38988	B	8677	877	2126	

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8621	38989	A	8678	1	1731	
8622	38990	A	8679	2	1675	
8623	38991	A	8680	1	2142	MIILDAEKAQFDKIQQPFMLKTL NKLIGDGTLYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGC LSPLLFNIVLEVLAAQIRQEKEI KGIQLGKEEVKLSLFADDMILY ILENPIVSAQKLLKLSNVSKVSG YKINVQKSAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGRGGIALVDIPNVNDKL MVLEVLARAIQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLSISNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYREN DIPIKLPMFTFTELEKTTLKFIW NQKRACIAKTLSKKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTEASEVTSIYNNH LIFYKPDKNKKWGNDSL FNKW CWENWLAICRKLKLDPFLTPYT KIHRSWKDLNVRPKTIKLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVIKLSFCTA KETTIRVSRQPTWEKIFAIPYS DKGLISRIYKELQIYRKKTNN PIKKWAKNNMRHFSKEDIYAA NRQMKKCSSLVIREMQIKTTM
8624	38992	A	8681	1	1242	

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8625	38993	A	8682	14	1785	FDQVEERVSVIEDQMNMKRE EKFRKRVIRNEQSLQEIWDYV KRLNLHLIGVPESDWENGTKLE NTLQDIIQENFPNLARQANIQQ EIQRMPQRYSSRRTTPRHILNA HKRK*ERYKIDTLTSQLEKEK QEQTYSKASRRREITKIRAELEK IETQKTLQKINESRSCFEKINKID RLRLARLJKKKREKNQTDVIKND KGDITDTPTEIQTIREYYKHLV TNKLENLEEMDKFLDITYLTPRL NQEEVESLNRPIGTGSEIAHNSL PTTKSTGPDRTAEFYQRYKEE LVPFLKLFQSEKEGILLNSFYE ASTILIPKAGRDTTKKENFRPISL MNIDAKILNKILANRIQHIKKL IHYNQVSFIPGIQGFNICKSIN VIQHINRTKDKNHTIISDAEKA FDKIQQPFMLKTLNKLGDGTV LKIMTAIYDKPTASTILNGQKLE AFPLKTGTGRCPLSPLLFNIVL EVLARAIQKEIKGILGKEEV KL.SLFADDIMIVYLENPVSAQT LLKLISNFSKISGYKINVQKSQV FPYTNNRQTESQIMSELLFTIAS KRKIYVVGQLTRDVKDLKFEN
8626	38994	A	8683	1	5127	
8627	38995	B	8684	1	1461	
8628	38996	A	8685	2	1879	
8629	38997	A	8686	1	1299	MKLPEEGSGSIICSAIFAVLQL PLVIHRQTGYGEDLQQTPTDLQ LRDLTDHSSSPAMEQSWMEND FDELNRSRLQKANKLENLEETD KFLDITYLPRLNQEEETESLNRPI TGSEIAIINNVPTKKSPPGPDGV TAKFYQRYKEELRTVNKNHMI SIDAEKAFDNIQPPFMLKTLNK LGIDATYLLKIIRAIIDDKPTANIL NGQKLEAFPLKTGTGRCPLSP LLFNIVLEVLAIRAIQKEIKGI QLGKEEVKL.SLFADDIMIVYLEN PIVSAQNLLKLINNFSGVGYKI NVQKSQEFLYNNNRQTENQIM SELPFTIASKRIKYLGIQLTRDV KDLFKENYNPLLEIKKDTNK WKNIPCSWIGRINIMKMAILLK VIYRFNAIPKLLMIFTFELEKAT TLKCI*NOGRAHIAKPILSQKNK
8630	38998	B	8687	1	2187	

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8631	38999	A	8688	1	1698	MMGDFNTPLSTLDRSMRQKVN KDIQELNSALHHMDLIDYRTL HPKSTEYTFPSAPQRTYSKIDHI VGSKALLSKCKRTEIITNCLSDH SAIKLELRICKLTQNHISITWKLN NWLNDYWVHNEMKAEIKMF FETNEIKDITTYQNLWDTFKATL NQEEVESLNRPIGTSEIQAMINS LGTKK/SPGPDGFTAKFY/P/E*H DCISRKPHRLSPKSP*ADKQLQ QSLRIQNCQSKITSILIHQ*QTNR EPNHE*TPIHNCIKDNKIPRSPY KGCEGFLQELQTTAQRNKR HKQMEEHPLMDRKNQYHEN GHTAQGNL*IQCHPHQATNDL HRIGKKYSKVHMEPKSLHCQ VNPKPKEQSWRHHTT*LQTLQ GYSNQNSMVLVPKQRYRPMH NRALRNATYLPKSL*ET*QK QEMGKGFP*QMVGLKLASHM *KAETGSLPYTLYKN*FKMD*R LKCT*TNKHHPRRKPRQYHSGH RHGQGLHV*NTKSGNKSQN* QMGSH*TKELLHSKRNYHQSE QATYRMGENFCNLI*QRANIQ NLQRTQTNLQ/RKKQPHQQVQ
8632	39000	A	8689	1	5073	
8633	39001	A	8690	128	1407	EKKASDDQTTSPSYRRKFKPKA KKLNTLKKI*TN/RITRITNREKC LKELMELKAKARELREECRSLR SQCDQLEERSVSMEEIQTTIRE YYKHLYENKLQNLLEEMDKFLD TYTLRRLNQEEVESLNRPIGTSE IVAIINSLPTKSPGPDGFTAKF YQRYKEELIPFLKLFQSIKEGI LPNSFYEASIIIPKQGRDITTK ENFRPIFLMNINAKILNKILANRI QQHIKKLIHHDQVGFIPGMQ WFNICKSRNVIHHNRTKDKNH MIISIDAFAFDKIQQPFMLKTL NKLGIDETYLKIJRAIYDKPTAN IILNGQKLEAFPLKTGTROGCPL SPLLFNIVLEVLARAIQKEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLFLISNFSKVS KINVQISQAFPLYTNYRQSAKS
8634	39002	B	8691	1	1443	
8635	39003	A	8692	1	1878	
8636	39004	A	8693	1	1479	

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8637	39005	A	8694	I	2091	MVFLEKISVGISRLSKQHPPFIR VALPLDADPTVSRIGSFQWVLG LADFRNEAVDPDRDVQMCPEFIP SGGFVVFLTSGVKPQTFTVSITA LKGEPTQMRNRQKTNNGNMTK LGYLTPOKNHTSSPAMSPNQEQ IPDSPEKEFRRTTEASLTGGTI NPIISWAVNGSGSKNLYHILGK GRKIFSSSGIKQKSIA SGERQNF QRNDQTAAFAVHENPLFCSHR CWYPGKQEKCLKELMELKAK ARELREECRLSRCDQLEERV SVMEDEMNEMKREGKFKREKRI KRNEQSLQEIWDYVKRPTLHLI DVPETLNAHKRKQERSKTDLT SQLKELEKQEQTHSKASRRQEI TKIRAELEIETKTLQKINESR SWFFERINKIDRPLARLIKRE KNQIDAINKDKGDIISDPTEIQT TIREYYKHLIYANKLENLEEMD KFLDTYTLPRLNQEEVESLNRP TGSEIVAIINSLPTKKSPPGPGST AEFYQRYKEELLISNFSKVSGY KINVQKSQAFLYTNNRQMESQI MSELPTTTSKRIKYLGIQLTRDI KDLFKENYKPLLNEIKEDRNKC KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLRMTFFTELEKTTL KFIWNQKRARITKSVLSQKNKA GGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNRTEPSEITP
8638	39006	A	8695	I	3514	MELKTKARELREECRLSRCD QLEERVSAMEDEMNEMKREG KFREKRIKRNEQSLQEIWDYVK RPNRLIGVPESDVENGTKLEN TLQDIIQENFPNLRQANIQEI QRTPQRYSLRRATPRHIIVRFTK VEMKEKMLRAAREKDRSTRQK VNKDTQELNSALHQADLIDIYR TLHPKSTEYTFPSAPHHTYSKT DHIVGSKALLSKCKRTEIITNYL SDHSAIKLELRINKLTKSRSTTW KLNNLLNDYW
8639	39007	A	8696	I	2091	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
8640	39008	A	8697	1	2781	MGKKQNRKTGNSKKQSASPPP KERSSSPATEQSWMENDFDEM REEGFRRSNYSLEREDIQTGKG EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRLRS RCDQLEERVSVMEDEMNMEN DGENGTKLENTLQDIQENFPN LARQANVQIQEIQRTPQRYSSR RATPRHIIVRFTKVEMKEKMLR AAREKDFKPTKIKRKEGHHYIM VKGSIQQEELTILKIYAPNTGAP RFTKQVLSDLQRLD
8641	39009	A	8698	1	1584	MSISGTVRMSAKSKGNPSSSCP AEGPPAAASKTKVKEQIKIIVEDL ELVLGDLKDVAKELKEQHWW HPISGDTATSICTVLESEKSKIK VTAFDVWLHLWGKGTDKQKD SSNFCRLKCPCLTALKRAVVLP ARSWRCENGQTASSSGSLTPDP RAANREAPPSSRGRLTPHTASDG ENGTKLENTLQDIQENFPNLAR QANIQIQEIQRTPQRYSSRKATP RHIIVRLTKVEMKEKMLRAARE KEIQTAIREYYKHLYANKLENL EEMDKFLDAYTLPRQNQEEVE SLNRPITGPEIVAIINSLPTKKSP GPDGFATAEFYQRYKEERHINRT KDNHMIISIDAFAKFNKIQQPF MLKTL.NKL.GIDGTYFKIIRAIYD KPTANIILNGQKLEAFPLKTGTR QECPLSPLLFNIVLEVLAIRAQ EKEIKIGLKGEEVKLSLFVDY MIVHLENPIISAQNLKLIISNFSK VSGYKINVQKSAFLYTNNRQ TESQIMSELPFTIASKRKYLGIQ LTRDVKDLFEEND

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8642	39010	A	8699	1	1722	MAGYPSEMKLPEELSGSNICCS AVFTVLQPLLIPRQTGSGVDL RQPTDQLRLVLTVRRKNNKQ KRTSTPKPHLYVTHKQDRSKKL TQNHSTTWKLNLLNDYVWV NNEMKAEIKMFFETSENKGTIY QNLWDTFKAVCRGKFIALNAH KRKQERSKIDTLTSLKLEKQ EQTHSKASRRQEITKIRAEQKEI ETQKTLQKINESRSCFFEKINKI DRLLARRIKKKREKNQIDAIGN DKGDIADPTFIQSTIREYYKHL YTNKLENLEEMDKFLDTYTLPR LNQEEDES LNRPTGSEIEAIINS LPAKKSPGPDRTFAEFYQRYKE ELHINRTKDKNHMTISVDAENA FDKIQQPFMLKTLNKLVLVLA RAIRQEKEIKGIQLGKQEVKLSL FADDVIVYLENPIVSAQNLLKLI SNFSKVS GYKINVQKSQAFLYS NNRQTESQIMNELSFTIASKRIK YLGQLTRDVKDLFKENYKPLL NEIKDDTNKWKNI PCSWVGRIN IVKMGI LPKV VYRFNAIPKLP M TFFTELEKVTTLKFIWNQKRARI AMTILS*KNKAGGITLP
8643	39011	A	8700	3	1033	
8644	39012	A	8701	1	1068	ANKLENLEETDKFLDTYTLPR NQEETES LNRPTGSEIEAIINNV PTKKSPPGPDVGTAFKYQRYKEE LRTVKNHMHISIDA EKA FDNQ QPFMLKTLNKL GIDATY LKIIIRA IDDKPTANILNGQKLEAFPLKT GTRQGCPLSPLLFNIVLEVLA RAIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLI NNFSKVS GYKINVQKSQEFLYN NNRQTESQIMNELSFTIASKRIK YLGQLTRDVKDLFKENYKPLL NEIKDDTNKWKNI PCSWVGRIN MKMAILLKVIYRFNAIPKLLMI FFTELEKVTTLKCI* NQKRAHIA KPILSQKNKAGSITLR
8645	39013	B	8702	69	1055	
8646	39014	B	8703	1	2301	
8647	39015	A	8704	1	3189	



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8648	39016	A	8705	92	1139	ASAADTQANRVWSGPPANSNR PAAIRVLTVRRKTNKQKGHPH QNPICTSPPSKKEIQTTIREYYQ HLYTNKLENLEEMDKFFDYT LPRLNQEEVESLNRPIGTSEIAI INNLP/TKSPGPDGFTAKFYQS VGSSGQGNQAGEGNKGHSIRK RGSQIVPVC R*HDCISRKPHRLS PKSP*ADSQLQQLRIQNQC AKI TSILIHQ*QTNREP NHE*TPIHNG FKQNKIPRNPAYKG CERPLQGE L*TTAQ*NKRGYKQMEHSM L MGRKNQYHENGHTAQGNL*IQ CHPHQATKNFLHRIGKNYFKV HMEPKKGPHCQVNP KPKEQSW RHHTT*LQTLQGYSNQNSI
8649	39017	A	8706	1	2199	
8650	39018	A	8707	1	2238	
8651	39019	A	8708	3	1889	RSMRQKVNKDTQELNSALHQA DLIDIYRTLHPKST EYTF SAPH HTYTKIDHILGSKALLRCKCRT EITNYLSDHSAIKLELRINKLTQ NRSTTWKLNLLNDYWWHN KMKAEIKMFETNENKDDTTYQ NLWDAFKA/EIQTTIKEYYKHL YANKLENLEEMDKFLDTY TLP RLNQEEVESLNRPIGTAEIVAIIN SLPTTKSPGPDGFTA EFYQRYK EELVPFLLKLFQSI EKQGILPNSF YEASTILIPKGRDTEKENFRPI SLMNIDAKILNKILAKRIQQHIK KLIHHDQVGFI PMQGW FNIHK SINVIQHINRAKDKNHIISIDA EKAFDKIQORF MLKTLNKL GID GTYFKIIRAIYDKPTANIILNQ KLEAIPLKAGTRQGCP LPLLFN IVLEV LARVIRQEKEIKGIQLGK EEVKLSLFADDMIVYLENPIVT AQNLLKLISNFSK VSGYKIN VQ KSQAFLYTNNRQTESQIMSELP FTIASKRIKYLGIQLTRDVKDLF KENYKPLLKEIKEDTNKWKNI CSWVGRINIMKMAILPKVIYRF NAIPIKLPMTFFTELEKTK/FIWN QKSAHITKGILSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN

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8652	39020	A	8709	1	1779	MGDFNTPLSTIDRSTRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFFSAPHHTYSNIDHIV GSKALFSKCKRTEIITNCLSDHS AIKLELRKKLTQNHSTTWQLN NLLNDYWVNNEMKAEIKMFF ETNENKDDTDQNLWDTFKA VC RGKFMALNAHKRQERSKMG TLTSQLEKEKQEQTHSKASRR QEITKIRAELEKIEI/QKTLQKIN ESR/TEIQTIREYHKHLYANKL ENLEEMDKFLDTYILPRLNQEE VESLNRPTVGTSEIEAII NSLPTKK SPGPYGFTA EFYQRYKEELHIN RTKDKNHMIIISIDAEKAFDKIQ QPFMLKTLNKLGDGTYLKILR AIYDKPTANIILNGQKLEAFHLK TGTRQGCPLSPLFNIVLEVLR AIRQEKEIKGIQLGKEEVKWSL FADDMIVYLENPVSTQNLFKLI SNFSKVSGYKINVQKSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGQLTRDVKDLFKENYKPLL NEIKEDTNKWKNI PCSRAGRINI VKMAILPKVIYRFSAPIKLPMT FFTELEKTKFIWNQKRAHIAKS ILSQKHKAGGITLP

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8653	39021	A	8710	1	2093	MEITTNCLSEHSAILQLRIKKL TQNCCTTTWKLNYLLNDYVW NNEMKEEIKMFFETNENKDTT YQNLWDVFKAVCRGKFIALSA HKRKQERSKTDILTSQLKELEK QEQTSHKASRRQEITKIRAELEK IETQKTLQEINDSRSSFSEKLNKI DRPLARLIKKREKTQIDAIAK DKGEINTNPTEIQTIREYYKYL YANKVENLEEMDTFLDTYTLPL RLNQEEVESLNRPTGSEIEAIIN SLPTKESPGPDGFTAIFY/HEGN QERERNKGYRIRKRGSHIVPVC R*HDCLFRKPHLLSSKSHEAVK QLQQLRIQNWAKITSMMPVH Q*QTNREPHE*TPIHNCYKEN KIPRNPTYEGCEGPLQGELOTT AQQNKRGQKEMEKHSLMDR KNHYHENGHTAHGNL*IQCHP HQATNDFLHRIGKNYVNFHME PKKSLHCQENPKQREQSWRHH AT*LQTLQGYSNQNSMVLVPK QIHRTMEQNRGLRNNTTHLQPS DL*QI*QKQEMGKQFPI**MVL GKLASYM*KAETGSLPYTLK N*FKMD*RLKC*T*NHKNPRRK PRQYHSGHRHGQGLHD*NTRS NGNKNQNRQMGSN*TKELLHG KRNYHQSAQTTYRMGENFCNL PI*QRANIQLQRT*TNLQEKNK QPHQKVGKGHEQTLLKRRHLC SQQTHEKMLITGHQRNANQN

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8654	39022	A	8711	3	1805	PLSTLDRSSRQKVNKDIQDVISA LHEAGLIDIVRTLHPKSTEYTF SAPHHTYYKIDHIVGSKALLSK CKRTEITTNCLSDRAIKLELRI KKLTQNYTTTWKLNLLSDY WVNNEMKAEIKMFFETNENKD TMYQNLWDITKAVCRGKFIAV NAYKRKQERSKIHTLTSQLEP EKQEQTSHSKASRRQETIKIRAE KEIDTQKTLQKISVSRWFSERI NKIDRLIARLMKKKREKNQIDA IKNDKGDITIDPTMQTTIREYY KNLYANKLENLEEMDKFLDTY ILPRLNQEEVELPFRPITGSENE AIINSLP/TKKSPGPDEFTAKFYQ RYKEELQGMQEKEREDTQLG KEEVKLLIFAEDMIVYLENPV SAQNLLKLINNFVKVSGYKINV QKSQAFHLTNNRQTESQIMSEC PLTIASKRIKYLGIQLTRDVKDL FKENYKPLLNKIKEDTNKWK IPRSWLGRNNIVKMTILPKVIYR F/NTLNFIVNQERARIAKTILSK KNKAGGITLPDFKLYYKATVT KTARYWKQNIKKGSVWPISLK SEKRGHRTPLWKLCHNDVQG ELLKTIQFLFGSPLGHSSLDPSA
8655	39023	B	8712	1	1743	
8656	39024	B	8713	1	1260	

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8657	39025	A	8714	1	1842	VPPPTTCGNYGSTIQDEIWMGTQ NQTISVSEEMMFQAEIISAQK MWNQHHITPSKVDHIVGSKAL FSKCKRTEIITNYLSDHSAIKLK LRIKKLTQNRSTTWKLNLLLN DYWVHNEMKAEIKIFFETNEN KDTTCQNLWDTFKAMCRGKFI TLNAHKRKKQRCIDTLTSQLK ELEKQEQTTHSKASRRQEITKIRA ELKEIEAQKTLQKINESRSWIFE KINKTDRLLARIKKKREMNQI DAIKNDKGDITNPTEIQTIRE YCKHLYANKLENLEEMDKFLN TYTLPRLNQEEIESLNRPIGTSEI EAIINSLPTKKSPGPDGFTAEFY QRYKEEMIEKKAFDKSQPFM LKTLNLGIDGTFKIRRAIYDK PTANIIILNGQKLEAFPLKTGRQ GCPLSPLLFNIVLEVLAREIRQG KEIKHIQLGKEEVKFSLFADDDVI AYLENPIVSAQNLLKLISNFSKV SGYKINVQLQAFLYTNNRQTE SQIMSEFPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLNKIKEDT NKWKNIPCSWIGRINIMKMAIL HKVIDRFSAPFKL/PKD/FFTEL EKTTLKFIWNQKRPRISKTLISK KKNAGGITLR

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8658	39026	A	8715	I	1593	MGKKQNRKTGNSKKQSTSPPP KERSSSPAMEQSWMENDFVEL REEGFRRSNYSELQEDIQTKGK EVENFEKNLEECMTRITNTEKC LKELMELKTKARELHEECRSLR SRCDQLEERVSAEMEDEMNEMK REGKFRKRIKRNEQSLQEIWD YVVKPNLHLMGVPESDGENGS KLENTLQDIQENFPNLRINKI DRPLARLIKKKREKNQIDTIKN DKGDITNTPEIQTTIREYYKHL YANKLENLEEMDTFLDITYLPR LNQEEVESLNRPTGAIEIVAIINS LPTKKSPPGPDGSAIEFYQRYKE E/PADKQLQQLSIQNQCTK/TSI LIHQQTNRPNHE*TPIHNCFK ENKIPRNPITYKGCEGLLPGLQ TTAQGNKRGYKQTEHSLML GRKNQYRENGHTAQGNF*IQ HPHQATNAFLHRIGKNYFKVH MEPKKSPHRQVNPKEQSWR HHTT*LQTLQGYSNQNSMVLV PKQGYRSMQNRALRNNAAYL QLSDL*QT*EKHAMGK/EFPI**
8659	39027	A	8716	I	1578	MGDFNTTLSTLERSARQKVNK DIQELNSGLHQADLIDYKTVKP KSTEYTFFGPHRTYSKIDHIVG SKALLSKRRTEITNCLSDHSA IKLELRICKLTQNRSTTWKLN LFLNDYVWHNMKAIEKMFEE TNENKDTTYQTLWDTFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKVSRRQEI TKIRAELEKIEIETQKTLQKINESKI QTTIREYYKHLYANKLENLEE MDKFLDITYLPLRLNQEVESSLN RPITGSEIEAIINSLPTKKSPPGD GFTAIFYQRYKEE/RPISLMNID/ AKILNKILANGIHDIKKLIHDD QVGFIPGMQGFNIRKSNVVIQ HVNRTDRKDNHMIISIDAEKAFD KIQQPFMLKTLNKLIGDGMYLK IIRAMYDKPTANILNGQRLEAF PLKTGTTRQGCPSPLLFNIVLEV LARAIGQEKEIKGIQLGKEEVK LSLSADDMIVYLEKPIISAQNLF KLISNFSKVS/GYKINVQKSQAF LYTNNRQTESQIM
8660	39028	B	8717	I	2982	

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8661	39029	A	8718	617	1155	SIAYQKSPGPDGFTAEFYQRH KEELLISNFSK/VSGYKIDVQKS QAFLYTNNRQTESQILSEFPFTI ASKRVGYLGQLTRDVKDLFKE NCKPLLEIKKDTKWKWNIPCS WVGRINIMKMAILPKVIYRFNA IPIKLPMTFFTELEK/TLRFIWN QKRDHIAKSILSQKNKAGSITLP
8662	39030	A	8719	1	1827	MGKKQSRKTGNFKKQRHLSFS KGIAVLHQWKNKAGQRLTFDE LREGFRPSNYSKLQKEIQTKGK EVENFEKNSDECITRITNTKKCL KELMELKAKARELREECRLRS RCDQLEERVSGMEDEANEMKR EGKFGEKRIKRNEQSLQEIWYD VKRPNLRLIGVPESDGENGTCL KNTLQDIIQENFPNLRANQIQI QEIQRTPQRYSSRRATPRHIVR FTKVEGKNIGSQRERAEIQTIT REYYKHLYSNKLLENLEEMDKF LDTYTLPSLNQEEVESLNRITITG SEIVAIINSLPTKSPGPDGFTAE FYQRYKEEVVPFLKLQFSIEKE VILPNSFYEARIIIPKGRDTTK KENFRPISLMNIDAKILNKILAN RIQQHIKKLIHHDQVGFIPGMAI RQEKERKGIQLGKEEVKLSLFA DDVIVYLENPVSAQNLLKLISN FSKVSGYKINVQKSQAFLYTNN RQRESQIMSELPFTIASKRIKW GIQLTRDVKDLIKENYKPLLEI KEDINKWKNIPCSWVGRISIVK MAILPKVIYRFSAIPIKLPMTFFT ELEKTTFK/FLWNQKRARIAKS ILSQKNK/AGGITLPDFKLYYKA

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8663	39031	A	8720	I	1551	MEKFLDITYTLRLNQEELES LN RPITGSEIEAIINSLPTKKSPGPD GFRAKFYQRYNEELVPFLKIF QSIEKEGILPNSFYEASHILPKPG RDTITKKDNFRPISLMNIAVKILN KILANQIQKHIKKFIIHDQVGF PGMQGWFNIRKSNVQIHINRT KDKSHMIIISIDEEKAFDKIHLPF MLKTL SKL.GIDGMYLKIIRAIY DKPTANIILNGQKLEAFPLKTGT RQRCLP.SLLCNIVLEVLARAIR QEKEIKGIQLGKEEVKLSLFD DMIVYLENPTVSAQNLLKLISN FSKVSGYKINVQKSAFLYTNN RQTESQIMSEL.PFTIASRKIKYL GIQLTRDVKELFKENYKPLLNK IKEDTNKWKNISSWWMGRANIM KMAILPK/VTWMKLEIIVLSKL P QEQTCKHRMFSLTGVFIEGRAL QNKSETSQSRHPGATHSLPEYTI PGSSPSNFYWFTLGLKEEVTSG WKREKKKKRKEGGKEGRKEG RKEGRKEGKKEGRKKGRKEVP
8664	39032	A	8721	I	1983	
8665	39033	A	8722	I	2436	
8666	39034	A	8723	I	3139	
8667	39035	B	8724	I	3558	
8668	39036	B	8725	I	2133	
8669	39037	A	8726	I	3051	MGDFNTALSTLDRSMRQKVNK DIQELNSALHQADLTDIYGLH PKSTECTFFSAPHHTYSKIVHIV GSKALLSKWKREIHTNCLSDH SAIKLELRICKLNQNCSTTWKL NNLLLNYYWTNK/KKREKNQI DA/IKNDKGDITNPTEIQTIRE YYKHL YANKLENLEEMDKFLD TYTLRLNQEEVESLNRPITGSE IEAIINSLPTKKSPGPDGFTAIFY QRMNYISFKSTWKIINKNAYS LA HSRELRDGGQ
8670	39038	A	8727	I	2706	
8671	39039	A	8728	I	2573	
8672	39040	B	8729	70	2029	
8673	39041	A	8730	81	385	
8674	39042	A	8731	301	515	SSWQAPAPVLGSSWASKK*MK KKYAAQIEKQKSP*CKSIKSP LRSASYAQLLSFSLSSCLCFSTC HSTLA WYCL*SSWQAPAPVLG SSWASKKRSLLWKESRSLPSF SITARS*ACCCCLCSSTEPQLLKA QYLLSHSRTRSFRLQ



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8675	39043	A	8732	2	4207	DTHRLKIKGWRKIYQANGKQK KAGVAILVSDKTEFKPTKIKRD KEGHYIMVKGSIQEEELTILNIY APNTGAPRFTKQVLRDLQRDL DSNTIITGDFNTPLSTLDRSMRQ KVNKDIQELNSALHQADLIDIY RTLHPKSTENTFFSAPHHTYSKI DHIVGSKALLSKCKRKEIITNCL SDHSAIKLELRIKKLPQNCSTIW KLNNLLNDYWVHNEMKAEIK MLFETNENKDTTYQNLWDTLK AVCRGKFIALNA
8676	39044	A	8733	1	2770	MGKKQNRKTONSKTQASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTGKGE VQNFENLEECITRITNTEKCLK ELMELKTKARELREECRSLRSR CDQLEERVSAEDEMNEMKRE GKFRKRIKRNEQSLQEIWDYV KRPNLRLLIGVPESDVENGTKLE NTLQDIIQENFPNLRANQVQI QEIQRTQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKEIQT TIREYYKHLYANKL

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8677	39045	A	8734	3	2169	FKPTKIKREKEGHYIMVKGSIQ QEELTILKIYAPNTGAPRFTKQV LSDLQRDLDSHTLIMGDFNTPL STLDTSTRQKVKKDTQELNSAL HQADLIDYRALHPKSTEYTFSS APHITYSKIDHIVGSKALLSKC KRTEIITNYLSDHSAIKLEIRIKN I.TQNHSTTWKLNLLNDYVWV HNEVKAIEKVFFETKENKDDTY QNLWDAFKA VCRGKFIALNAH KRKQERSKIDTLTSQLEKEKQ EQTHSKASRRQEITNIRAEKKEI ETQKTLQKINESRTEIQTIREY YKHLYANKLENLEEMDKFLDT YTLPRLNQEEVESLNRPTGSEI VAIINSLPTKKIPGPDGFTAIFY QRYKEELVPFLLKLFQSIEKEGI LPNSFYEAIIIPKPGRDITTKKE NFRPISLMNIDAKILNKILAKRI QQHIKKLIPHDQVGFIPMGQGW FNIRKSINVIQHINRAKDNHMI ISIDAEKAFDKIQPFMLKTLNK LGIDGTYFKHRAIYDKPTANIIL NGQKLEAFPLKTGTTRQGCPLSP LLFNIVLEVLAIRAEKEIKGI QLGKEEVKLSLFADDMIIYLEN PIVSAQNLLKLISNFSKVSGYKI NVQKISQAFLYTNNRQTENQIM SELPFPIASKRIKYLGIQLTRDV KDLFKENYKPLLNEIK\EDTNK WKNIPCSWVGRINIVKMAILPK LIGNCSKISGYKINVQKSQAFLY
8678	39046	A	8735	1	5166	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDEL EEGFRSSNYSELWEDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELHEECRSLRSR CDQLEERVSAEDEMNEMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIHQENFPNLARQANVQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAARQKAPH HTYSKIDHIVGSKAL

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8679	39047	A	8736	1	4553	MGRKNRKLDSRQHSYTSQSRSHEDPAAVLQALSSSGVVIIYQSLVAVQSPLAAPGCDGSRCEVRGLTVGSRYGSRWLAGCRDNEMVNACQSGWCYQNLTVLRGWKV LLEMTPHHTYSKIDHILGSKAL LSKCKRTEIITNYLSDHSAMKR ELRIKNTQNRSTTWKLNLLNDYVWHNEMKAEIKMFFETNE NKDDTTYQNLWDIFKAVCRGKFI ALNAHKRQKERSKTDTLTSQL KELEKQEQTTHSKASRRQEI
8680	39048	A	8737	1	2673	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDINRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNTQSRSTPWKLN LLLNDYVWHNEMKAEIKMFF ETNKNKDDTTYQNLWDFAKAV CRGKFIALNAYKRKQERSKIDT LTSQLKELEKQEQTTHSKASRRQ EITKIRAELEIETQKTLQKINES RSWFFERINKIDRPLARLIKKKR EKNQIDITIKNDKGDITDTPTEIQ TTIREYYKHL YANKLENLEEM DTFDLYTLPRLNQEEVESLNR PITGSEIVAIINSLPTKKSPGPDG FTAEFY/PESYL*QTHSQYHTEW AKTGSI PFENWHKTGMPSLTAP IQHSVGSQGGQNGAQEGGNKY SIRKRGSIQVPCV*HDCLSRKP HRLSPKSP*ADKQLQSLRIQN QCTKITSILIHQKQTNREPTHE* TPIHNCFKENKIPRNPYKGCCEG PLQGEQLQTTAQRNKRGHKQME EHSMLMGRKNQYRENGHT/SQ GNLQIQCHPHQATNDFLHRIGK NYFKVHMEPKSPHRQVNP KP KEQSWRHHTT*LQTLQGYSNQ NSIMVLVPKQRYRSMEQNRL RNNAAYLHYSDL/*QT*EKQA WGKGIP/IYKMA/LGKLA/PM*
8681	39049	B	8738	1	2792	
8682	39050	B	8739	156	391	
8683	39051	B	8740	1	2824	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
8684	39052	A	8741	3	4167	PLSTLDRSTRQKVNKDIQELNS ALHQVDLIDYRTLHPKSTEYTF FSVPHHNYSKIDHIVGSKALLS KCKRTEIITNCLSDYNAIKLELR TEKLTQNRSTTWKLNPNLLND YVWHKEMKAEIKMFFETNENK DTTYQNLWDFAKAVCRGKFIA LNAHKRKQERSKIDTLTSQKLE LEKQEQTTHSKATRQEITKTRA ELKKIETQKTLQKINESRSWFFE KTNKIDRLLATLIKKKREKNQI GARKNDEGAITTN
8685	39053	A	8742	1	1107	MKVEIKTFETNENKDTTYQNL WDTFKAVCRGKFIALNAHKRK QERSKIDTLTSQKLEKQEQT HSKASRRQIQTITIGEYKHLTY NKLLENLEEMDKFLDTYTLPRLN QEEGESLKRPMAGSEIEAIINSL PTKNSPGPDRFTAIFYQRYKEE L/PDKQLQQLRIQNQWEKITSI PIHQ*QTNREPHE*TPHNCFK ENKIPRNPTYKGCEGLPQGELO TTAQRNKRGHKQMEHSMMLM DRKNQYCENGHTAQEETAFC HSRRESSRLGLLVANFRACHQE RFRRRERSVPAGVHAEAHPCWE NRGREERHWEQHPGPETVLLQ AGGHVCDQGLHHGQPQVGQV PRGSRGHSQHFLPSVQDRSWL
8686	39054	A	8743	1971	5654	RSPTAGRNTNYPKRDYKHLTY A/NKLENLEEMDKFLDTYTLPK T/ITQEEVESLNRPTIG/SEI/AVI NSLPTKKSPGPDGFTAKFYQRY KEELHINRTKDNHMIISDAEK AFDKIQPPF/MLKTL/NELGID GT/YFFKII/RAIYDKPT/ANIRLE WGQKLEAFPFKLAQEQGMPL LLNPLPQSNIVVGKFLA/RAI/RQ EKEIKGQVEKQEVKLSL/FADD MIICLENPIVSAQN/LKLSISNVS

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8687	39055	A	8744	1	4901	MTGSNSHITILTLNINGLNSAIK RHRRASWIKSQDPVSCCIQETH LTCRDTHRLKIKGWRKIYQAN GKQKKAGVAILVSDKTDKPT KIKRDKEGHYIMVKGSIQEEEL TILNIYAPNTGAPRFIKQVLSL QRDLDSHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHPKSTEYTFFLAPH HTYSKIDHIVGSKALLSKCKRT EITNYLSHSAIKLELRINKLTO SRSTTWKLNLL
8688	39056	A	8745	2	1887	SASVVPASGLRPSSTSLTSRQP RFLGLLRSHPALVA VPGDW DLAVCCIVAPSHVCRMVFM RTLGLSLPGLLKREEDACWVEA NINGRVLAQCNIDELKKEMNM NFGDWHLFRSTVLEMRNAESH VVPEDPRFLSESSSGPAPHGEP RASHNELPHTELSSQTPYTLN FSFEELNTLGLDEGAPRHSNLS WQSQTRRTPSLSSLSQDSSIEI SKLTDKVQAEYRDAYREYIAQ MSQLEGGPGSTTISGRSSPHSTY YMGQSSSGGSIHNSLEQEKGD SEPKPDDGRKSFLMKRGDVIDY SSSGVSTNDASPLDPITEDEKS DQSGSKLLPGKKSSERSL FQA SLK\KGRGLRLSKLP/SEEDEC GAEEEDNTPLLKDDKDRKPEG KVERVPKSPHVSVEPIRTFIKAK EYLSDALLDNKGNSSDSVSD PRES\SPNHVSAQCKCADLDP LKRHNLELEDSDSHSGKRGIPH SLSGLQDPIIARMSICSSEDKKSPS RIASLD*PSSPLEENW/PACQKA YNL\NRTPSTVTLNNSAPANR ANQNFDMEGIRETSQVILRPSS SPNPTTIQENLKSMTHKRSQR SSYTRLSKESPELHAA/SSSESTG

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8689	39057	A	8746	1	385	EGNEAQTCSFWNTRQLASS DPSLSVSQRMDPSWRRSSHSWP QPMPPDSGRAPVRPHLAKLEED VWPCPQFHQTAAASGPPFVTFQ PANCFPSVISFHLCHTWSEQD RAYHPVYQMR**GSDVQLLEY EASAAGLRSFSERFPEDGPELE EILTQLATADARFWKGPSEAPS GQ/ALRK/SVWPCPQFHQTAA SGPPFVTFQPANCFPSVISFICT AIRGVSKTGLTILSTR*NGSSE KSLV
8690	39058	A	8747	2	2015	QDFLDSQNLASAYNTRLFKEVD GEGKPYEYVRLASVLGSEPSLD SEVTSKLKSYEFRGSPFQVTRG DYAPILQKVVEQLEKAKAYAA NLSHQGQMLAQYIESFTQGSIE AHKRGRFWIQDKGPVIESYIG FIESYRDPFGSRGEFEGFVAVV NKAMSAKFERLVASAEQLLKE LPWPPTFEKDKFLTDPDTSLOV LTFAGSGIPAGINIPNYDDLRTQ EGFKWVVFAGGIVLGCGLTPRK REK/LTFLEEDDKDLYLWKGPS FDVQVGLH/ESLLGHGSGKLFV QDEKGAFNFDQETRDPQKRG EQIQSWNRTGETWDSKFSTIAS SYBECRAESVGLYLCLHPQVL EIFGFEGADAEDVIYVNLNM VRAGLLALEFYTPFAFNWRQA HMQARFVILRVLLEAGEGLVTI TPTTGSDGRPDARVRLDRSKIR SVGKPALERFLRLQLVKSTG DVTTEGRALYEGY*STVTDAPPEA CFLTLRDTVLLRKESRKLVSQP NTHLEGNE/VSDVQLLEYEASR AGLRSFSERFPEDGPELEEIFIQ LATADARFWKGPQ*GPHSGPS LRKIVVALPPKFHQTAA/SGPS HSVCVFRGWGGGAGAWTLV LPQLEGW*HNPLPICQHVSSLP NCFPSVIL/SFICTAIRGVSKTGL TILSTKMRNGSSEKSLV
8691	39059	A	8748	1	519	
8692	39060	A	8749	786	864	
8693	39061	A	8750	1	468	

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8694	39062	A	8751	128	605	MTWGTVPPLHFQMRCCWVSC QGIMRGWGLCSQTLNCLLSK C*TCSSGGGQIWSRKFRVVRVE *G*GNFKTPQLQPGVPPGLPP PGSCFKCRKSGHWAKECPQPGI PPKPCPICAGPHWKLDCPTRLA ATPRSPGTLAQGSLTDSFPDIDG LAVED
8695	39063	B	8752	1	615	
8696	39064	A	8753	1533	1767	PSPTCPAIYS*KGGWSQRHSQG ACYTCRKSGHWAKECPQPGIPP KPRPICVGPB*KSDCSTHLAAN PRAPTLAQGS
8697	39065	C	8754	84	329	
8698	39066	A	8755	911	1497	SQRKARDQRRKRNRASSIAK HKEPKRPILPSGKNSQEGVATH TKPLAQGGVWLD/NETNEIPN ANFRQQIRKLIKDGILIRHRKPV TVHSRAQGWKSTLARRKGRHL GIESKKIDRHMVHSLYLKLGKN VFKHKRILTEHSHKLKADKAR KKPLADQAEARGSKTKEARKL REEHLQTKKEEIKTLSQEEKAK
8699	39067	A	8756	34	280	EVIHAAIGEEKGSY/NA**PWVE EQLTRQPLIHHQPASLHVSYY/RC RYHSLYLKVGKGVFNKRLIM EHIHKLKADKARKKLLA
8700	39068	A	8757	1	692	AFLQELCLKSSTGELFPFAAV AAALSMLRLQKRLASSVLCCG KKNIWLD/NETNEITNANSRQ IRKLIKDGILIRKP/TVHSRLRC RKNT/LAR/*KGRHMGIGRKV PANA/RMP/KEVTWMRENEGF CRR/ASEDTRES/KKIDRPHVVT ALYL/EVKGNVFKNKRL/MEHI HKLKA/DKARKKL/LAD/QAEA RRSKTKEATKRREERLP/ARPK REII*TLSKEETKK
8701	39069	A	8758	46	131	
8702	39070	A	8759	5	447	PATELPGLPTRPGMLCIWRGAP DWPEGPPSSGELSSIQPTQGLHN CFQPDGARPAAPGPVPQGLGAL PWSCRPPAEPTLFMESLVQWPP GDGIRQ*CEDAAELREPGVQRH QGSPG*VRTLPPLRGPSQVPA/G SSSSASPRSPGSRG

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8703	39071	A	8760	1	201	MPNIYTMEEYAAVKKDEFMSF VGTWMKLETHLSKLSQGGQKTK HRMFSLIGTRMKLETHLSKLLQ GQKNQTPYILTHRISFEDVRNY MPLAVIHSDESPILPLHEQQDAS ENGWIKDTERDADLEIYIVSGIG SFRWVLGLADFKSEAADPCGM KLQTFVAVSVTALKGGASRVVH SSWWVCVLTDFRSEAAYLSVT ALEGGASRVVAHSSRFVVSLSG VKLQTFVTNATAHKGSADPKS EQHQDLLQRAKKHTFHSMKGE PRRVVAAGWGAIAKADSNLI LLFQTIEKYCPWFPDKGSDVLL DWDVRVGTTLQLMRDGVLLPI SVWTDWALIRVALLPFQSGDTL QLPQVNADVEPLPLPCIGGITG PEGGDPGPGSFHYLVGVYYFLT CRSTWEQRKSPVALR**KLGPG GSPSGPVMPPMHRGKSGSGTS ALTCGS
8704	39072	C	8761	42	179	
8705	39073	A	8762	11	1713	PKTLKMGGGTAGLVGMGFSTT GRTPSAPGRPHPCRGAP/GSPG KAGLFLQRPRLGTGL*GSAPRG PG*MGCPGTGRGNSNRH*RGPP RRPQAS*AAPFQPGPLETWTPG *SQVPGAAPSCNFSYPHREVPP WGPVPPAPHGSCGWALALPR RKRAAVFSSWAPGQAGQLLDA ASVGAAP*QDIPPCRGSAPS SPHPPPGLESGBK\PGAASWAGP QTPFSGRAQQLCQEGPAGAGN TSGRSA*AASAGTCDGPRSGGR VRTYPGLP*CRWTPGSRSSAAS SHHCRMPSFGGHCTRLSMKRV GSAGGRQLQGRAPS*PARGT*Q RPRGGQSLGAAPLESRH*DGEC *AFWRAETVRSSVQRRREFATG LSGPSS*PRWSTCSVP/ASSPGG GDVAGPQEGPRSFHCLPSCL*V RPSHPEGDAAP*GALHK*RMII EEGRPGPCGGWGLV/GSWEPV QGCRRLNLRWGRAWNCLQFPE *PPGGPGLADSGFIQTARLNFQ GWASVSFSIKRPGRAILRPCPTS EFLLPESFVSGNCSSITERAMWP FWAPPSPAPGAENFPCASVPCK



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8706	39074	A	8763	1	409	LTHLTAQNVPNLFARNERVICL FDTEFGPMAQILVGATIVGSIET VWAGTITPPREGIIRWTWPAG ENDGVSALLKGQEMGRFKLGS TVINLFAPGKVNLEQLESLSV TKIGQPLAVSM*SKATQLGNPR
8707	39075	A	8764	1	1528	MTFVNAQAEDSQIFLYKRRVVP VEGYAPWLVSNGASELERIHYE GMDDVILLDFLPKELGDFMNM HILSFAPGANHGYYIEHTFKEHG GATQAFAKENNHKAYKDTYG VSHITRHDMLQIPKQQQYKEYQ DTHIDTPYCEPLPGETRLWGD DVIGLFDAAETDMNDVVAILENH PLLGAGFAHKIEQLEDKDWERE WMDNFHMPRFGERLWICPSWR DVPDENAVNVMLDPGLAFGTG TIQTLSPAMLDSTHTRRMRS TLNLYEITRMSTVSTSEHSMTY TLVQVDMKEAQKPDATASYRTF NEFFVRPLRDEVRPIDTPNVL VMPADGVISQLGKIEEDKILQA KGHNYSLEALLAGNYLMADLF RNGTFVTTYLSPRDYHRVHMP CNGILREMIYVPGDLFSVNHLT AQNVPNLFARNERVICLSDTEF GPMAQILVGATNGGSIETPESE GATVDES FVVGPGVGDPELLLC IQERSALSGRCVI*SFNSAKVRFI QQSRRPVKS A
8708	39076	A	8765	2	420	QNFKEIFVRPLRDE/VRPIDNDP NVLMVPADGVISQLGKIEEDKI VSNLFARDERVICLFDTEFWPN AQ/ILVGATIVGSIETVWAGT/IT PPREGIIRWTW/QAIEEDSWQ NLGRVAG*NKLPTELNNFDW AQTLSRRNRG

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8709	39077	A	8766	1	1130	MHFAKKEDVSEITGSDGEKPK ARAGCLIGNSERLFSVTFVQF QATLPLSYTIMKHKDTGTSSVP ESIDASLEASQQNP AFLKTLTRS CSPSWPCSRNWP HLLIPLTCPA QAGATPQLPGLGPPGHLPMNQ PASSFPFRPNAASQILTSTFHKP PPGSSLACCCCPGCDWQEDSQ *PTPACPSWPPWPTQLSPSAAGS PNIHSPIQGFHSQLLS* RSPG TEE P*EANKLPWWTGHRPEPHPLG PGHIPCAAG/MHRPLAPTTRPL ATLHGERQRHLHPGQRRRVPR APAESTEAPALWLHRPPECPEC SGHGPAAL EQGAGMA*CRSCR HLPFCFGEADAGSREGPHQEV PRSKICQPPQAASFRICLHSIF
8710	39078	A	8768	179	1908	KKQNKSRGCVNVNWMRRALK MCIPYRNGHSIFLVMVKVERSK RFALKLSVAEKNQMPRNATVIE NSAGYSYGKMAFS*PRICTQIV GPRIISTTAVIS/QPATHHRRATR GAIIRTAFCGPGCFGAGDTPINNG LSIRHTTRNFPNREGSKPANGQ MSAVALMDARSIAATAANGGY LTSASELDCWDNVPEYAFDVTP YKNRVYQGFVKGATQOPLIYG PNIKDWP ELGALTDNIVLKVCS KILDEVTTTDELIPSGETSSYRS NPIGLAEFTLSRRDPGYVSRSK ATAELENQRLAGNVSELTEVFA RIKQIAGQEHIDPLHRVYRHCS RSGNCPSDVFDSKDPVQDHRP QKRVTLIWGYDIHPQIEIIQTGD NFFQFRAIANNFGFLRFYQIRHF GLSGQHGVQIFTADVERGVGL RLQRFPVVKHAI VQRQVEVIAV AHIEVQADIFRSFRAIEANGHK VEQHFDHRPANGVRGTGGAVA ELMHPFAQLFRAGQVETAPCG GLGLIAQLFKVIRLQILRGESKK FSANLTALKLPLPMVYEGDKV LKHLRLPKFNLPLVPQPKKML
8711	39079	B	8769	1	1881	
8712	39080	A	8770	2093	2287	

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8713	39081	A	8771	1	1358	MKINLKLTDNSKVADGQFANI VVFLINWFYIHATTCEIDNGGVI VADGQASKAYSADSIVDYN AHYKTSVDQDAWGFVPGGDN PWKKYEPAKAWSASTVYVKG DRVVDGQAYEALFWTQSDNP ALVANQNA TGSNSRPWKPLGK AQSYSNEELNNAQFNPETLYA SDTLIRFNGVNYISQSKVQKVSP SDSNPWRVFVDWGTGERVGT PKKAWPKHVVYAPYVDFLTNNH HRRTDSFRSKATAELENQRLAG NVSELTEVFARIKQIAGQEHDP LQTEIGSMVYAVKPGDGSARE QAASCQRVIGGLANIAEEYATK RYRSNVINWGMPLQMAEVPT FEVGDYIYIP/GIKAALDNPGBT FKGYVIHEDAPVTEITLYMESL TAEEREIIKAGRIRHLLSDAMLA HLIRPTNRIESVGQIRHFRSIRHL LSDAMLAHLIRPTNRIEP
8714	39082	B	8772	21	1623	
8715	39083	B	8773	32	1850	
8716	39084	A	8774	1	1193	MSEVEAAAGATAVPAATVPAT AAGVVAVVVPVPAGEPQKGGG AGGGGGAASGPAAGTPSAPGS RTPGNPATAVSGTPAPPARSQA DKPVLATRLVPGTAKRFNVRS GYGFTNRNDAKEDVFVHWA VKRNNPRKFLRSVRDGETVEFD VVEGEKGAQATNVTGPRAAGV PMKGSRYAPNRRRFR*FIPRPPS VAPPPMVAEIPSAAGTPGSKGE RAEDSGQRPRRWCPFFFYRRR FVRGPRPPNQQPIELTGAFACS QGTDRVEPKETAPLEGHQQQG DERVPPPRFRPRYRPRFRPRQ QPTTEGGDGETKPSQGPADGSR PEPQRPRNRPRYFQRRRQQA PPGQQAAGPRQPAAPAEAPTEAIK P MIAHDGHAPPNPSTCCLEPSY QLVDVN

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8717	39085	A	8775	3	933	RHQESLCAPLEILQKKKCPCLE EPLQROPCPCQSSSEVTA**NISF RFASPGGN/SPWASH*APSVRG AAPAGPVGLEAAAGSEPHGP/ PDAGGARVPVGGAGSRPRMVL/ SPRSAPHLGGGRSA/PAMRTGN PCTHTQVVTTSPNLPNIP*GAKS HPI/VERPLS*KGTGPSAQIATE NIYP*QLHGKGLIRD*KIVPHD GAAGQSPLLPVRSCQRGYLP SAK*FFDALKIKFTLKFHLRRFSC TSLRLGLLVSPLLPVRLLAG WAHAWMHGCGGWEPRTQQR ASCQLPDRTKSKMRVKIPAANS SWLCH
8718	39086	A	8776	3	925	RGSEQIPSSIPGAP*KMLFSPG/ SSEPEHL*TVPASSLGCRRPGGPV ASRSRPPRPPARAALRGPPASSP IRFP*GASPRAPPTS*MRSGAGS KT/TPRPGPSASGDRPRAPCVRG PGCGSEPAASSTPGPAGVPRA R*GPGHGQTSPHGW*PSSMQQ RTRRCSPSSVPGQFPLP/LSCS QVSPWTW*GLPYSLIPVSSLLP WPEDRVPSFVA/GPLPSFDNTS LPVEGGS*LHPVCLLYVYQENS SKHIPYSCRGSRIFPFSQRQVRM AGQRKLCDHPGGLISKPLAWT RIPEAPVVAAMVEGGGGL
8719	39087	A	8777	144	503	
8720	39088	A	8778	15	427	
8721	39089	A	8779	1	1055	
8722	39090	A	8780	280	1480	FQTRMGISVATIPGTSCSWSMR ASEKEKDTFESTVQVSKLQDLI HRSKMARCRGRFVCPVILFKGK HICRSATLAGWGELYGR/QATT YFFSGGADDAWADVEDVTEED CALRSGDTHLFDKVRGYDIKLL RYLSVKYICDLMVENKKVKFG MNVTSSEKVDKAQRYADFTLL SIPYPGCEFFKEYKDRDYMAEG LIFNWKQDYVDAPLSIPDFLTH SLNIDWSQYQCWDLVQQTQNY LK.LLLSLVNSDGGTDSKSLVAI RTSVGVALAQTSGNALAYGTK KAQEQSQDGLIHTSLKPTILYL TVAYDWLFGHMLVDRLSKGE EIFFFCNFKHITSEFSALKTQ RRKSLPARDGGFTLEDIC*DE RTVAVPPDLVCDCLPGHGEFPR

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8723	39091	A	8781	2	588	HSFFFFNPREKCKTKR*RLSASRF PP*PWSRLPSG/QPAGGASAGSP SAPRGTRGAGSRPAHG/VQPP RAHPEAPCPACPRSVGGAR/RA PEPSSNLSGEAPASGDRDVPVPPS PLAR*VPLGGREFGWPWANA L.RPGKTP/RSDRV/SRSPWS/PAG FSVPASWPRRSTSGNRGPPSRFS RLSRTSGPLNRLGEPFDVQGPL
8724	39092	A	8782	1	198	
8725	39093	A	8783	1	275	MAGAPAPASLPPCSLISDCCAS NQRDSDMGVGPSEPGAGYNLVP VIEKRSIRVGVTFGRCCPSPSL TRKGNLTPWASQVRQCLAL QLAH
8726	39094	A	8784	349	478	KLKSFYTEELSSGLYIGISLCP HKYNCLVSSHRCCKN*VTGY
8727	39095	A	8785	1	325	FSEGNLYLVGIMHPLKAMLPL QYQTETFPFGYLM/PCRLQQ SHLLTLRDCCASNQRDSVGVGP SEPGAGYNLVRRFLSLLEKRSI WVRVTRFSSALNHELKVNNDH
8728	39096	A	8786	113	313	
8729	39097	A	8787	2	1991	
8730	39098	A	8788	512	1178	
8731	39099	A	8789	135	1562	DTLVPTSGQDISRGLEGNLNSC PT*Q**RAPFLWCQ/PKAEWGT WIFNPEAEESLEPRSLISDCCAN NQRDSDMGVGPSEPGAGYNLVP RSFLSPSEKRSVRGVTRLSRCR PSPLSLTQKGNPLTPCASQVRQ CLALLRLRHVYFYFNGWKDYG VASLTTILDMVKVMTFALQEG KVAIHCHAGLGRGTGLIACYLV FATRMATDAQIIFVRAKRPNISQ TRGQLLCEAQSGAFSADVSGS HSPGEPVSPSFANVHKDPNPAH QQVSHCQCKTHGVGSPGSRVQ NSRTPRSPDCGSSPKAQLFVE HETQDSKDLSEAAASHALQSEL SAEARRILAAKALANLNEVEK EELKRKVVEMWQKELNSRDGA WERICGERDPFILCSLMWSWVE QLKEPVITKEDVMDLVDRAD AAEALFLLEKQHQHTILCVLHC IVNLQTPVDVEEAFLAHAIAKAF TKISIIIVNQNPVETVLL
8732	39100	B	8790	563	2017	
8733	39101	A	8791	108	194	
8734	39102	A	8792	1	164	

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8735	39103	A	8793	1	1068	MEESSRYWGTGRNRRREGKIQ WAQAPALFNIRQGPNEGDNQQ GSYWEALASIMQIHLVPSGLG MVTAFHCSWYLSTTATFPGLV NPALTEIKSGNYYVHGSFILQV ADYKEFQTLMLMITKATFHQKTQ CWACEEGVQQSFHCPCRMQAA ASVERYTELLKEFLKEHTCDN QEPTSTLHYHSLKTVHIHVYSS RCTLPCQPSQAAQAEIGSPAP ACEDFVFAALAPP/ESG/RCPTL RLLGGLCTPTNARRTRTHSTTA CWARAQWDSLGLPLKLSHR/PR VCGGTRAPGRQCGMGNQRLGT SNSEARDPGGLRVKHR/CEAIQ EPPNRSRRQGAPLHSPPAY*MS SWRP*SFSKRHNLS
8736	39104	C	8794	78	331	
8737	39105	A	8795	129	1734	QWMHRMLDIFKGSQQHPSVPR VSSRPPLGPQGYSLHHFGTQGI HSATPINTQGLQAPAMGTQQPQ PEGKTSAAVVLADGATIVANPIS NPFSAAPAAATTVVQTHSQSAST NAPAQGSSPRPSILRKKPATDG MAVRKTLIPQPHDVASPRVES SMRSTSGSPRPAGAKPKSE/STC LWPLRSLCPWRLYPIKIMISLPL PSLKLPSSPHRPFQL*LQQPVPR HNQPLPFQPFLESPSLHPSPLA HCTTSISHCGWQSFRLGLPSRS* N*SERRSRTNGYHEASF/SVPPL ATNTVPSPLALLANNLSMPTSD LPPGASPRKKPRINNSMWISTEE GDMMETNSTDDEKSTAKSLLV KAEKRKSPKEYIDEEGVRYVP VRPRPITLLRHYRNPWKAAYH HFQRYSDVRVKEEKAMLQEI ANQKGVSCRAQGWKVLCAA QLLQLTNLEHDVYERLTNLQE GIIPKKKAAATDDDLHRINELIQG NMQRCKLVMDQISEARDSMLK VLDHKDRVLKLLNKNGTVKKV SKLKRKEKV
8738	39106	A	8796	1	169	RPTRPKSNKRQCLVFVTPKEE EPVRNILEKFTNISGKVRSLYL HAPLLPLER
8739	39107	B	8797	156	398	

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8740	39108	A	8798	20	723	VWGGELPRIFWFLPTSHQWM LFSVFLGWGSCQWSCSHLLSCL WRAAFSEFPLGPEPGEGIPELC LCFQMEAIELSVDPKSNKRQCL VFVTPKKEEPPVRNILEKFNTISG SK/CTEVQRGVYIPGHIR*R**SI PRGF*FYSK*GRPDSAGGHGPG GVLQGEKGHSACARQGGRFQE GAAFAQRETAGRRVGQRWCG DCFRTPVHRKSLSSPNFGGFGA GSEAVPCHLVLYLVW
8741	39109	A	8799	79	256	LRLLTLFFQNLGGKSSMLWTA HPCPEGACSSCTSLGSHLLSS FPVLGR*PGPSGDH
8742	39110	A	8800	402	996	TFFKFPPDSGAQLASPRGSRIGA AGGAA/SSPEPSAALLSPWVVD GTGRPGAGGGARRGGSGCTGA HGGGGSSGM/VG/PAGPEPCPA GRQLRPGEKSSAAPLREPASAL AGPERGSHSAAAG*RAPO/GRQ SGSPGRGGAESERGL*GLPSCC HLSPGSGAAAVPRSVGSRWPC GA/PTLATPPTSAFFSAATPEGP PLAS
8743	39111	A	8801	7	602	TFFKFPPDSGAQLASPRGSRIGA AGGAA/SSPEPSAALLSPWVVD GTGRPGAGGGARRGGSGCTGA HGGGGSSGM/VG/PAGPEPCPA GRQLRPGEKSSAAPLREPASAL AGPERGSHSAAAG*RAPO/GRQ SGSPGRGGAESERGL*GLPSCC HLSPGSGAAAVPRSVGSRWPC GA/PTLATPPTSAFFSAATPEGP PLAS
8744	39112	A	8802	262	349	KEGEGGK/DP*PVRMCPKPSG HWKHPGE
8745	39113	A	8803	2271	2863	GGASGVVRSWWARGLAGFRS EAADLRGLPVELRASAPCVRT PQPLGGR/GIGRPGAEGGPCWG GSGRTGAHGGAGAGSSLGQP RKGLPQCSGG/PEGLLKCGQSG SPGRGRAQSERGL*GLPACCHL SH*PQGRQI*PRTCPTPFQSKTS DQGGPSGPAVSGSERQV*LHHQ *PGCRDYLCGFCSWEINPVWG

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8746	39114	A	8804	3	561	NCPSLLVESCFCQECGSSIPFALPS TQVEHALYASER*QRAGSPHSP HSLSVPLPGLPLWRHLRSPS/G PPLH*PP*ASTLTGGPQ*RLGSA GINVSSEPVSSSRPNV*SFFFPQY TVTLVKGWRSREPSPKSSVLGS/ MVP*STKSEP*REPI*SLTGKA GERGEKGREKAIGSGR*GVAKCS SDHVR
8747	39115	B	8805	298	380	
8748	39116	B	8806	1	1292	
8749	39117	A	8807	1	1224	MKPRTLAVSVTALKVARLEFV PSDVRMCSEFLPSGGLVVSLAS GVKLQTFVSVTARNVDPKN SGAQLASPGSSTRAASGAAC* SPSPPPCARTPQPLGGR/GTGCP GAGGGTRRGGSGRTGAHGAAE GVGSGLGQPRKGPPTVQWWAE GLLCKRQSGSPGRGGAESKRGL *GLPASTLSMPPGIECAGKSENS HMNLNCSGGSLPGGTGAHLPL GPDGQPAETLLWGPCGCGPG TGLTSGQTISLGCQGGQPRRE VKPPVPQRVSVLLVAVNPPDS RCRVETDRPWLRCIQSCLCGTL KRDVLHSPSVFNTTRGGTAE WSREDKDALLPEYALHMPFAV GFKLEYKEGVLSNLAAGPEK ELCEAKRNQCPKSGVSHTSRPL KPEWSDFVAEIDESKLPRDS
8750	39118	A	8808	1	1298	ESLRAGSFQEQIPELAPLIILRG FGTWPGWSFQATGFCVGVVRGS PGSGFRGCGAYRAP*SFRTQLW PWQPLQGLDPKPLKDALARPSPL GRRACAEHHLCSADERPDLGFE GLQRWGGCRGSQKPAVHQ WGRGCEGTGGGHTGSPPPRLTP P/PGGSGFRAQPGERRPAACGQ QRALGPMRPPAC/GPSPT*GCA LNPTSPPALV*GFIHIVAAFCF VTPVSKSHSFQLGGELRVAGSD VGGRWGERENTQGSTLPPSSPAS SPGSPSPDPATPPGPATPGLIDIL LLLPMVASSRKHDFSGFSGRLP PQGEFFQ*GPTGWQSWVWPLD PSYLGCGCGGCGQGPRTGRRG ASSHCCVPAAP/GLSMDCSRGS GGSPRSPPWALLGDLPSLET VCLVMMFPCPIWMASEFAMEI QLLGPFWQIMLIGLCW



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8751	39119	A	8809	2	662	RIPLLVTRLKINEKVLQVLTNIF LFHDFSVQNFIFGLQLSLEHFY SQPLSVLCCNLPEAKRRINFLSN NQCEINIRRLPSFRRYVEKQASE KQVALLTNERLYKKEETQLLEN VLHVYHMNYFLVLRCLHKFTSS LPKYPLGRQIRELYCTCLEKNI WDSEYASVILQLRLMAKDEL MTILEKCFKGFKSYCENHLGST A*RIEEFLGQFQSLDEPRGR
8752	39120	A	8810	326	1215	NPILHGNFIFMLDHSKLVQDQ E*TLN*/HYGPQVVTMCQCSFIE RNKRIPVVQGIIRGRGHVQWG RYVEKQASEKQVALLTSECL KKETQLLENLHVYHMNYFLV LRCVHKFTSSLPKYPLGRQIREL YRTCLEKNIRNSEEYASVLQLL KMLAKDELMTILEKCFEVFKSS CEKHLGSTAKRIQFLAQFQSF DETKENEALKREEGCPNITPDI CIAAYKLYLECRRLINLVDYSQA FATILTAEEKMDANSTSEEMN EIIYAWCIRTVFLELLGFIKPTK QKTDHVARLT
8753	39121	A	8811	70	613	SLEMKELRRSKKQTKFEVLRE NVVNFIDCLVREYLLPPETQPL HEVVYFSAHAHLREHLNAAPRI ALHTALNNPPYYLKNEALKSE EGCIPNIA/PDICIAYKLHLECSR LINLVDWSEAFVVTAAEKM DANSASSEEMNEIHARDIRAVS ELELLGFIKPTKQKTDHVARLT WGCG
8754	39122	C	8812	598	762	
8755	39123	C	8813	138	296	
8756	39124	A	8814	1	395	

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8757	39125	A	8815	2	1289	DDLALAFKVLHDKQRGPTGF YAPFNSRPL*KPQLAHSIILMET ATERISRLLLPFADQHVEIPSLT AGNIALTVGLKHTATGDTIVSS KSSALQLQ.VEPNGREKRSTDK TMKAERLLLAGSGRFQEPVFFC TIGTPITV*GSQIWEHAFEMSFS VRIPVLKVRLDPDSSGQTVLCLG MGELHIEIIHDRIKREYGLETYL GPLQVAYRETIINSVRATDTLG *EL*GDKRHLVDLLGSGKARPI ETSSVMPVIEFEYAESINEGLLK VSQEAIENGIHSACLQGPLLGS IQDVGNYLYIP*QIHPWAPSTTY DFCLCLKMPCKKALERKADKQ VLEPLMNLVTVARDYLSPLV ADLAQRRGNIQEIQTRQDNKV VIGFVPLAEIMGYSTVLRITLTSG SATFALELSTYQAMNPQDQNT
8758	39126	A	8816	545	849	LAIHLSSLNRSRHDDEATRTSTSE GLEEGEVE/GETLLIVES/EDQAF S/VDLSDHQSGGISLNSDEGDVS WMEEQLSYFCDKCQKWIPASK ELLNSFDLSIPV

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8759	39127	A	8817	1	2395	MDSSIHLSLISRHDDEATRST SEGLEEGEVEGETLLLIVESDQA SVDLSHDQSGDSLNSDEGDVS WMEEQLSYFCDKCCQKWIPASQ LREQLSYLKGDNFFRFTCSDCS ADGKEQYERLKLTHQVVMML ALYNLSLKGSGRQGYFRWKED ICAFIEKH*TFLLRNKKKTSTCR STGAGCLSVGSPMYFR*GA*EF GEPRWWKLVHNLPLTMKPERE KTAASTLNIFAASKPTLDPITVE GLRKRASRNVPESAMELKEKR SRTQEAKDIRRAQKEAAGFLDR STSSTPVKFISGRRPDVLKLG EVIDFSSLSSDRTPLTSPSPSPS LDFAFGTPASHSATPSLLSEAD LIPDVMPPQALFHDDDEMEGD GVIDPGMEYVPPAGSVASGPV VGGRKKVRGPEQIKQVESEEE KPDMDIDSEDTDSNTSLQTRA REKRKPQLEKDTKPKEPRYTPV SIYEKLLKRLAECPGAVAMT PEARLKR/KLIVRQA/KRDRGL PLFDLDQ/VVNAALLVDGIYG AKEGGISRLPAGQATYRTTCQD FRILDYQTS/LPSRKGF/HQ/T TKFLYRLVGSEDMADVDSIVSP YTSRLKPYIRSDPHWTEPDAP LDYCYVRPNHIPTNSMCQEFF WPGIDLSECLQYPDFS/VVVLV KKVIIAFGFMVP/DVKYNEAYI SFLVHPNWRRAGIATFMIYHL
8760	39128	A	8818	3	364	GDSVPTAEGGDQVCVILSSVPQ TVWEPMFNKRACG/P*SP*SLSA TSIYPRELKAGTKDTCPPVFR AVLFTTATQCPSTDAWMNKM WYSRTMECYSALKRKEIPPHAT ARHPMCLQFCRW
8761	39129	A	8819	292	508	ARPGDQATSGGQGTTFQHPLFC FELGGSQNPALQ*PFAAACPVG AD*TKFTAFCCRLK*KRTCCCL SLGSR
8762	39130	C	8820	253	369	
8763	39131	A	8821	295	393	IYFGCLLGEPVVAAEAGIWDN DCVKKQLLHSW
8764	39132	B	8822	91	479	

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8765	39133	A	8823	I	544	ARHPDMKKRRVEDASILPCNVSL EYEKTEVNSGFFSKSAEEREKL VKAERKFIEDRVKKIILKRRKV CGDSDKGFVVINQKGIDPFSLD ALSKEGIVALRRARRRNMERLT LACGGVALNSFDDLSPDCLGH AGLVYEYTSAPCPKQSGLCILSS TLGEEKFTFIEKCNNPRSIVTLII KGPKNHTLTQIKDAVRDGLRA VKNAIDDGCVVPGWCRCRKGW AMAEALIP*APVLKGRAQLGS PKHLLDAFAHYFPKVLCFRNSG FLTQGNILKFKAEHSRIQVQL VGVDLNTGEP/MVASRSKAVW GHT*LW*KKTSLPSTPTW*IA\ TNILLGLNEIMRAGMSFS*KGF VVINQKGIDPFSLDALSKEGIVA LRRAKRRNMERLTACGGVAL NSFDDLSPDCLGHAGLVYEYTS PACPKQSGLCILSSTLGEEKFTFI EKCNNPRSCHIIDQRTK
8766	39134	C	8824	636	1025	
8767	39135	A	8825	33	1505	KCISASVKVDFSDLLLSNNTS*S AFTPTRTQKSSSKLLRKESHYS GMMSIQEKSSENSKVTKKSD DKNSETEIQDSQKNLAKKSGPK ETIKSQAKSSSESKINQPELETR MSTRSSKAASNDKATKINSKNT VTVRGYSQESTKKKLSQKKLV HENPKANEQLNRRSQRLQQLT EVSRRSLRSREIQGQVQAVKQS LPPTKKEQCSSTQSKSNKTSQK HVKKRVLEVKSDSKED/GKSSN **SNKFS/SKGKNAR*NIR/SACA CSSQCTQGSEKCPQKTTRRDET KPVVPVTEVKKRSMATSVVPK KNEMKKSVHTQVNT/KHNTPK KSTAISA*TK**AGASRKEQTR *YSPA\REEIAGEIESDNVEVKK ESSQMESVKEEKPSKLEETSV ERQILHQKGTNQDVQCNRRFFPS RKTKPVKICILNGINSSAKKNNS WTKIKLSKFNSVQHNLDSQVS PKLGLFTNQFFTSFRNASSSDS KYIFRDKAT
8768	39136	A	8826	I	394	AISRALGRYVLPCLIQDGFVA HTAHAILTSLED/SL*MFQPKTC WCL\AN*HDTLSVNMETPHPSF QEELSGLLLLKMLRSPIEASKD KDKVKNSAVRALGNLLHFLQP SHIE*PTFAQINEEAIQALIS

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8769	39137	A	8827	52	730	KSACDALSSILPEAFRNLPNDR QMLCITVLLGLNDSKNRLVKA ATSRVALGVVYLFPCLRQDVIFV ADAANAMVMVMSLEDKSLNVRA KAAWSLGNLTDTLIVNMETPD PSFQGRVLWSPALENGYDQAL EASKDKDKVKRHA/VRA/LGNL LHFLQPSHI/GKTPHLQKFJ*GSL SRALNELLF*QKLA MKVRWNA CYAMGNVFNKPALPLGTAPWT SQAYNALTSVVT
8770	39138	B	8828	47	1576	
8771	39139	A	8829	2	2753	
8772	39140	A	8830	1	273	
8773	39141	B	8831	104	206	
8774	39142	A	8832	1	987	
8775	39143	A	8833	111	2187	DERRVGAADMFGRSRSWVGG GHGKTSRNIHSLDHLKYL YHVL TKNNTTVTEQNRNLLVETIRSITE ILIWGDQNDSSVDFDFLEKNMF VFFLNILRQKSGRYVCVQLLQT LNILFENISHETSLYYLLSNYYV NSIIVHKFDFSDDEIMAYYISFL KTL SLKLNHNTVHFFYNEHTN DFALYTEAIKFFNHPEMVRJA VRTITLNVYKVDNQAMLHYIR DKTAVPYFSLVWVFIGSHVIEL DDCVQTDDEHNRGKLSDLVA EHL DHLHYLNDILINCEFLNDV LTDHLNLRLFLPLYVYSLENQD KVFLIIHHAPLVNSLAEVILNGD LSEMYAKTEQDIQRSSVLP TLSS LWQGSLSLNLQSLGHLKCSS HLCGAQAAADS VTGEIPAIRSL EWLISAGSKARTFFFLKMLIGF WEKVDCEYQRRQVLSTRLQEA LPSNRLTDVA AVHSSCMLGFGS TAPRGSWIGDPA AVHLPLPGEI AEHLGSKGTTT VTKHQPAKPS IRCFIKPTETLERSLEMNKHGK RRVQKRPNYKNGVEEEDKEG PTEDAQEDA EKAKGTEGSGKI KTSGESEEIFMVIMERSKLSELA ASTSVQEQNTTDEEKSAATCS ESTQWSRPFLDMVYHALDSPD DDYHALFVLCLLYAMSHNK/G KSPEKEEGLSGTQSHPGKAGTF GKEGAEEERKRAQV

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8776	39144	A	8834	1	3050	RNLLVETIRSITEILIWGDQND SVDFEFLEKNMFVFLNLRQKS GRYVCVQLQLTLNLFENISHET SLYYLLSNVYNVSHVHKDFDSD EEMAYYISFLKTLKLNNHT VHFFYNEHTNDFALYTEAIKFF NHPESMVRVIAVRTITLNVYKVS LDNQAMLHYIRDKTAVPYFSN LVWFGSHVIELDDCVQDEEH RNRGKLSDLVAEHLHLHYLN DILINCEFLNDVLTDLHLNRLF LPLYVYSLEN
8777	39145	A	8835	111	270	
8778	39146	A	8836	240	406	
8779	39147	C	8837	86	286	
8780	39148	A	8839	172	243	DPS*EARSMLLLFLPPDHSLP H
8781	39149	A	8840	280	526	GRNAVVSQ*AHCRSQTGPQK*S SL/LVFPS/WTYRHPHPLAN* KKFFLHRDGLDMLPRLVWNS WPQVILPQPPKALGILL
8782	39150	A	8841	3	1785	VLDARNAGAGGLAGPAGVLR RASRCDPGAAVAGQGGAARVR PGRAAAPSPGPPGGA*CVPTDA GAGPGSAGARQPLPFAAGALS HSGHC*RGLRGPGLASPAQAK AAWSGILLSPAAAGRDGGRGH NPRDPPPLREHGPPIPGFHGDR G*ELYQCHLGGEGG/GPDKPGS PCASCGLDGHWYRALLETFRP QRCAQVLHVVDYGRKELVSCSS LRYLLPEYFRMPVVTYPCALYG LWDGGRGWSRSQVGLKTLIL GKAVNAKIEFYCSFEHVYYVSL YGEDGINLRVFGVQSCCLAD RVLQSQATEEEEEPESTSQSPAE EVDEEISLPALRSIRLKMNAFYD AQWKENGYYRAIVTKLDDKSV DVFLVDRGNSENVVDWIINMLL RFLTNOEQEGETISKVIAQAGY AKYQEFETKENILVNAHSPGHV SNHFTTESNKIPFAKTGEQEQ AKRENKTTSVSKALSDTTVVTN GSTELVVQEKVKRASVYFPLM QNCLIEIKPGSSSKGELEVGVTE VRVSYVENPGYFWCQLTRNIQ GLKTLMSDIQYCKNTAAPHQ RNTLACLAKRTVNRQWSRALIS

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8783	39151	A	8842	2090	2901	THLLVPGMQPLTWQMPFSPFLS ISPTRSNLPSAATPVIAQWA/HE QSGHGGRDGGYTWAQQHGLA FTNTDLA FVNAKIGFAYPVCDA SAKTTIRGLLECLIRCDGIPHSIA SDQARIHRSRNQEEVEVEVAPLT ITPSDPLAKFLISVPVTLRSAGL EVLVPGEGMLPPGNTRTIPLNW KLRLPPGHFGLLLTLSQEAENG VTVLAGVIDLDYQDEISLLHN GGKKEYARNTGDPGLRLLVLP CPVIKINGKLQPNPGGTNGS DPSGMKV
8784	39152	A	8843	1	585	
8785	39153	A	8844	1	1697	MDKYFMIKTPKAMATNTIDK WDLIKLKNFCTAKETMIRVNR QPIECKMFAIYPSDKVILLFKM APKRNAEGLSTVSTCKKAAMC LIEKGCELVGPGVQTHPVVTS PVSECIIGIDILSGWQNPHTSLT GRVKAIMVAKDKLPLEPLPG KIVNQKQHCIPGWIEISA TIKD LKDAVIGIPLTPFNPSPIWPQK TNGSWRMTVDYHKLNQVVTPI AAA VPDVVSWEQINTSPGTCL HWWPHGEFPLVDREERTRW FTDGAQYAGTTQKWTPAALQ PLSRSTLKESECFIHGHGIPHSIA SDQGTHFMKKVRQWAHAHEI HWSYHVPHYPEAAGLIEKWNG ILKPQLQCQLGDNLTQGWDKV LQKALYALNQHSVYGTISPIAR IHRSRNNQEEVEVEVTLIITPTD PLAKFLLPVPSTLHSLDLEVLVP EGGMLPPGHTAMIPLNWKRLR PPGHFGLLLPLSQAKKGVIVL AGVIDLDYQNEISLLHNGGKE EYALNIGDPLGHLVLVPCPVIN VNGKLQPNPGRITNGEDPSG MKVCVTPPGTITTTKKP
8786	39154	C	8845	1	720	
8787	39155	A	8846	57	261	WNF/CDPGGPMMKL/FISFKLKT ISSTFLSPTCLVL*RRPSRSASSL TVLCTTTTRSSSPLLALV*TWTP
8788	39156	B	8847	1	1158	
8789	39157	B	8848	1	2523	
8790	39158	A	8849	3	375	
8791	39159	A	8850	3	169	DFQPFRVTVHWGKNDQTFR GLLDTGSELTLIPGDPKHHYGP PVKVGAYGAQQL
8792	39160	A	8851	3	376	

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8793	39161	B	8852	1	592	
8794	39162	A	8853	1	319	
8795	39163	A	8854	1	1071	
8796	39164	C	8855	1	862	
8797	39165	A	8856	1	1488	MGRARRLTVPVIALWETADGS RALTVETTVTLQHLNVTGII FRGGRGQVAAVNCQKRDIQPF TRVTVHWGKRNDQTFQALVDT GLELTLPQDPKHHCDPPVKVG AYGHQVINGVLAQIQTIVGPVG PWTHPVVIFTVPKCIIDILRW QNSHTGSLTGRMKAIMVGRK WKPLELPLPRKTVNQKPYHTPV GTAEISATMKDLKDAGVVIPTT TLFNSPIWSVQKTGGSWRMV DYCMLNQVVSAAVEIVLDVVS LLEQINTS/P/WP*SGSCTAAFHH QMEVVHT*SGSSRS*RHNCTN GLMGSL*SVDRGREYDGLVH RRFFTC*HHPKLDSCSTTVPF* DIPEQL*REIFPPVSWRGWR LCMGSAWTFTTHQG*PGYGHG *VPNLPAAETNTEPSIWHSSG* SASYLVAG*LYGTSSIMERAEEV CPHWNRHLF*IWVVCLSTLCF C*DYHPWTLEMPYPSPYSTKL CCCPRHILLYG*RSAAV
8798	39166	A	8857	1	1056	MSSVLLRLIYQLTKQTASFEGG PEQKALQQIQAAVQAALPLGPY DPANPMVLEVSADRDVWLSL WQVPIGESQQRSLGFWSKVLFPY SADNYFPFERQLLACYWALLET DRLTVGHQVTLQPELPMNWV LSDPSSHKVGHVHQHSIIKWK WYIRDQTRAGPEGTTTPVITQ/ WDAHEQSGLSGRDGKGRFV LTGVDYSGYWFAYPAHNAS KTSIVGFTECLIHCHGIPHSIASD QGTFLTAKEVWQWAHAHGIH WSYHIPPHPHPIAAGLIEWNGLL KSQQLQCQLGDNLTQGWGKDL QKAMYSLNQRLLIYSTVSPISRIH GSRNQREVEVEVAPLITLSDPL AKFFFFLP
8799	39167	B	8858	603	1785	



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8800	39168	A	8859	3	467	RIHVRPEITLTA/ANTARPY*IDP HDTLLSHSNFGSSDCPSSSKMR QALELVRERAPELMIDGEMHG DAALVEAIRNDRMPDSSLKGS NILVMPNMEAAARISYNLLRVSS SEGVTGVPVLMGVAKPVHVL PIASVRRIVNMVALAVVEAQ TQPL
8801	39169	A	8860	1	1878	
8802	39170	A	8861	3	684	MPNYLRFVRGLIDSSDLPLNV REILQDSTVTRYLRLNALT KRVLQLLEKLAKDDAEKYQTFW QQFGLVLKEGPAEDFANQEAIA KLLRFASHTDSSAQTVSLEDY VSRMKEGQEKIYYITADSYAAAK SSPHLELLRKKGIEVL LLSDR IDWMMNYLTFDGGPPFQSVSK VDESLENLADEVDESADAEKALT PFIDRVKALLGERVKDVR LTHAGSGLVGENV
8803	39171	A	8862	2	393	LEFGKKLGNAADYFIANKIDQ PKIAVINCEAFVVCVQR RKGFEVLKSRVPGAQIVANQEGT VLDKAISVGEKLIISTPDLNAIM GESGGATLGAVKAVRNQNRPE KLLFSVRI*QPKLLRSWK TIRCTPSRVEGNQEP SLVYIP/SQAP/
8804	39172	A	8863	414	805	WNM*TRDHKHGLNLYVQ RVFIMTDAEQFMPNYLRFV GGLIDSSDLPLNVSREILQD STVTRNLRLNALT KRVLQMLEKLAKDDAEKY QTFWHQFGRGIIIFTSQ FNR
8805	39173	A	8864	3	684	MPNYLRFVRGLIDSSDLPLNV REILQDSTVTRYLRLNALT KRVLQLLEKLAKDDAEKYQTFW QQFGLVLKEGPAEDFANQEAIA KLLRFASHTDSSAQTVSLEDY VSRMKEGQEKIYYITADSYAAAK SSPHLELLRKKGIEVL LLSDR IDWMMNYLTFDGGPPFQSVSK VDESLENLADEVDESADAEKALT PFIDRVKALLGERVKDVR LTHAGSGLVGENV

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8806	39174	A	8865	1	624	AKLLRFASHTHTDSSAQTVSLED YVSRMKEGQEKIYYITADSYAA AKSISPHLELLRKKGIEVLLLS RIDEWMMNYLTFDGKPFQPG AKVDESLEKLADDEVDESAKEA EKALTPFIDRVKALLGERVKDV RLTHRLTDTPAIVSTDAD*M/TP RMAKCFGGAGQKVPEVKYIFE LNPDHVLVKRA\ADTEEEAKF CVWGKNCVLPF
8807	39175	A	8866	471	659	
8808	39176	A	8867	638	834	SSNTMMHFQIHMKESTEQQT MTARR*Q*SEVDE*REDTTLAA RGRTEA*SARYQLT*QSVPSPH
8809	39177	B	8868	1	1383	
8810	39178	A	8869	4452	4896	SQHSEVFVCHMLSQPRAPGAG RYL/LQRKA/SEALEVEV/VDTW QADAVRDTRTLVGESFLVSL ALALALSDLVSHKTRIDSLFLD EGFGTLDSETLDTALDALDALN ASGKTIGVISHVEAMKERIPVQI KVKKINGLGYSKLESTFAVK
8811	39179	A	8870	31	185	GHRRRPFKRGRKSR*RGGSQRR VNEDARRSAWMRKKQRRLISK ISDR\ARK
8812	39180	A	8871	1744	2670	

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8813	39181	A	8872	1	1680	MGFWVENGEIQYPVSEITIAVSS LVFSSASFAADLEDNMETLNDN LKVVEKADNAAQVKDALTKM RAAALDAQKATPPKLEKSPDS PEMKDFRHGFDILVGQIDDALK LANEDVFTRTLGDADALYQFQNI RHVLRMQRIAAGEGNTLAFDT SVIQIVNDLVFHCFGKWLGTGY PPCAFIATGAFMNTPGDKQGA TSAGAVDDVDRISNEITIGIPML TGYILLHVKGVRKSSADHRR RPLASLATPPHKSWTCTLLFFR LPNVVCYANRQQLTPILETLQP SDELPHEETVVLNWRQVHE QCLALHSQQQTLQQQDVLAAQ SLQKAQAQFDTALQASVFDDQ QAFLAALMDEQTLTQLEQLKQ NLENQRRQAQTLVTQTAECLA QHQQHRPDDGLALTVEQIQ QELAQTHQKLENTTSQGEIRQ QLKQDADNRQQQTLMQQIAQ MTQQVEDWGYLNSLIGSGEGD KFRKFAQGLTLDNLVHLANQQ LTRLHGRYLLQRKASEALEVD VVDTWQADAVRD/TRLTSGGE/ SFLRLRLR*VTRRHQLWLHLRLH
8814	39182	A	8873	3	823	
8815	39183	A	8874	287	426	YSGLSAVNPVNDAYGVRFQLP SVNRIPVS***VKLAPPAHQIKRI SGKCRFIPLC*YAPPGFSSASTM RATGILSTASQPPGKLCMEEST AERRVGLPLAKW
8816	39184	C	8875	1	2058	
8817	39185	A	8876	1	1989	
8818	39186	B	8877	1	3132	
8819	39187	A	8878	194	789	LTKLPSLFTFTRLSSDNDLRRGG DKRGGANGARIAL*PQTRTGD VTRRQPIRVCTVIEMFELLE/PIA DGRFNRYARLDVST/TESLLIDK AQQLTLTAP/EMTALVGGMRV LGANFD/GSKNGVFTDRGVLS N/DFFVNLLDMRYEAWKATD/ES KELFEGRDRETGEVK/FTASRA DLVFGSNSVLVFRILGGFFCEYS LTIRILH
8820	39188	A	8879	1120	1395	

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8821	39189	A	8880	1	629	THRPPKSGPPCAKTRTTHVTA KPLFPQTNPKQTVRRMQGELY LVDESQGQFVSALNYRRRKTR NNATAYPIRLFYLSVRPRAGSK SSRTIWILLAD/AKITPYERRQL VARIEA/LSTEIPAQVRPLYQLW RDGQALQLQLAEERQR/YTGG ADTKQDGATTTKDKQQR*TKG TRSQPSTREVQQSQTKHSTSR PPNHAQPSNSALVTRQ
8822	39190	A	8881	3	307	
8823	39191	C	8882	161	337	
8824	39192	C	8883	34	168	
8825	39193	C	8884	172	456	
8826	39194	A	8885	174	516	VSGVRCWIHSSAFPVPFPGFFLP VAFFDRPPARLYRMHTWSHME SQEPARLPSHYAD*GQGSQKR\
						DSCSSGWAGLLFISQFVLWSA EIEGSLNHITLGFRLSHGTTSD GMTF
8827	39195	A	8886	1	2964	
8828	39196	A	8887	1	2724	
8829	39197	A	8888	3708	7098	
8830	39198	A	8889	115	339	
8831	39199	A	8890	445	634	VINTFSLHMTGST*HQGNWR HLTLHPRNSKHLEQPTPGVLQ LRPPTASLRQLLSNAGCSG
8832	39200	A	8891	1663	2234	GEGLRRGLFPGAEEAQGRAETA GCLRRGRGALALALPGSPGLSP WVEDAGGHRVLHGRAVLRCA RAPVPQPAGLAKVEPYSGVSS LTAFPQAPILLSGGQSRAGERT TM*G*PEMEKL*SCIGEGHQPC HR/KSRPAAPCPPPSAMLFLT SSATLLSSSKGASGGWEPSSAA PLGGSGQPFREMVSH
8833	39201	A	8892	202	542	
8834	39202	A	8893	564	1179	QHRLTYRTALWIHYRPDPKPL MSFRPGHQRLSVTSLVCHGLL MVGTSGLVLVALPVRLSSPSL PPVELL*HSVCVSVCRGISCL*W RLWDQISDWISRTLQPPRPSPC CPVVASPGPGKGPQCNGDPKW KSCEAAVSKGTSPATGKSRPAA PCPPPSAMLFLTFRYSATLLSS SKAASGAREPSAAPLGGSGQPF REMVSH
8835	39203	C	8894	321	539	

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8836	39204	A	8895	630	983	NLETNGKIPFENPWSKVPIRFGRL QNLRRVCLTTGGQIPTGRWVT ATDSRGAGDYRLCLHHLR*PD GARLSAGSADCAANRRDVGDS GRGLPGRLSVQQPRRVRGQP DVQPVSWPGC
8837	39205	A	8896	31	144	MEISFTRVALLAAALFFVGCDQ KPQPAKTHATEVTVLEKTMG TFWRASIPGIDAKRSaelKEKIQ TQLDADDQLLSTYKKDSALMR FNDSQSLSPWPVSEAMADIVTT SLRIGAKTDGAMDITVGPLVNL WGFGEQPPVQIPSQEQIDAMK AKTGLQHLTVINQSHQYQLQK DLPDLVVDLSTVGEGYAADHL ARLMEQEGISRYLVSVGGALNS RGMNGEGLPWRVAIQKPTDKE NAVQAVVDINGHIGISTSGSSRG D*DGYGQGLSRVIDPQTGRSIE HNLVSVTVIAPTALEADAWD GLMVLGPEKAKTCSPPGLRGT ESLNTLRDRITQINGIDEVRMD DSWFARLAALTGLVGRVSAMI GVLNVAAVFLVIGNSVRLSIFA RRDSINVQKLIGATDGFILRPFL YGGALLGFSGALLSLILSELVL RLSSAAVEAVQVFGTKFDINGL SFDECLLLLSSMVTFWCRNLF TSLELWTHADKQDDNSCLSS ASVYLKAKMMKVMPLMQLLS SGTGFYRDRLENSGGRYESRRS LTRQFREETAIPRECSQRIDFL LFETPSVASASSAGFWLRFGSTA
8838	39206	A	8897	1	1775	
8839	39207	A	8898	10	300	PTSIPRESSSGTWQFVASTTVLF SAILAGLGSASAFCLGPQIPQAR PNNASVNSKNSRFGIPRQAE*P EQGGVYHHTAGVLKKLIPPSAR QHPDRC
8840	39208	A	8899	1657	2061	QMPGNPFAFSALLVAFKHQFAI AGGIFIKEVTFIAIKTSQLLWFGQ PIFNNETTHQTACFLSVEADDL KFAVLLIEEHLRLDNI.GIQFLRLH RFKILI*QINHHIALCCEERLVQ LVGDDISPEFELELRFSEVH
8841	39209	B	8900	26	1540	
8842	39210	A	8901	1	3396	
8843	39211	A	8902	1	3522	

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8844	39212	A	8903	1	105	SPQPRHYRHHRGQLVCIVIF YFCAKRWMAAIL* <sup>Q</sup> HRHRFL TTDDGKFVANGSFS* <sup>R</sup> GLHH/ ATGLRRFPIC* <sup>G</sup> PLVCIVIF FCAKRWMAAIL
8845	39213	B	8904	1	960	
8846	39214	B	8905	1	2618	
8847	39215	B	8906	1	490	
8848	39216	A	8907	2820	3332	ATEGYRQQRQFHAAAYDESP HRNRKRWRPTYRCHPAPDHR TACLRSAFYGNAPGCVQTGPV RRSGAASASSPAVFLSGTSPWS FARTIALVRGRS/LKIDTNSPWA YFSALLM/F/DLLSHVHEWCGR YISPPRFAQTGETLPCRRHQGSR YSAYLSASRYPARRKWYFSPR
8849	39217	A	8908	3	716	EVDDTAKHRRRDSFPQ* <sup>D</sup> P/LM NIRYAPS/HLPATVALTGA <sup>V</sup> IT VLYALAGKRLFCWSVCLNPIT DLANWLRRRFDLNQSATIPRHI RYVLLVVLVGSALTGTLIWVW INPVSLMGRSLVMGFGSGALLI LALFLDLLVVEHGWCGHICPV GALYGVLGSKGVITVAATDRQ KCNRCMDCFHVCPEPHVLRAP VLDEQSPVQVTSRDCMTCGR VDVCS <sup>E</sup> EDVFPITRWSSGAKS
8850	39218	A	8909	3	323	
8851	39219	B	8910	94	2205	
8852	39220	A	8911	504	694	FNQLGRDWRTRYRKSDPPR/Q WLRHSPV* <sup>V</sup> LKMPMAIRGL LWMLSAQPAICSSRQTKMV
8853	39221	B	8912	1	2031	
8854	39222	A	8913	3	190	FIATPGYTGEAGYEIALPNEKA ADFWRALVEAGVNPCLGARD TLRLDGDSEYG/QEM/DETVP* AMKLRCPMKKRPSIGVRWWK RVLTHVAWARVTRCVWTGMN LMARDGETVSP
8855	39223	A	8914	1	621	MWPSVSHLTQMNIPSRFSEPSG AIEVPPDKVHELRLRLAQQGLP KGGAVGFELLDQEKFGISQFSE QVNYQRALEGELSR <sup>T</sup> ETIGPV KGARVHLAMPKPSLFVREQS PSASVTNLLPGRALDEGQISAI VHLVSSAVAGLPPGNVTLVDQ GGHLLTQSN <sup>T</sup> SGRDLNDAQLK YASDVEGR <sup>I</sup> QRRJEA <sup>I</sup> LSPIVGN G/TAQLDFAS
8856	39224	A	8915	1	2274	
8857	39225	A	8916	957	1067	

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8858	39226	A	8917	1	1242	MDGLNTDKGSSVFHTPTDRLVI CCPVDADERMTTPRLWDHEP SKPLFFTNYPVSAFFVGL/PPGK RPQGGFRAGNL*TSKTTIGRDL NDAQLKYASDVEIGRIHRRIEAF LSPIVGSNGNIPAQVRAQLDFASK DQPEEQYRPNGDESHAAALRSR QLNESEQSGSGYPGGVPGALSN QPAPANNAPISTPPANQNNRQQ QASTPSNSGPRSTQRNETSNYE VDRTIRHTKMNVGDVQRKLGII GQGKNEKPLQLERVEEKPNG EGWEKKWQGEVWKKEDGTI YLQKNKLRAPTDSTLWFAKNG RVAKIAKALVEPANNFNPGVD EDDTEKLLLEVPEELTNEKLDL EQKCIHIYDDKRRQTKQTPQDV FLKRVTSPPQEPQPGSGGIPEEG IVIIGEDSSVQVLAPEDLPVEKL
8859	39227	A	8918	256	1510	RRFVGFRGTGVTKEDAIQGRGV DQFFRQSQYRLVGVTVAGMPE LTRLFVQRFTQFRMRMAQRVH RNATREVDILFLLIPQARTFAT YRYKGCGRSVNRYHPFIKVFTRN WREADLSLKRVTLLNDTGYQ EVITYSFVDPKVQQMIHPGVEA LLLPSPISEMSAMRLSLWTGL LATVVYNNQRQNRVRIFESGL RFVPTQTAPLGIRQDLMLAGVI CGNRYEEHWNLAKETVDFYDL KGDLESVLDLTGKLNEVEFRAE ANPALHPGQSAIYLGKERIGF VGVVHPELERKLDLNGRTLVEF LEWNLADRVVPQAREISRFP NRRDIAVVVAENVPAADILSEC KKVGQVNVVGVNLFDMYRGK GVAEGYKSLAISLILQDTSRTL EEEEIAATVAKCVEALKERSQ
8860	39228	B	8919	47	156	
8861	39229	B	8920	139	993	
8862	39230	A	8921	1	284	MRRKRLIRPTVQAQVCRPDKTR KRRIRQWC/YGCRMRRKRLIRPI KYANRQAETA*GLDALHLCSS HG*KGPT*SSGHGFRGCKPQAL EASMWC
8863	39231	A	8922	1	813	
8864	39232	A	8923	1	1176	

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8865	39233	A	8924	3	618	AGGPPLNPIEMA*KS/WDEIIVK LEKDPQLKQTFLFVYPQFSGE NITDAIAEFKLTITPDSPFDKW LRGDENALTAQQKKGYLQFKD NKCATCHGGIILGGRSFEPLGL KKDFNFGEITAADIGRMNVTKE ERDKLRQKVPGLRNVALTAPY FHRGDVPTLDGAVELMLRYQV GKELPQEDVDDIVAFHLNLNGV YTPYMRDQ
8866	39234	A	8925	2	212	QYPGLDLHGAKGLGDLAGKR YRQLLVSCVRHVLRYHPAGPGT RK*RRSGIRWLHRLCGNEPRGK LLVDQ
8867	39235	A	8926	1	640	
8868	39236	A	8927	1	704	MSSFQFEQVIRSPYKEKFAVP RQPLVK SANGELHLIAPYNQA DAVRGLEAFSHLWLFVFHQT MEGGWRPTVRPPRLGGNARM GVFATRSTFRPNIGMSLVELK EVVCHKDSVILKGLSLDLVDGT PVVDIKPYLPFAESLPDASASYA QSAPAAEMAVSFTAEEVEKQLL TLEKRYPQLTLFIREVLAQDPRP AYRKGEETGKTYAVWLHDFN VRWR/VSP*ACSTFQLEP
8869	39237	A	8928	3	313	AQRGGI*RGSLATAGLRSFGL HPRTSQQFCLPVRGKPPQTQAS VMVDAPHSTKLKHLRSISDCCT GSKNFKPVDLSLLGSMGVGSTE LDHLAPWLQAPFGE
8870	39238	A	8929	13	453	
8871	39239	A	8930	380	966	LRHAVLLTEGF/SYKPHAFALG FVEAPRGEDVHWSMLGDNQKL FRWRCRAATYANWVPLRYML RGNTVSDAPLIIGSLDPCYSCD RVTLVDVRKRQSKTVPYKEIER YGIDRNRSPNLNRSLYPREVPSTT LQPLRTPRCPGKNLALAVNVST GTNGQKPESCGPGRCRMKGGE YKRTISGGRTIIRVHIARLLRTF



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8872	39240	A	8931	1415	2085	SQVPICQRSTSCRVKRLFSWKMA AYRSALVTWPWRVFRNPAVPR TSPVVFTGGDVFSRVMVRVKE T/FDSLAMLEFALDNMPDTPLL TEGFSYKPHAFALGFVEAPRGE DVHWSMLGDNQKLFWRWCRA ATYANWPVLRVYMLRGNTVSD APLIIGSLDPCYSCTDRVTLMP QCIACGACACAPANALTIQTD DQQNSRTWQLYLGRCIYCPST NNNGPVISFN
8873	39241	A	8932	1	1127	MKKRKTVKRKYVTALVIVIA LMTLWRIRNAPVPTYQTLIVRP GDLQHSVLAPGKLARTSKNFA Q/FIRVRYSAFSLAGEKKR**P RVHGVQNASSGRYRGTCRLG SDSRKKLVEIL/LATPNMEQRT QGIGILDPQIARDLRFDPHYAEY DNIPK/TLFTFTAADVFSRVVVR VKETFDSLAMLEFALDNMPDT PLLTEGFSYKPHAFALGFVEAP RGEDVHWSMLGDNQKLFWRWR CRAATYANWPVLRVYMLRGNT VSDAPLIIGSLDPCYSCTDRVTL VDVRKRQSKTPYKEIERYGID RNRSPNRRCTGEGWTRAWITL PLLKPLTPLMIASFAFNFNFFV LIQLLTNGGPDRLGTTTPAGYT

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8874	39242	A	8933	1	2466	MLRGVNVLADAVKVTLGPKG RNVVLDKSFQAPTITKDGVSVA REIELEDKFENMG AQMVKEVA SKANDAAGDGTATVLAQAII TEGLKAVAAGMNPMDLKRAS RSRKGYGPARIQELNQKGISR EATEKAMRECDIDWCALARDQ ATRKYGELPTVFSEKSRKLI GVKRAFTHQAVNAGFCTQPAV SVIAGDFDRHGFNTRHFTRLF DDFSFETTRFCPAQIHTLKHARP VLCFRTARPLNIEVAVGAVIF AREHTAELKLRQFFQGAPOKA VISIPVVPQVTGVVIEVTDKKNT LIKKGVLFRLLDPTRYQARVDR LMADIVTAEHKQALGAELDE MAANTQQAATRDKFAKEYQ RYARGSQAKVNPFSERDIDVAR QNYLAQEASVKSSAAEQKIQS QLDSLVLGEHSQIASLKAQLAE AKYNLEQTIVRAPSDGYVTQVL IRPGTYAASLPLRPVMVFIRSET SLRTHCPGHADYVKNMITGAA QMDGAILVVAATDGPMPQTRE HILLGRQVGVPYIIVFLNKCDM VDDEELLELVEMEVRLLSQY DFPGDDTPIVRGSALKALEGDA EWEAKILEL/RWLPGLFLYSGR ACD*QAVPAADRRR/SSPSPVV VPLLPVV*NAVSSKLVKKLK/R WYPRDSEVLYWR*NVPPTAG RRPCW*ERRCSAAWYQT*RN

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8875	39243	A	8934	1475	2904	FWRAAAPIDCWRSGAVKKQH VEVTQLDWTTPGRQYAGPIPCS RRGYCPLPRSGSVRWADL/FPP A/LD/LAGHPG/AKVANLVPKTT FIDGVDQTSFFLGTNGQSNRKA EHYFLNGKLAAVRMDEFKYHV LIQQPYAYTQSGYQGGFTGT MQTAGSSVFNLTYDTPQESDSIG VRHIPMGVPLQTEMHAPGLPLA SSMKRWIRATGFIIFGKEQFED VVPVLGSKVNGVQFNALVAD SLGISQIRCRCAIFLTVVFFVLH KQAFDLISLLQPPGRNGGIDT AGHADDYFFCGFRHWITHDIEL QGGARQKDAADHYLAGDIESL PLATATFDLAWSNLAVQWCGN LSTALRELYRVVRPKGVVAFTT LVQGSLELHQAQWAVDERPH ANRFLPPDEIQSLNGVHYQHH IQPITLWFDDALSAMRSLKGIG ATHLHEGRDPRJLTRSQRLQ LAWPQQQGRYPLTYHLFLGVI
8876	39244	A	8935	1	920	MARADTVSVPFMGLAAKPC WRDTEPNTGYRGPHVRNIQLT HDPRLDYRSI/LIDINDIGQTFHE RLHPDACLSNAILVHNKGGP LADGIVITPSHNPPEDGGIKYNP PNGGPAADTNVTKVVEDRANAL LADGLKGVKRISLDESDGIRSK NDVIDTSDDDM**QCLSRRSN GHPGAKVANLVPKTTFIDGVD QTSFFLGTNGQSNRKAHEYFLN GKLAAVRMDEFKYHVLIQQPY AYTQSGYQGGFTGTVMQTAGS SVFNLYTDPQESDSIGVRHIPM GVPLQTEMHAYMEILKKYPPR
8877	39245	A	8936	471	668	
8878	39246	A	8937	1	1233	
8879	39247	C	8938	1	1548	
8880	39248	A	8939	1	1260	
8881	39249	A	8940	1	1468	
8882	39250	A	8941	261	596	RSESCCGHEPDGPETROP*PQR LWTCAYSPGTESERYFPRSDRK SDA*M*HRLVRTGARSGDAKI WRTFANCLFRKIKKTYRRSQGT FYAPGGERRFLYASRKRNR F

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8883	39251	A	8942	2	1356	CLPGLKLVRLLYRLEERNARRT SAAVDAT* RAGAWLAQCGLTV EQLARIQVDPDMITTRAHLHYHC DHRGLPLALISEDGNTAWSAEY DEWGNQLNEENPHHVYQPYRL PGQHQDEESGLYYNRHRYYP LQGRYITQDPMGLKGGWNLYQ YPLNPLQQIDPMGLLQWTWDDA RSGALTWYGWGDGRLTTIQND RSKIQTIIYQPGSFTPLIRVETATG ELAKTORRLADALQSQSGGED GGSVVFPFVLVQMLDRLESEIL ADRKRAATTWSHNHYANKKE GIKATGYRLAQLTGKCEESSV FRVTRKSHSSFVWLDKAVTPHP TSNVRAGCLMRRWRVLSGLHR CEVLHPHTPHPAYHAGCGVSL QRNIRHFFLNGLRFRQLRFRRTIC CLRLVVVQPHFAGVLQLAFC CRYITVQLASIRNRDRFQRLPL RAGNTIAKYFFQIQHNRGG
8884	39252	B	8943	1	1159	
8885	39253	A	8944	1	1304	MAETQQQFKRMAASGLETRF DEVGNLYGRLNGTEYPQEVVL SGSHIDTVVNGGNDGQFGAL AAWLAIDWLKTQYGAPLRTVE VVAMAEEEGSRFPYVFWGSKN IFGLANPDDVRNICDAKGNS/IC RCDFGLRIYSSERPTNS/VVRIL KPLLNCILNRA/DVLERITAWD KPDCHTLHHHADLSGHFPPEIG PLLFAFGSSAWQNGPSAFSWQK HGSAQTSSIAVLHRTPRHAGCL AQCDFTRAFFQIMLKNYLRKK RWKKKIHFPNASGKSS/RAIFEG YVTTYGDVAKLGGIAPGRAPG GR/VQRQALLAEGAGTAEDGFT *VGEVEDAARDGP*TAERTG* TYADAGRQDPQSAEDRQRANL HGNADR***RFASGGFHRGYHP RAAAGFCDHRKPACGNARRAG WPDRA*SKSSAYAFRYRYEHR HAGRSG

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8886	39254	A	8945	1	1695	MRSDDPTSVNEIETKLSALLGS ETTGEILFDLLCANGPEWNRV TLEMKYGRIMLDTAKIIDQDV PTHILSKLFTLRNHPEGVVMK NFEVLQPLQNSLSGLPLWVSE ILQQINQLTHYEPVIGIMGKTGA GKSSLCNALFAGEVSPVSDVAA CTRDPLRFRLQIGEHFMTIVDLP GVGESGVVDTEYAALYREQLP RLDLILWLKADDRALATDEHF YRQVIGEAAYRHKMLFVISQSDK AEPTSGGNILSTEQKQNISRKIC LLHELFPVHPVCAVSVRLHPV VALLQQFRITDDERTHYHYDS QHRLVDYTRTQYEEPLVESRYL YDPLGRRVAKRVWRRERDLTG WMSLSRKPKQVTWYWGWDGRL TTIQNDRSRIQIYQPGSFTPLIR VETATGELAKTORRSLADALQ QSGGEDGGSVFPVPLVQMLD RLESEILADRVSEESRWLASC GLTVEQMOMQMDPTEGTTAW Y/AEYDEWGNLLNEENPHQLQ QLIRLPQQYDEESGLYYNRHR YYDPLQGRYITQDPIGLKGGW NFYQYPLNPISDIDPLGLSMWE
8887	39255	A	8946	605	1395	SMSLLKNIRLSSASKQCAACSG WPAAGIRGVSGGQG*ARVSSS ANTATALSSRLLPQNSVTVPH A*RMNCVLRVTPLSKNRGGKP APSGTEGKGLPEVQPGQLRAH GLPVSENLEQDFYASGPNQK WAGDITYLRTEGWLYLAVVI DLWSRAVIGWSMSPRMTAQLA AGCPKPLWGTPSFPGPACGLAP SSAGVLPGRGFPAVWLDSDEPE EYVGSSDFLTQMOSMKKVDLK KNRAATDADGQFSRCCMPEK YAGSHN
8888	39256	A	8947	1	1914	
8889	39257	A	8948	1	4767	
8890	39258	B	8949	1	2294	

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8891	39259	A	8950	115	3551	NPALTRIVPAQONLYTNTLLAA RIKQRLTEQFELMLRQAQIDFA GKAHSLTEAQANTTQVSAERD RLFKNYQRYLKGSQA AVNPF ERDIDDARQNFALQDALAQIS QLDSL VNGEQSQIVSLKAQLAE AKYNLEQTIVRAPSNQVVTQVI IRPGTYAASLPLRPVMVFPDQK RQIVAQFRQNSLLRLAPGDDAE VVFNALPGKVFSGLAISPAPV PGGAYQSTGTLQTLNTAPGSDG VIATIELDEHTDLS
8892	39260	A	8951	845	1213	DKGEIGGWAAQTHRSHEQGA RRVPEDRDARARRKNNEEPAAR PRTTNTNRNGSRKGPERK/WADG RGHKAAGRRKRRKRQ*KEEM RKIRQESGGKKRGLCGRPPG GGNNCMEGERRGRKKR
8893	39261	A	8952	843	1061	NRPPPVCACHRQVVLPPVPNR APAEKWQVPRVTLPGRQSTSW FAAVVYRN*YQYCALTAQRGR RSRQLPHR
8894	39262	A	8953	1	682	MIRIFGCEDKLGADQQPAFVLY LEIDPHQVDVNVHPAKHEVRF HQSRLVHDFIYQGVLSVLQQL ETPLPLDDEPQAPRSIPENRVA AGRNHFAEPAAREPVAPRYTPA PASGSRPAAPWPNAPGYQKQ QGEVYRQLLQTPAPMQKLKAP EPQEPALAAANSQSFGRLTIVH SDCALLERDGNISLLSLPTGIW CSD*H**PMIPRLIPASVRSSSM VESAK
8895	39263	A	8954	1	1887	
8896	39264	A	8955	189	552	LFRGEKGARNEVLATRYRQT VSGDFRHLHCLADQYALGGAY QF*AGLY*LHQAWEMNRGLQL LSDALGEQYAHGNWRLRNN DRFVFQILRSFEHDNSDEKPGP GMPPHGWRTQFWGG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
8897	39265	A	8956	263	3549	TGGPSSPSSHWKTPVVIYWDGT ALRCVFVPLVGETGAQRKRISA RKGSILTTSCPGALSEHCPTTP APLPSQRRNHWMENISPFERSVG VSASRCSES*MRPWNSRMRPLG RSQGDSSAL/MSTGVAFGRGF LKGGLPQAPAVAAATPWLCTQ GVAGETTPAVNVKYNVVRVRS EYISMHVHREVTARNVYVTQT RRPMTTFTPLAWETPHYHRRY GVSLSSAVVQVGPFRYCRQT NALSNLPNFKSGADTQ
8898	39266	A	8957	1	1799	MMRDLINHAIRPACE*QLGA DQQPAFVLYLEIDPHQV/DVNV HPAKHEVRFHQSLRVHDFIYQG VLSVLQQQLETPPLDDEPQPA PRSHIPENRVAAGRNFHAEPAAAR EPVAPRYTPAPASGSRPAAPWP NAQPGYQKQQGEVYRQLLQTP APMQKLKAPQEPALANSQ SFGRVLTIVHSDCALLERDGNIS LLSLPVAERWLRQAQLTPGEAP VCAQPLLIPRLKVSAAEKSALE KAQSALAEGLMVNSTRFSLHE HPDAERSPGQSGEQRQPAVD DYAIVDEYGRHYRRAVAGTLL HVSVDSGTTQTVMYTWLSMA LIALPAFIFARVPNDTHQNVAIS RRKTESRNEVLATRYHRQTVS GDFRHLHCLADQYALGAPIPPD GTRRPILVNGAEVGAVIASPVE RLTRNTDINFDKQQRQTSWLIV ALATLLAALATFLLARGLLAPV KRLVDGTHKLAAGDFTTRVTP TSEDELGKLAQDFNQRASTLEK NQTPITSRGHPRIFLARHPAPAP TTLTSLALKIIRSPAFLPDTASEC AMAIIDCYILAASTQAYKAASSL SLSVVLATSARFKTSSTSIWVKS SSTNSCE
8899	39267	A	8958	1348	2190	
8900	39268	B	8959	1	105	
8901	39269	A	8960	1	781	
8902	39270	B	8961	1	1716	
8903	39271	A	8962	754	807	
8904	39272	A	8963	821	875	FFSLFFFISLASGLSIL*W*FVFL WDRW*YPLYHFLHLHFDSSLSFS SLLVLLVVYQFC

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8905	39273	A	8964	1	315	SGSVMPPALFFWLRLDLAMQALFWFHMNFVVFSNSVKKVIGSLMGTALNL*ITLGSMAlFTILILPYP*AWNVLFPVCVLFYFLEQW FVVLLEEVLIHPCCKLDS
8906	39274	A	8965	42	403	GLCSVPLVVISVLVAVPKLFW*L*PCSIW*SQVA/SIPPALFFWLRLDLAMWALFWFHANFKEVFSNSVEKVGISLMGMALNL*MTLGNMAVFTILILPTHEHGMFFHLFVS SFISLSSGL
8907	39275	B	8966	179	1225	
8908	39276	A	8967	342	407	
8909	39277	B	8968	143	3122	
8910	39278	A	8969	692	1360	MCGIIEGSLFHCISITLFWYQS HAVLVTVL*YFLKSGGLMPPALFFWLRLDLGMLALLWFHMNLKVVFSNSLNKVGSLMVMALNL*ITLGSMAlFTILILPIHEHGMFFHSFVSSSFISLSSGL*FSLKRTFTSLVSWIPGYFIFFVAIVNGSSLMIWLSVCLLLVYKNACDFCTILYPETLLKLLICIRRFWAETMGFSRDTIMSSANRDNLTSFFPN
8911	39279	A	8970	2116	2418	FFSLFFFISLASGLSIL*W*FVFLWDQW*YPLYHFLHLHFDSSLFS SLLVLLVVY/PILLIFS KIKNKKPAPGFIDFFEGFFVSLSPVLL*S*LFLAFC*LLNVFALASLVLLIVMLGQCF*IFPAFSCGHLVL*ISLYT
8912	39280	A	8971	1	558	LYKNSVKYFHN*PVGNIMSNIPV GALFSGPAFGIGILAAGVILAI MIIPYIAAVMRDVFEGTPVMM KESAYGIGCTTWEVIRIVLPFTKNGVIGGIMLGLGRALGETMAVTFIIGNTYQLDSASLYMPGNSITSALANEF AEESGLHVAALMELGLILFVITFIVLAASKFMIMRLAKNEGAR
8913	39281	A	8972	1879	3735	
8914	39282	A	8973	16	452	VGQLFWKGYPLAGFPDPCAQS WKVAHVLLRLGLHIKSVSANGKEVTSKFHRKENI.ARG.LHSRPRRGQVRVGGVAQHCEPR*TPPPACRVR.LPGCPVDPASPRGRRTSAGTPEPALRHPTPRGPVAARTLP AEPGARPSGLPP



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8915	39283	A	8974	158	531	CSLRRGPDP/PGAYCKRRATG AASTRSLSGAVAGSPAHRCESR PLQAMGAGGLPHPEGGRGSG GRKRTDGPVCGGERAPREYP DPSRSWRGPQRKPAPSQHPCLP RLSRGPGRHPGPHQVR
8916	39284	B	8975	22	387	
8917	39285	A	8976	241	389	VASQAPGVRALQVGAHSC*G RGHVSWPPWPWGPPCCCLCL LNLGPN
8918	39286	A	8977	1620	1936	TLFFFESESHSVTQDRVQWYDL VNSLQPPPPGLK*FSCLSLPSWD YRRPPPCPANFFLVELEFHHV GQDGLLELTSGDPPALASQSR ITGMSHCAQQNKHIL
8919	39287	A	8978	3	105	
8920	39288	A	8979	1	1821	MLKNFKKGFNGDYGVTMTPTG KLRLTCEIDWPTLEVGWPSEGS LDRSLVSKVWHKVTGKSGHSD QFPYIDTWLPQWVRGQAAAVL VAKGQIVKEGSRSTHRGKSTPE VLFDPTSDDLQEMAKVIPVVP SPYQGERLPTFESTVLVPPQDK HIPRPPRVDKRGGEASGETPPL AARLRPKTGIMPLREQRYTGI DEDGHMAERRVFCQPFSTAD LLNWKNNTPSCTEKQALIDL QTIQTHNPTWADCHQLMLFL NTDERRRVLQAATKWLGEHAP ADYQNPQYEGKEESPAQFYER LCEAYHMYTPFDPSPENQRMI NMALVSQSAEDIRRLKQKQAG FAGMNTSQQLEIANQVFVNRD AVSHTGAHVSVTGPVAPLSK KTIDIIGAMGVSAKQAFCLPRT CTPGTKDYRLVQDLRLVNQAT VTLHPTVPNPYILLGLLPAEDS WFTCLDLKDAFFSIRLAPERQK LFAFWEDPESGVTTQYTWTV LPQGFKNSTPIGEALARDLQK FPTRDLGCVLLQYVDDLLLGHP TAVGCAKRTDALLRHLEDCGY KVSKKKVAQICQQQVRYLGFTI RRGVRLGSEKQVICNLPEPKT
8921	39289	B	8980	209	2272	
8922	39290	B	8981	1	228	
8923	39291	C	8982	375	472	
8924	39292	C	8983	266	408	
8925	39293	A	8984	1	1105	

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8926	39294	A	8985	108	708	LTNQKSRSTRRIHSRILPEVQGG AAADRHCPIDRLGSLQDHHRRS RLLSQWSP*KSTHD*HGFSYQS AEDIRRLKQQQAEEFAGMNTSEL LQIANQAFVNRDAVSRKNIHR DNERQAQRNTDLLAAAIRGVPP KRQKGKGGPKETQPGCQSLQR NQCA YCKEIGHWKNKCPQLKR KPGDSEQEAPDKDEGALLNLA EGLLD
8927	39295	A	8986	125	444	DCLAVKRASVWQPTGYSCPKL L/QGVLT YQRRQAAPPLRRR LASSSRDKPKCAGKHTSSLVRA GDMQGTIVTGTTEVLRLDMEPK FEDDQLRPVLLEHKVPRREMA
8928	39296	C	8987	80	325	
8929	39297	A	8988	566	1857	
8930	39298	A	8989	1	1037	MEEGWIRLPDGRVAAPQLLGA AVVLAVQETHRGQESLEKLL GRYFYISPLSALAKTVRQRDFA DFGTTIKQDFRLLGQTSVDRL QLSQGQAVKGNQLLPVSLTSQ CQVYKCVWNWVVLGLTDFKN EAKELRLYKQEKREKAKRWKE TEKGFNGDYGVMTTPGKWRT YFEIDWSKLEVGWPSSEGNLERS LVSKVWHKVTGKSGHSDQFPY IATWLQLVLDPQWLRGQAAA VLVAKGQIPRKDPTPPAEGNQ LLK/SLFDP TSEDPLQEME/PSDP SGALPLPGKDAPH S*AHSPCAS TRQTYP*ATRSRQERR*SLERNP YIGSFKTQNWDTNAPERAVV
8931	39299	B	8990	1	2082	
8932	39300	A	8991	6	367	ENLNIKAPHAVVTMLTTTGPD WISNAILTKDFCLLCENTHISRW GCNTLNATTL LVSSEPVKHNC LEVLD SVYSSRPNL RDHP*TSV DWELYVDGSGFANPCKVTLKK ETSPAPVTPRS

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8933	39301	A	8992	1	2991	MLKNFKGFGNGDYGVTMTPTG KLRITLCEIDWPTLEVGWPSEGS LDRSLVSKVWHKVTGKSGHSD QFPYIDTWLPQWVRGQAAAVL VAKGQIVKEGSRSTHRGKSTPE VLFDPSTDDPLQEMAKVIPVVP SPYQGERLPTEFSTVLVPPQDK HIPRPPRVDKRGGEASGETPPL AARLRPKTGQMSLRQRYTGI DEDGHMAERRVFCQPFTSAD LLNWKNNPTSCTEKQALIDL QTIQTHNPTWADCHQLL
8934	39302	A	8993	1	444	SSASTPETRAKFT*DNLCASW QRLASANFRVLVDCLSDTFED LRLQCDAVNLAFGRRCEELED ARYKLHHHLHKA VE*GGGA EH VPHRLREKLLEAEQSLRNLEDI HMSLEKDIAAMTNSLFIDRQKC MAHRTRYPTILQLAGYQ
8935	39303	A	8994	1	1576	MVQTDVLLPEPAQPTVSPCELP CKEYDVARNMGPGHRQLVEVW FQNCYARYHQAFADCNQSERE LQGREGQLAAETQALAQPTQ QDSTCRVGERLQDTHSWKSEL QHEVEVLA AETDLLAQKRL ERALDAMEVPFSIATDNMQCS QRHQHANLVRDYYVETELLKAY PPAPSQCLKNCCSSRKPSACNK GACEVMETLTVQEEANPGTEG CRTRALAHKEEA EPIRNIQELLK RAIVQAVSQIQLNREHTEICEM DWLDKVEAYNLDETCGRHHSQ STERP/WTKFTQDNL CRAQRKR LSSANLWVLVDCLRDTSEDL GLQCDAVNLA FGRRCEELEDA RHKLQHHLHKMLREITDQEHN VVALKEA IKDKKEPLHIAQTRL YLP SHRPNMQLCREAAQFRAA FPG*ESQWRLPRTSLPAPNWE FWVPFHPSRCILLSPAPAH TTP TPPSW*VRWRSLYKSITALREK LLQAEQSLRNLDIHMSEKDV TAMTNSVFIDRQCKMAHRTCY PTILQLAGYQ
8936	39304	C	8995	99	442	

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8937	39305	A	8996	177	622	TESSASEKTTGEDGTRVVFVSL RSLLSLLPSAPLRHHPPSA*L SCLSCVSD*AVALIPQSAHHFPNIS *PFPLHCF/AHAKPPVWIFHSH/S LWLP*AFLAPMTSFTDQVAVD DFLSIVYLFITFTPLAFCEPST ALATREQVWVESAS
8938	39306	A	8997	1	329	AAARPGRGSETGDWVLLCYPG WSAVV*S*LTTA/SELLGSRG*G SLLSLPSSWDYRLSAPCLANSK KPSEK*GLSMLP*LVNSWPQVI LLGPPKALGLQAPGTMGRLP
8939	39307	A	8998	1	814	
8940	39308	A	8999	57	274	TASSSLTLVYGHRLCWLGSPH *PSLWLP
8941	39309	A	9000	1	1236	
8942	39310	A	9001	1	1095	
8943	39311	A	9002	1	2313	
8944	39312	A	9003	166	494	FSQQLCGENHPLHRTENTQAQR AGVPLGVRLSRPGFP*LSTHSC FSCPLV*PPSQGPGLSLWTLC SAIQAPAELESCRSSCDRDRSH WPRVSGGLWLSQVPRPR
8945	39313	A	9004	3	974	MGESPAV*GYFVLQGMNSAGL SFGGGAGKYLAEMWVHGYPSE NVWELDLKRFALQSSRTFLR HRVMEVMPLMYDLKVPWAF KTVSQLRTSLLYDRDLAQEAR WMEKHGFERPKYFVPPDKDLA ALEQSKTFYKPDWFDVIESEV KCKVEAVCVIDMSSATKFEITS TGDQALEVLQYLFSLNDLDV GHIVHTGMLNEGGGYENDCSI ARLNKRSFFMISPTDQQVHCW AWLKKHMPKDSNLLLEDVTW KYTGTVRALYGDVEHESWLS CVRHAHHPDPCIAHTYLHLRS FSQADGREWRKVLDKHKILF ARSLC
8946	39314	A	9005	1	1872	
8947	39315	A	9006	1	2250	
8948	39316	A	9007	1	1257	
8949	39317	A	9008	1	1596	
8950	39318	A	9009	1	1584	
8951	39319	A	9010	1	1461	

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8952	39320	A	9011	110	993	TSTELSTPSQQNIHSSQHHIALV PKLTT*LERIKYLGQLTRDVKD LFKQNYKPLL/NKIKEDTNKWK NIPCSWTGRINIVKMAILPKVIY RSSAIPKLPMTVTFTELEKSTLK FIWNQKRAHIAKTLSQKNKTG GIMLLDFKLYYKATVTKTAWY WYQNRDIDQWNRTEPSEIIPHC NHLIFDKPDKNRKWGKDSLFN KWCRENWLAICRKLKLDPLTP YTKINSRWIKDLNVRSKTIKTIE ENLGNTIQDIVMGKDFMAKTP KTMATEAKIDKWDLIKLRASA QQKKLPSE
8953	39321	A	9012	1	1185	
8954	39322	A	9013	1	185	
8955	39323	A	9014	2	1321	
8956	39324	A	9015	2	1757	
8957	39325	A	9016	1	1008	
8958	39326	A	9017	1	1311	
8959	39327	A	9018	1	1152	
8960	39328	A	9019	1	526	MPSLTTPQHVSQGSSGRAIRQEK EIKGQLGREEVKLSLFADDMIV YLENPIISAQNLKLIISNFSKVS YKINVQKSQAFLYTNNRQTESQ IMSELPFTIA/KRIKYLGIQLTRD VKDLFKENYKPLL/NKIKEDTNK WKNIPCSWVGRINIVKMATLPK MTWIANWLRNSLQAQ
8961	39329	B	9020	1	1626	
8962	39330	A	9021	1	2361	
8963	39331	A	9022	1	1140	
8964	39332	A	9023	1	2112	
8965	39333	B	9024	1	1065	
8966	39334	A	9025	1	1416	

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8967	39335	A	9026	1	1690	MPMVEELYGNYGIMADTTERV GQHKDAYQVILDGVKGGTKEK RLAAQAYFILKFFKHFTELADSAIN AHLQTVSGRQQVLKLVAEQAD LEQTFNPSDPECVGRLLQCTQQ AVPFFSKTVHSTRSVTYFCEQV LPNLGILTTAVEGLDIQLEVLKL LVEMSSFCGDMKLETNLGLK FDKLL EY MPLPPEAENGNGNA GDEEPKLQFSYVECLLYSFHQL GQKLPDFLTAKLNAEKLKDFKI RLQYFARGLQVYIRQLHLALQ VKQCFAYMEKENGIDAKILN KILANRIQQHIKLIHHDQVGF PGMQGWFNIRKSNVIQHINRA KDKNHMIIISIDAEKAFDKIQPF MLKTLNKLIGDGYFKIIRAIYD KPTANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLAIRAIQ EKEIKGIQLGKEEVKLSLFA DD MIVYLENPIVSAQNLLKLSNFS KVSQYKINVQKSAFLYTNNR QTESQIMGKLPTTIA/S/KRIKYL GIQLTRDVKDLFKENYKPLLKE IKEDTNKWKNIPCSWVGIRINIV KMAILPKNWKKLL
8968	39336	A	9027	1	1575	
8969	39337	A	9028	1	2682	
8970	39338	B	9029	1	2088	
8971	39339	A	9030	1	2406	
8972	39340	A	9031	1049	1500	
8973	39341	A	9032	1	4341	
8974	39342	A	9033	103	366	NHPQLKVAGLKNCCVCMCV CVC/CVCCVRVWVWVCVVCVC VCVCVC/CVCCVC/CVICVCI*V WVCVCVCLCLSLPKCWDYRHE PQRPA
8975	39343	A	9034	232	735	YLSGNGGEGKFCHALPDHRLR VLHQHPHACVETDTVDLGITS ISLADRVVCVCMCVCCVC/CVCV RVWVWVCVVCVCVCVCVC/C VCVC/CVICVCI*VWVCVVCV CVCVCVCICVCVCVCVCVCV CICVCI*VCVCVYVCVCVCLCT VLGIHSFLTARNAHQPIGH
8976	39344	A	9035	163	795	

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8977	39345	A	9036	34	758	RVPHRHGMKRVVRQRHGMKRV PHRHEMKRVPHRHGMKRVPHR HGRKRVPHRHGRKRVPHRHGR KRVP AQVQDEEGHCQKPGRCV CMCVCVCVCVCVRVWIVCVC VCVCVCVCVCVCVCVCVCIC VCI*VWVCVCVCVCVCVCIC\ CVCVCVCVCVCVCICVCI*VCVC VYVCVCVCLCLFYLVLCFCIS/ CIISGGQRWC*RKTMCSLPFAH SHHSFPGHFFLIFQSRSFQVSFHP
8978	39346	B	9037	34	156	
8979	39347	A	9038	3	419	GGENVKAINQQTGAFFVEISRQL/ PPN/GDPNFKLFIIRG/SPE/QIDH AKQLIEEKIEVGWGG/LWGFL TARIPAHLPWLLSFLG/PLCTV G/PGPGGPGPAGPMGPFNPGPF NQGPPGAPQ*VSSASWVLRP/E GLLSWQEE*QTPFFFP*KCRAG ALIAHFCEGYHQALSCL/PGR ACAFQHPSVHVQVSRLLSCPQA DAARPPSSCFLSRFPFGAPLSLVV WVSGASPLKNIPTPGGPAA/PPP HHCSSIPFFSPA VPGGPLLTSTH PRAGAIPTPSGS/QPAPHDPSK* WALQPGATRGSPVLSILCLLGF EAGLLSWQEE
8980	39348	A	9039	1	445	ATADPNAAWADDYSHYYQQP PG/PVPCAPAPAAPPAQGEPPQ PPPTGQSDYTEWAWEEYYKKI GQQPQQPGAPPOQDYTKAWE\ EYYKKQAQVA/TGGG/PGAPPG SQPDYSIAAWAEYYRQQAAYY GQTPGPGGPPPTQ/GQQQA

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8981	39349	A	9040	38	1297	TCVSALSVLASDDGTGPEKIAHI MGPPDRCEHAARIINDLLQSLR VGGPGC*RGWQGLQGSARFDR LPGFIHLLLLSCRVVPPQGPVGG PGMPPGRRPKKEGGN/WGSP WAGKMTFSIPTHKCGLVIGRGG ENVKAINQQRGAFFVEICRQLPP N\GTANFKLFII\RGSP\QQIDHA KQLNEIEKMKGPLCPVGGPGPGG PGPAGPMGPFNPGVPPNQGGPG APPHAK\PPPHQYPPQGCNGT YPQWQQHAPHDPISAGKAAA AAADPNAAW/AAYYSHYYQP PGFVP/GPAPAPAAPPAQQQQP Q/QPGAPPQQDYTKAWEEY/YK KQAQV/ATG/GGPGAPPGSQPD YS/AAWAEYYRQAAAYYGQ/T PGPGGPQPPPTQQQQQQWVA PETPSPRGVPLMPAAGAVWPE VPGVPTHRQGSIRWVQR
8982	39350	A	9041	1	1777	MPVLPVTATEIRQYLRGHGIPF QDGHSCRLRALSPFAESSQLKGQ TGVTTSFSLFIDKTTGHFLCMTS LAEGSWEDFQASVEGRGDGAR EGFLLSKAFEFEDSEEVRIWN RAIPLWELPDQEEVQLADTMFG LTKVTDCTLKRFVRYLRPARS LVFPWFSPGGSLRGLKLEAK CQGDGVSYEETTPRPSAYHNL FGLPLISRDAEVVLTSRELDL ALNQSTGLPTLTLPRGTTCLPPA LLPYLEQFRRIVFWLGDRLRSW EAAKLFARKLNPKRCFLVRPGD QQPRPLEALNGGFNLSRLRTA LPAWHKSIVSRQLREEVLGEL SNVEQAAGLRWSRFPDLNRILK GHRKGELTVFTGPTGSGKTTFIS EYALDLCQGVNLTWGSFEISN VRLARVMLTQFAEGRLEDQLD KYDHWADRFDLPLVFMTHFG QQNIRTVIGTM\NHAVYVYDIC HVIIDNLQFMGMGHEQLSTDRIA AQDYIIGVFRKFATDNNCHVTI VIHPRKEDDDKELQTASIFGSA KGGWSAPHSTSSRPSAQPKSD STVAEAAPLASDFATYWIWFLT WGRGRASRDREFGYLAALN



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8983	39351	A	9042	3	679	SPLIVSSARMHAGRDI.PLYFMT FHGQQSIRTVIDTMQHAIVYGAY DICHVIDNLQFMFMGHEQLSTD RIAAQDYIIGVFRKFATDNNCH VTLVIHPRKEDDDKELQASIF GLSQRQAREADNVLDPAAGTGK LGNRGQGGKRYFAGVPKEPF*W EM*GVFPLEFNKNSLTFSPPKN KARLKKIKDDTGPVAKKPSSGK KGATTQNSEICSGQAPTPDQPD TSKRSK
8984	39352	A	9043	90	317	GTLRKRYRAFHCRITIFKALTEV CKNFSAHCEFSWGFFFCFSFFF LASS*G*NCLPSQPQPCWFLQPP CPWQIL
8985	39353	A	9044	2	2136	PRLSVSLSEFITTHIYFLLSETTY NYEWNLSISLYVVDPSRLAC*TV QLFFMLQLSVGLYVFNVDNDIC LHKMGSVTVLFFVTARRVNLPP VAVIKLMSSSSCISFLSLFLNLV ESTDDTEIVSYHWEEINGPFIEE KTYLCFFTLFCVFIFVFAIT*G VQTPYLHLSAMQEGDYTFQLT GLQT*CKEIIHFTVSVIPENNRP PVAVAGPDKELIFPVESATCLS YSKPHAPSLMLTTSMFYRGPSA VEMENIDKAIATVTGLQVGTY HFRFYSITGVNLQSLCFHFAIFD LENNSPPRARAGGRHVLVLPN NSITLDGSRSKPRNWDPRIDSC PVIRVLSQDVIDGSDHSVALQL TNLVEGVYTFHFLML*SLCKCP SANPVSSLSPPDKSGVELTLQ VGVGQLTEQRKDTLVRQLAVG VSW*SPSDHVAVLSHCLLHSTV IVFYVQSRPPFKVLKAAEAVARN LHIS*SRDSLFCMLPSALHTS/S AGCLLKCSGHGHCDPLTKRCI* K*SWSTNSL*LCPLWFSCVSEW SIFYVTVLKS*LSVTLKI*VELF IVPFRQKRKIRKKTLLNMY*VH LKYYFH*ILILPIAVRGMCDNDYP HD*QLEVNHGVPQMLLCFSLG IKHRSTEHNSSLMVSESVRSFD RDCLQSLNYLLSGLLQKEKNLQ KAGLTSPAPSLWEDKCSGRTEH AQ SARLPLKEDTEKTLMQF
8986	39354	A	9045	47	157	FDKICIFKRQVTKSEVILNLTN* VL*YLEYHIRNIN
8987	39355	A	9046	1	393	
8988	39356	C	9047	274	357	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8989	39357	A	9048	727	1089	
8990	39358	A	9049	175	608	CGWEYGN* AIDTMDQEYCKVC QAYKAPRSHHCTKCNCTCYMK MDHHCPWINNCCGYQNHASFT LILLAPLGCIIA AFIVMTMYT QLYSFGMENNFFRKQNFYLLS WDWKEEGLKDPDFSIQLGWK SFVFFHMDMGEVDGEGTF
8991	39359	B	9050	780	1166	
8992	39360	A	9051	3	681	HIRGPRYSGHHSFAGCPYSMDN LKKEATLHDLRREQTQANLES DSSHKS KSLCSLNFNGKHEKV NSQPRLVQQA CKLIK GKEDID LDNLFREYSVEQAQQV LHQSV SMSTVSAHPFRDLPLGREQHCK LLPGVADIRASQVARWTVDEV AEFVQSL LGCEEHAKCFKKEQI DGKAFLLLTQTDIVKVMKIKLG PALKIYNSILMFRHSQELPEEDI ASGQEV RG
8993	39361	A	9052	30	981	TQDPWPSPVLVWSRASSDPAAG HRAEH*TYWPWKLEGTDIWL VLYMPLVQPDNFIKKHSHLPTY CLFKEDVKFPFRTCLTYCWLN YTEEITYLHTKKVSVGQSAVRE EFAAACTWSIRIGEKLAILLSLY LCRQQALLNMRMSVPIHESGV AQRSPVMDKLAQYSVEQAQQV LHQSVSMSTVSAHPFRDLPLGR EQHCKLLPGVADIRARQVARW TVDENLHGLIQTKQTPHLDISIS KGESPALVVTLMCMMTATEP LVPTKNPYQERGHIGDSFLHYT DQEPQPDQSSVHPTAPIYSV SSGFRVTRGSDI
8994	39362	A	9053	1	864	MVSALPEVGRAQLRLIAYIRSP APPVVGVERAARRPAQAFGLV ALPSTDATVFANQPLARACIGA ARHREPDAPGQSAWVGEECLK DALRSPETPKLGLSLPPCQDTRP GRASNDFSLEMGYSLSAARLK IHGQVFQCCGPGPLRTLHWQ S*TYLNI LALET*GAQNQP*EW QAVD*GAPGLFSLTLGVFPR/RL PQHPKQIICFQNYEYSVEQAQQ VLHQSVSMSTVSAHPFRDLPLG REQHCKLLPGVADIRASQVAR WTVDEPYSSAPRGPELSAGANS SRGA

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8995	39363	A	9054	1	1737	MKEKPAVEVRLDKWLWAARF YKTRALAREMIEGGKVHYNGQ RSKPSKIVELNATLTLRQGND RTVIVKAI TEQRRPASEAALLYE ETAESVEKREKMALAQMIMPQ IIDQLHRYLFENFAVRGELVTV SETLQQILENHDPQPVKNVLA ELLVATSLLTATLKFDDITVQ LQGDGPMNLAVINEINERAQNP LLCAFRVCNTYGSYECKCPVG YVLREDRRMCKAVFPYCQNES SDVLWQFDSTSQIFLKGTPKTT VRRGGEHNLKNPDECEDNPNIC DGGQCAGIPGRNRLCYDGF ASEDMKTCVDIDECSLPNICVF GTCHNLPLGLFRCEIGYELDR SGGNCTEDPDHKSRSRGRSQND WGRRRKT/S*KRSAVYR*RQLY IRRQPYAERPSLR*RQRP*IPCIR SQHGNRKRMRRRRJI/STKRRT AAARTSSVKARSFSRALKNA MLS*RTAPSVS*S*IMITH*KK** SR*SLQTR*LMKSSARVFSK*TA NGTWSL/HSRGSKVTIDGINSND IYMLGYVSNLSLTGPYPVDKGTG LGLEMGLDPNDVTLTYSHFRVP EAEAMWVSHAT

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8996	39364	A	9055	1	1743	MTTSTMTHMMTMHFPIIIVCAD SRDDVDVNTDNDVNDHDDSAKR KSHRERPIAAKRTETK/KRRRRA RPKR/RTKARS*SAK*QTAQHT RTTAAIHMRDTQARRV*RP TKH AAEQRQNTTGKQRR*TKRVKA AKKEGE*RRRKMARRTTPTQR R*TRAKRRINRPRHGAKKRA*N /RRLKSAPKRHRVNRNRENART TTRHKKRRNRVKAERSGAE RTPYKQRHQQTREKRTCKRRQ TK/RRTKAK*T*RDHENDGTRA YNKTPKKAARKTRNNLRHNA TKGGDNRGQTRRA*TKPRKYR PDENRYNTSSPERTPRKRRGKS E/RDKTAQRAQ*ADRYNSRKT QQRL*KGHTHTER*RQARMHT RHAQNLDTOHSTRLCNA*ST/C HRRSSSTMCHRYDQLYSRSH ALTMIIIVNKPLRQCIRMLSFHD RHRSLAIDGDSASTGSPAFCV NTYGSYECKCPVGYVLREDRR MCKDCTCEKAFAPAGCEVDKT HTVPQERAYIHRTLRGRARTKK RDLYRRAHNDRRRQKSAAYYE STSVRRRAHKYNSGKSDTQNGS HHRQKLRQYGDAGKSHYLQY NIHFMYPLFNT
8997	39365	A	9056	3	451	FFEMKSHSVAQAGVQCSGVILA HCNLHLESDDSPASAFRVAGII DARPHAWLIFVFLVETGFHHVG QAGLELLS*VIHPPWPPKVLRL QHETPCPAVSLYLNQSPENNLE EDSLAMSNNRRSGPGIWWQNP GFEILALSTFLVESDLK
8998	39366	A	9057	53	343	
8999	39367	A	9058	14	234	CLFIRIFNVICYSKTCKNSICIGV IEIVDGCMTGGEDGGGGGGSV TAGGAPSPJETGSHGPPQAVYF WRF

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9000	39368	A	9059	3	865	INFSVCVLARFFLGVVVLCVSC CWFRCCVACVICALAFPFCSCC VVVLCVPVGRCTLFAV/CCCL/ CVICALFCGFLRLFLCLCV/CPC S/CSARCRC/VCLALGAVVCFPP CSVVASCGCCDWWVWLCGGAV VALVGLI.CCVLVCAWSFRGC/C V/CLC/VCVVVVLVVRCC/VCW CGSCVVDCAAGVVLVCCLLVVL MMSL/CGCRVYSWYGVWCWCS VVCRVIDL/CPCCLCW/CVT*RG CWSVWCM/CTCCG/CVCGLA V/CWCRCVVRLVCLCAV*FIC ACVCFEAVGGFVGGCFLGSCL
9001	39369	A	9060	1606	1849	QGVSAFLCREAGLTKISPGAPL WLPCSPGVTAECSGERTVRHN VTDRCVGLGAVTSPGRN*RG HVTHKFCILCTDTVRDC
9002	39370	A	9061	2	682	ALEAVFGKYGQIVVHLMKDC ETNKSRGAFITFERPADAKDA ARDMNGKSLDGKAIVKQATK PSFESGRRGPPPPRSGPPRVL RGGRGSGGTREPPSRGGHMD D/SGRDSYRGPPRESLPSCR/D APPTRG/PPPSYGGSSRYDDYSS SRDGYGGSRDYSSSRSDLYSS GRDQVGRQERGLPPSMERGY PPRDSYSSSRGTTPRGGRGGS RSDRGGGRSY
9003	39371	A	9062	90	443	NVYYIQFIVLPYYLTIDPAGNSR SAPPTRGPPPSYGGSSRYDDYSS SRDGYG*SRDSYSSSRSDLYSS DRIVSTLFFVSLNWDGPKFCLF LVASASPSIRSASSRSTSWCS AA
9004	39372	B	9063	12	1373	
9005	39373	A	9064	2	206	

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9006	39374	A	9065	2	1423	IHFREMAKSWLNFLLTFLCGSAI GFLLCSQLFSILLGEKVDTPQNV LHNDPHARHSDDNGQNHLEGQ MNFNADSSQHKDENTDIAEKIL EEKVRILCWVMTGPQVLEKKA KHVKATWAQRCNKVLFMSSEE NKDFPAVGLKTKEGRDQLYWK TIKAFQYVHEHYL*DADWFLK ADDDTYVILDNLRLWLLSKYDP EPIYFGRRFKPYVKQGYMSGG AGYVLSKEALKRFVDAFKTDK CTHSSIEDLALGRCMEIMNVE AGDSRDTIGKGNFFHFPV\PE\H HFNKGYLPRTFWYWNYYYP PVEGGELRFLFSTVTIRHSAKLS LGVAQCSWLLKQVVISDDKTK RPDFPDRSRIMKERVQIVLYES GQAPVESSPPLPGYCSALFATCF QVTGKNFSQDPTQAILYTQADK IEGWMRASGERVAEQSQGTA MDGGKKEAEWKRTKAKYRD DVCSKHHPPYPTPVPPSLED
9007	39375	A	9066	1	311	
9008	39376	A	9067	1	493	ITRQHMRKAVPFQVPRKEILKL LKGGVVVGHALHNDFFQALKI*S TLGARPGDTTYVPNFLSEPLH TRARVSLKDLALQLLHKKIQVG QHGHSSVEDATTAMELYRLVE VQWEQQEARSLWTCPEDREPD SSTDMEQYMEDQYWPDDLAH GSRGGAREAQDRRN
9009	39377	A	9068	45	365	NQAAASRPHCAARTMAGEEQA ACVHEDRTQCRGDKAAPQAAH LCGPPRGSVSTAPRAR*CPV CSSCPGPGAPEDTPEEVDVGAA SAHRSPRLCCSHLTHRWPKH

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9010	39378	A	9069	3	1687	ICVPKSVPSFLWAGRGPHCLLP CGSSSP*SGGLARA*GVFQGRA GVARAPSHLSFHNSPCVWSLST CCRAGSQDGPCHAAGQGP GK QTSSGTGASSSPWTSCL*KSLPK VCS*GLETITIGRGRVKPIKVT TAQ*CAASVTAPL.LSS*LQDGG STAKVTRCT/TAGGRAVYGTAE GKAFPEAPELTCRS/ALAAAGT WPLPPLQVSCGLRNPSPDLPSV VGSRAV*TKSGSPPAKVWPLA EWFKSGSA/PVTGQEA WLLWA SDSSSELSLCPRKHAAPPHSAEH RQISQGLASSCWGAGGDKVVS ASMVGSAPGQCPMSALMTGSA SGQCPGHPCWSGTNADS*GRDP HRASRLALPTASYEQ*PQPHW GSWTAHQNGLGIFFRVSWF V*GQTMVSRPRISGLGQPVCLS AASPQAAPLGSHDPTAGR*GL EPGGRQPSSS*YVWEAPPGLW VPPGPFLSH*SWRFGRTKAAPL KEPRPGGRCPGDRPSPRAEAGL PQTRKPAIPAIGR/PKKACSLRR PRVILEQSSQHLAAALSSWMQP ALLETGGKAVFFTPGGL

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9011	39379	A	9070	66	1956	PLLAIPAHSTFPARKPEEPPRPD* LCPHIIHCAAV*GEIRTVP/SKTV RGVATRTPRSSASLGIITGLR VSSVRRVQLSIKPGCSRVENSS NSPCSSSQPGTSLPCPTVCRE AGP/AGP*PPG*ALSLPAAGFTT ATEWKQSLSSGG*THSGEDM GRATAAATEKAQEQCMLREKL GTRQKAESGSRGA/VGLQHFCS APRTAWQPRASRA/RAGVRAW PCADPM*PPSHSPSPKPFIPAA/ PGAQTLGAAGVEHVAGSARIPC CRTGLE/PHPHSPRRTLERQARI SGAGRRSSPNAATGARPRPAA SPVSARRAPRRRPA*SSPCSGPW TAVSAPRSPGPRGGRRPSPGR RRPCCSVFSGGASPSARVSSPS GSCSASPAPAPA/PASGAVVA GPVVGSPREHGG*LRPPLPRLG VPGLLAARTSGAEVIHEQAAAQ GTAADTPGAPGLLLAPAAAGA V/TRPGPPGASGCPRPAPRPPT ASRSGRP/VPGGGRGRRGGRGA GGEALQGA/VVGGQVGGSGAL A/ATARGSPAAGVSRWTAPRCR HRRSDASASGTPARFPGAGRKG RTLWQ*SWRSAPPPGLSELL*G LPRPLPESGRSKAPLPSGSTPLPS GRTPLPSGRSPSTRSSPS
9012	39380	A	9071	95	1423	GLENKRAKGTEAHTRACP*GK STEQDITWNTGRNEQQGPRP KGEQTQRKTERKPGRERQVQV LSPPGRWC*DVGPLGGLPSRA KAEAAALTAQKAQGRGSPGS LPKSSPLSAPGKR/TPPRGHLL VPLPSPIYPALLSQHPQGPCCG ASAPPSALLQRAPPPGRTRLQR PPGPRVTCGTP/MAAKAKSQS NAPRGSLLKKSNSFYNIPLKQV SCLITISKHSRNEVSYYQTSRPR AAATDVPRTPSLSVGCSWSCT RGHWPSSCCPTAPRGQGL*EHS QGPGSRSKLPWPTGPCGGLTPS CWSLAGSAGERVDLNQAAASR PHCAARTMAGKTLSGCGCVD VGAASAHRSRRLCTTSPIDGP NTERGSRKTGWTPGPGFWPCP RPPTSTNTTPLGLMDSARPGKA PAPFTDFRTPSGLLLPGWAVRA RREEDGCG



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9013	39381	A	9072	42	380	LGAPCTPPRSPRTGRPEYA*ARG*PVGDLRCRGEAVVSTQVLLPRGLQ*NFAVLLQLMQSCATPPPNCALKGCV*VPLEQSPFFHQAVACREWKRKGGMVCGGNASPO RTEA
9014	39382	B	9073	116	341	
9015	39383	B	9074	52	190	
9016	39384	B	9075	70	310	
9017	39385	A	9076	1349	2456	HCSVPGA EWPRKPPAQICPQLTSRPHLSSPRSLSPGCGHSPGPG*SPQPPVMSLHEGP PRGPQV/PSPVANPQPKPWLLRSVDLPVPWHLPTVDRITSL/APLSQSDV/PAPSGAL*PSGRACSGV/PPID*APEAALSA AAPRPSLGGGQNASGLPAASLPQDSSQPHKTVPSPARSVPLGAQARAAPPRLWCPHALVSG*EASPEAVSVAAGPPVPGPTPS TSGSTASHSRRC*SPR*TPAPP RRDHGRSAAFEVLAAAASAQPCASQGGPRPTGAGRTPSPLGLPFSRGPPAASARPF CRHPSL*FSW*SSPSGLSLSDTPHSPRRPLGPVCGLRAPCPPQIPACRVPA AHSQRWPGSSSRSCRCQCC
9018	39386	A	9077	462	739	ACEPMVLFCLLALLQDLFLGSYPRVLA AFDIQVFFLGTSDRM*NTG/LEYFMLNSWLWLLNRL*SWGELCHFPLHSPVKRGLNFYLOEFFI
9019	39387	A	9078	1	678	GTRVNMILMKMGFSGIVVHQESVCATYGSGLSSTCIVDVGDQKTSVCCVEDGVSHRNTRLCLAYGGSDVSRCFYWLQRA GFFPYRECLTNKMDWLLQLHL/KRNF LFSRSTRSLGFRMTSFRFRHPDS PALLYQFRLGDEKLQAPMALFYPATFWICWTGK*RPLHTDLRA ILKILTMNITCWPHKAHENS LQKLLLTESLHPNLLDLKGIFVASP LIFQKDSIPR

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9020	39388	A	9079	227	1980	GERLRYGVVTENGKEKGGEKEK EQRGVKRPIVALVPESLQEQIQ SNFIIHVPSTTLRIGRATDITLP ASIPHVIARRHKQQGPPLYKDR WLLREGLNKPESNEQRLNGLIM VDQAIWSNKMMSGTRRNVPSP EQARSYNKQMRPAILDHCSCN KWTNTSHHPEYLVGEEALYVN PLDCYNHWPIRRQQLNHGPG GGSLTAVLADIEVIWSHAQKY LEIPLKDLKYRWRILVIPDIYNK QHVKELVNMILMKMGSGIVV HQESVCATYSGLSSTCIVDVG DQKTSVCCVEDGVSHRNTRIFS WRSGHLWVQDHEFQIRHPDSP ALLYQFRLEDEKLQAPMALFYP ATFGIVGQKMTTLQHRILRAILR ILTMNITCWPFRANKNSLQKLL LTESLHPNLFERGFELWASPLI FQKDSIPRR*IWGLHREMA*WP ATIPRRPLTALMSRKTAISLFEG KALGLG*SPSSAIDCCSSDDTK KKMYSSILVVGGFDFVIFKASR IFCSTEFSTKCPPSLQADYDKM WM*SQGLKMDMDPRLIAWKG AVLACLDTTQELWIYQREWQR FGVRMLRERAAAFVW
9021	39389	A	9080	1	756	MRRIVALVETGEQPFGAATVGS RFGCLEDLGTDQREHHDHEMA AAHTYFIGDGDITLDEDEDIT WGMAGKHAINIEGFKLARVE DEMVFQEREPEKVKIRGRTRGY TFIMLAALAAAEADMVQVGE L/C*KVSLKASQLGQMALMLQS VTVQIGMVYGLPACGAQVNLQ DDKGSVMVLMCASKHGHMEIK LLLAQLGCNVHLQDNDGSTML SIALEVGHKGITVLLYAHISFAK AQSPGTPRLGMKPKQSF
9022	39390	B	9081	5	5440	

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9023	39391	A	9082	1	4294	WAVFDGNYYYLPWAHTKPV VTLSYWEDISHRLDAVNALLA MAERLQTNIEALKSGIQGKIPA NQLAELWLKLIDEVIEDTRYTL PLTEGKANVTVLDTOIRKLRSR SLSQIHEAAVRMRSEATDVKST LAEIEDWLDKLMQLTEEPQNS MPDIIWMIRGEKRLAYARIPAH QVLYSTSGENASGKYCGKTQTI FLKYPQEKNNNGPKVPVELRVNI WLGLSAVEKKFNSFAEGTFTVF AEMYENQALMFGKWG
9024	39392	B	9083	1	339	
9025	39393	A	9084	2	1767	KLYRGKSDENEDPSVVGFEKGS FRIYPLPDDPSVPAPRQFREL DSVPQECTVRIYIVRGLELQPQ DNNGLCDPYIKITLGKKVIE/DR DHYIPNTLNPVFGRMVELSCYL PQEKDLKISVYDYDTFTRDEKV GETIIDLNRFLSRFGSHCGIPEE YCVSGVNTWRDSLRLPTQ/LLQ NVARFKGFPQILSEDSGRIRYG GRDYSLDEFANKILHQHLGAP EERLALHILRTQGLVPE/HV/ET RTLHSTFQPNISQGGKT/LQMWG GMFFPKSLGPPGPPFNITPRKA KKYYLRV/IIWNTKDVILDEKSIT GEEMSDIYVKGWIPGNEENKQ KTDVHYRSLDGEFNWRFVF PFDYLPAEQLCIVAKKEHFWSI DQTEFRIPPR/LIIQ/WDNDKFS/ LDDYLGFPRTLTCRHTIHFLOK SPGGNCRVWT*FPGSKAMNPL KAKTASLFEQSMKGW/PCY AEKDGARVMAGKVMETLEILN EKEADERPAGKGRDEPNMNP LDLPNRPETSFLWFTNP/CKTM K/FIVRRFKWV/IG/LL/LL/LL LFVGRAP/TL/LL/PNYFVQWKIVK PNVLT/KGKG/FISRV/IIQ
9026	39394	A	9085	2	407	

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9027	39395	A	9086	15	759	SARPSHDYSHYYGTIEYLCYKI LGDIIENSRIVLQINNACLAADD F*TKYEREQT/LA/RTDLEMQTE GLKEELA YLKKNHGEINALRG QVGGQISVEVDSALGADATNIL SDMQSQYENRKDAERWFTSCT EELNWEVVGHMEQLQMNRSQ VTDLRCLNQLGLEIELQWQLSM KAALEARFGPQLAQIQAIISSIE AQLGDVRADSERQNEQYQLLM DIKLWLEQELATYLSLLEGGEE HYNLSSTSKIL
9028	39396	A	9087	3	2026	AGPWDRMGAMGSLVGGDLGL VWGCAGEGFAGIPFSCALTCQ EGNQGTAKWVQTSTRIKGGQ VKQARGAQVTPYSPLWHGKLG RAAFTFNAPGRWLLPLLLPPL L*ITTCLLGKRTLQEALSLKLE LRKVCLQEA VRAWP*GYQAGR LGGGEELGPLGRPPTARAYPPP HPNQAHHSLCPAEV/MQMGEV SKRVGRGDRYRGVARRIMALA PDLSTEQRRRRRQVQADALRRL HELEEQLRDVRARLGLPVLPLP QPLPLSTGSVITTQGVCLGMRL AQLSQGEHPLVRVGEWTLANG RGRAGMGDSYPPNLPPTPTSL* PIPIFIHPVSGGSPERRTPWKPPPS DL YGDLKSRNRNSVASPTR*E*A PPPLRRSWEWDSKPGLAEGPAS DRASLFVARTRRSNSSEALLVD RAAGGGAGSPPAPLAPSAGPP VCKSSEVL YERPQPTAFSSRTA GPPDPRAARPSSAAPASRGAP RLPPVCGDFLLDYSLDRGLPRS GGGTGWGELPPAAEVPGLPSR RDGLLTMLPGPPPVYAADNSNP LLRTKDPHTATRTKPCGLPPE AAEGPEVHPNLLWMPPTTRIP SAGERSGHKNLALEGLRDWYI RNSGLAAGPQRRPVLPSVGPPH PPFLHARC YEVGQALYGAPSQ APLPHSRSTAPPVSGRYGGCF
9029	39397	A	9088	1	136	
9030	39398	A	9089	14	310	TFLFIYFFFTETESHVPRLECS GVISAHCNHLHLLGSNNATSAS *VAVITGACHHAWLIFVFLVEA GFCHVG/RRLVNS*PQVIRLPW PPKVLGLQA
9031	39399	A	9090	1	436	
9032	39400	C	9091	75	410	

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9033	39401	A	9092	1	6691	MVNTYREVKEGPVIL EDVLIEV FRTLYSQCKAELDLQTEPPFSK DHAQLSSKLRENKKTAEILKTA NLLFNSFEPYMWWDYVARWFE ECCRRTLHVRLQIGPGDSNDSS ELQLTNFCLLVDLFDIVSLITY IEIQTEHLPQLLRMISALTSHL QTLHLSELTDLSRLCSKILSKVQ PPLL SASTGGVLQFPSSGQNNV KEWEDKKVSSVSHENPTEVFE DGENPPSSRSSESGFTEFIQYQA DRTDDIDRELS
9034	39402	A	9093	293	687	PTAKVYIFSLFITYHIVCCINTSS LFGFLQKNPEEDNSGRTLGWE PGHLLALTICTVRSMEQLLPFFN VLSQVFNKVTSRCCGHSGSPI LYSNAFPNKDMKLENHKPCSS KARQKIEEMVEKDFLEGMKT
9035	39403	A	9094	3	4173	IPMVVDFDLDPDQIEILQSSDS GCSQSSAGDNLSEYVDPETVNA QEDSQMPKESSPDDDVQVVF DLICKVVSGLVEVASVTSQLEI EAMPPKCSDDPDDEETIKIEDDSI QQSQNALLSNESSQFLSVSAEG GHECVANGISRNSSPCISGTHH TLHDSSVASIETKSRQRSHSSIQ FSFKEKLEKVSSEKETIVKESGK QPGAKPKVKLARKKDDKKKS SNEKLGKTSVFFSDGLDLENW YSCGEGDIS
9036	39404	A	9095	5	1055	FDLERVRNLTYMVTTRREIKRS VCKVQEQIFNLTYKLEQERVS GVPSSCSSLNMLLFNSPSVG PDAPKIEDLKW/PFCISSENKVV LPWVSFG*KRPKISRILLQN*PW K*RQNPAAEARPVW*KGDDGG PRELFGFRKDLCRSTSHISTTEK WCGDARPEWKKRQSFL*SH*R RLKGRIF*TESQAS/PGPQMCP GIWTTQELPPLEWGSQHLGTR KEIVPKCNGSLIKVNYNQTAVK VPTTPASPVKNWGGFRIPKKGE RQQ/PGRGRWGLPPALRLPIFG LRPSS/TKERAKSKLSDNEND GYVPDVEMSDSESEASEKKCIH TSSTISRRTDIIRRSILAS

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9037	39405	A	9096	3	1136	FDIPFPKIGKLIKSNVPELRGHFP LSITLVLRMLLASKGDDPEDA KAKVLSVLKHSLLSFQPRVM DMLKLYFLFSLQFLGGKRAI*IQ EG*SYGVCWDLVFTFGIYPWNL SNLVFVSFLVNGLFHDLCOPT KGSKHFSQDVMKELVLVLAHL FGRRYFPKFDQAHFEFYQSKV FLDDLPEDFS DALDEYNMKIME DFTTFLRIVSKLADMNQEYQLP LSKIKFTGKECEDSQLVSHLMS CKEGRVAISPFCVCLSGNFDDDL LRLETPNHVTLGTIGVNRSQAP VLLSQKFDNRGRKMSLNAYAL DFYKHGSLIGLVQDNRMNEG AYYLLKDFALTIKSISVSL/HVT YCENEDDNNVLA FEQLSTTFW
9038	39406	A	9097	2	522	
9039	39407	A	9098	3	1080	FLLPFSHQSKKENS DQMLTFT SFNSLHSA MESFFQATGNS TNL ADDGKRRTV VTPVILTKIDGVN VDTHHIPVNVTLRRIAHGADAV AARWDFDLNQGQGWKSDGC HILYSDENITTIQCYSLSNYAVL MDLTGSEL YTQAASLLHPVVY TTAILVLCLLAVIVSYIYHSLI RISLKS WHMLVNL CFHIFLTCV VFVGGITQTRNASICQAVGIILH YSTLATVLWVGVTARNIYKQG H*KS*KMPRI PDEP/RTFNQDQW LRFY PDLVGGYPPSLV LRA*LA AANIKELRQSAKPHPY/WLGW HGNPPWEAFYGPASFSTFVNC MYFLSIFIQLK RHPERKYELKEP TGQQRLACQ
9040	39408	A	9099	1	307	
9041	39409	A	9100	2	286	

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9042	39410	A	9101	35	1211	EKDLLWEEKFPDRTTVTELQPT SHVSFSEPDIPSSKSTELPVDWSI KTRLFTSSQPF TWADHLKAQE EAQGLVQHCRATEVTLPKSIQD PKLSSELRCTFQQLIYWLHPAL SWLPLFPRIAGDRKMAGKTSF WSNDATLQHVLMSDWAVSFTS LYNLLKKNFSPYFYVCTYQFT VLFRAGLAGSDLITALISPTTR GLREAMRNEGIEFSLPLIKESGH KKETASGTSGLGYGEYVVIKIL/S SSTDLTWTHEIDLHRNSL*NRDS NCSNF/LREQAISDEDEEESFSW LEEMGVQDKIKKPDILSIKLRKE KHEVQMDHRPESVVLVKGINT FTLLNFLINSKSLVATSGPQAGL PPTLLSPVAFRGATMQLKARS VNVKTQALSGIQRPI
9043	39411	C	9102	48	464	
9044	39412	A	9103	1	140	MNRLKKEWMLEHIVENNSGM ESQDIKGHFHAADKDLLEMGY LQKRGLIGLTVLHGWGGLTIM AEG*KRSGCLSTLWKITPAWNL KTLKAIFMLLIKTYLKWAIYKR
9045	39413	B	9104	1289	2767	
9046	39414	A	9105	3	1278	INNTNTFRVLPHPSFVYTAKFHP AVREL VVTGCYDSMIRIWKVE MREDSAILVRQFDVHKSFINSL CFDTEGHMYSYGDCTGVIVVW NTYVKINDLEHSVHHWTINKEI KETEFKGIPISYLEIHPNGKRLLI HTKDSTLRJMDLRILVARKFVG AANYPGEDS*YFD/VH/GGTFLF AGSEGDGIVYVWNPETGEQVAM YSDLPFKSPIRDISYHPFENMVA FCAFGQNEPILLIYIDFHVAQQ EAEMFKRYNGFTPLPGIHQSQD ALCTCPKLPHQGSFQIDFVHT ESSSTKMQLVNQRLETVTEVIR SCAAKVNKNLSFTWPPAVSSQ QSKLLQSNMLTAQEILHQFGFT QTGIISIERKPCNHQVDTAPTIV ALYDYTANRSDELTIHRGDIIRV FFKDNEWDWYQGHRERQEG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, v=possible nucleotide insertion)
9047	39415	A	9106	1	1249	MAVLIFLGCLLGGAIGLPIAWA LLLCGAALMFWLDMDVDVQIMA QTLVNGADSFSLAIPFFVLAGE IMNAGGLSKRIVDLPMKLVGH KPGGLGYVGVLAAMIMASLSG SAVADTAAVAALLVPMMSA NYPVNRAAGLIASGGIIAPIPPSI PFIIFGVSSGLSISKLFMAGIAPG MMMGATLTGKRARFTEDDTR ERDAISVINHQRNAVLIRQVRK LQQLFVIRVLAMRIFYGSLRH KQGNSHWMTNAQLLGDFSIDN YQLYSLGHYPGAVPGNGTVHIG EVYRIDNATLAELDALKTRGGE YARQLIQTPYGSAMWYVYQRP VDGLKLIESGDWRVLRWLRVH SIDVPDPFGLTVTGDRDTRAG KTSPAQAGCKLFLTNPLGIGVL TTAEKKSLLKPEHQGLATEVM CRMNIAGASFANIEGVKAMTD VTGFGLLGHLSEMCQGAGVQA RVDYEAIPKLPVVEEYIKLGAV PGGTERNFASYGHLWLR*LAL AP/LEVVEANGSL*CSGERGCL YGQTTTIQLNFRPAFCPEHAIG QKVAILRLNMQIDIKRVSSRTH GNHFTNFKFTVQHYRSCLT



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9048	39416	A	9107	162	2106	KMSKLLKIAVSDSCPDFCTTQRE CIYNESNRNIDVAAIVLSLNDVT CGKLDEIDATGYGIPVFIATENQ ERVPAEYLPRIQGVFENCESRRE FYGRQLETAASHYETQLRPPFF RALVDYVNVQNSAFDCPGHQG GEFFRRHPAGNQFVEYFGAVPC RLVIPALKKQKRLSDLETAIVV VDRFSGEVRAMVGGSEPFAG YNRAMQARRSIGSLAKPATYLT ALSQPKIYRLNTWIADAPIALR QPNGQESVRVMLVDALTRSM NVPTVNLGMALGLPAVTETWI KLGVPAKDQLHPVPAMLLGALN LTPIEVAQAFQTIASGGNRA'PL SALR*TIAEHGKELYQSFPQAE AVPAQAAAYLTLWTMQVQVQR GTGRKLGAKYPNLHLAGKTGT TNNNVDTFWAGIDGSTVTITW VGRDNNQPTKLYGASGAMSIY QRYLANQPTPLNLVPPEDIAD MGVDYDGNFVCSGGMRILPV WTSDPQSLCQSQSEMQQQPSGN PFDQSSQPQQPQQQPAQQEQ KDSGDGVAGWITDMFGSNEHLS GYELDSYPLSSARRRARFTEDD TRERDAISVINHQRNAVLIRQR VKLQQLFVSNHIACWIRRPQDA NHPGFFANMQMLKIDVVFKLA FRQQFNIRTRRDQIQQSGVT
9049	39417	A	9108	1	66	
9050	39418	C	9109	79	150	
9051	39419	A	9110	2	475	GRGRWGAPRLRGAL*DP*GHF LGQQPRPQLHSPAPDR/PAPTPT DAEGL/PPAAAAAAGATARVP GSRGG*GQAAELHEAGEAQA CRGGTEDEEHG**HLCHGRAS* CPGVSGSTGSPHPSMAPDDT SGLLEFVGVPQLTLFAVWSPAE AAEQQL
9052	39420	A	9111	171	462	PTSMGHLYSFPGN*SHAHYHPI KT*SPLPHSTPISNPSA/PLKGLK PVITRLIQHGLLKPINSPYHSPL PVLKPKDKAYKLVQNLRLINQIV LPIHSM
9053	39421	A	9112	1	573	
9054	39422	C	9113	100	297	
9055	39423	A	9114	1	1401	

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9056	39424	A	9115	24	482	VGSGDLPWEGNPLSSCSLLHEK DPPTTSGPQT/GP/GPRNISPILNR AAPRQAQLGPNSSASAPPYPN PFITSPHTWSALQFRFVTSPPPP AQQLTLKKVAGAKGTVEHFC HDLPASSMQSNYPVHDSGHILT TGPSLFKPTLNIEYSTGHAP
9057	39425	A	9116	1	489	
9058	39426	A	9117	1	642	
9059	39427	A	9118	237	748	ETNPLSSCSLLRKDPPTTSSPQ THQPKKHPPISNPAAAPHQAE LG PNPSSASAPPYNLFITSPHTW SGLPFRSVTSPPPPAQQFTLKKV AGAKGTVKTITDIELQVTLTVE ARLRPGEINSHVAHTKPVWWS LHTDTCDIWCRPGTGGLLQET SPLSPSLCEEHL
9060	39428	A	9119	63	255	WVSGSVQVKVERGWDEGCKGI VKKACLTYTNRMHCVGRY*A *ESIWVWHHGVNRQNNLVDKA
9061	39429	A	9120	24	389	SDVKANLSTGGPVGCGGDTL/P VAEKPSDAVEAPGV*APSAGG AGPA\PSPGLEPSGAPPP/ALPP RAVLDSGLAPGRPLPLASSNP/P PAGRRLLCTSPGRRGGAAAGSG PRCPESKSIPLRCL
9062	39430	A	9121	704	867	CVKECLDVRHLRPFAYFTTRII* ILQDQGIQSAIF/CVIWNYCRVCI GVKRHSRRK
9063	39431	A	9122	1	7068	
9064	39432	A	9123	2	165	LLKRELNFDFYKISTTKERHLQ QS*PKDS\VPSSLASQTPNAPFL APQRRCLLA
9065	39433	A	9124	1	148	IRHSVNLRLAG/RIFVFEPPLGLK ANTQRTFESGMKHKVRIIYMMEF HVF

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9066	39434	A	9125	1	2340	QFGIWLDSSEPEQTVPYLWSEE TPATPIGQAIHRLLIQAFRPRD LLAMAHMFVSTNLGESVMSIM EQPLDLTHIVGTEVKPNTPVLM CSVPGYDASGHVEDLAAEQNT QITSIAIGSAEGFNQADKAINA VKSGRWVMLKNVHLAPGWL MLEKLLHSLQPHACFLFLTME INPKVPVNLRLRAGRIFVFEP GIVKANMLRTFSSIPVSRICKSP NERARLYFLAWFHAIQERLR YAPLGWSKKYEFGESDLRSAC DTVDTWLDDTAKASGRQNISP DKIPWSALKTLMAQSIYGGRR DNEFDQRLNLTFLERLFTTRSF DSEFKLACKVDGHHQIMPDGI RREEFVQWVELLPDTQTPSWL GLPNNARVLLTTQGVDMISK MLKMQMLEDEDDLAYAEATEK KTRTDSSTDRPAWMRTLHTT ASNWLHLIPQTLSHLKRIVENI KDPLFRFFEREVKMGAKLLQD VRQDLADVVQVCEGKKKQTN YLRTLINELVKGILPRWSWHYT VPAGMTVIQWGVPIARRIKQ LQNISLAAASGGAKELKNIHVC LGLFLVPEAYITATQYVAAQAN SWSLEELCLEVNVTTSQGATLD ACSFVGTGLKLQGATCENNKL SLSNAISTALSLTQLRWVKQTN TEKKASVVTLPVYLNFTADLI FTVDFEATKEDPRSFYERGGG
9067	39435	A	9126	3	6375	HKVAAPDVVVPTLDTVRHEAL LYTWLAEHKPLVLCGPPSGK TMTLFSALRALPDMEVVGNLFS SATTPELLLKTFDHYCEYRRT NGVVLAPVQLGKWLVLFCDEI NLPDMDKYGTQRVISFIQMV HGGFYRTSDQTVVKLERIQFV GACNPPTDPGRKPLSHRFLRHV PVVYVDYPGASLTQIYGTFR AMRLIPLSLRTYAEPLTAAMVE FYTMSQERFTQDQPHYIYSPR EMTRWVRGIFEALRPLE

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9068	39436	A	9127	3	617	SWFQPPSGPPWPGA\PPPPPLAR VNPGVVPSLTTSMDVEP* A Q V ELPSHPRVPSAPGPAP* VLEPP RSLTTSVVGPPQGPSWAGGMA VRQALEEAACRDPCIAISSWAG GDRPLWWLDGLLLRRVYPDSC PPCPSRIPIFGASLQGSINPILQ MRKLFPHDMDLL*GQDPFSCR RPESWNRDVGWLGALGVFCLVP FSLVGSGLN
9069	39437	A	9128	1	702	
9070	39438	A	9129	1	1317	
9071	39439	A	9130	1	2641	MGLKARRAAGAAGGGGDDGGG GGGGAANPAGGDAAGDEE RKVGLAPGDVEQVTLALGAGA DKDGTLLLEGGGRDEGQRRT QGIGLLAKTPLSRPVKRNNAKY RRIQTLIYDALERPRGWALLYH ALVFLIVLGLILAVLTTFKEY ETVSGDWLLLLETFAIFIGAEE ALRIWAAGCCCRKYGWRGRRLK FARKPLCMLDIFVLIAVSPVVA VGNQGNVLATSLRSLRFLQILR MLRDGPGEGGTWKLGLSAICA HSKELITAWYIGFLTILSSFLV YLVEKDVPEVDAQGEEMKEEF ETYADALWWGLITLATIGYGD KTPKTWEGRLAATFSLIGVSFF ALPAGILGSLALKVQEQHRQK HFEKRRKPAELIAAWRYYA TNPNRIDLAVTWRFYESVVSFP FFRKEQLEAASSQKLGLLDRVR LSNPRGSNTKGKLFPLNVDAI EESPSKEPKPVGLNNKERFRTA FRMKAYAFWQSSEDACTGDP MAEDRGYGNDFPIEDMIPTLKA AIRAVRILQFRLYKKKFETLRP YDVKDVEIQSAGHLDMLSRIK YLQTRIDMIFTPGPPSTPKHKE VFRKGQHFTFPSQSSRGLNHH *ARPSTSEIEDQRH*WGKFVKS LKGVVQGLGRKLDLVDMMH QHMERLQVQVTEYYPTKGTSS PAEAEKKEDNRYSDLKTIICNY
9072	39440	A	9131	353	477	QNEILPQISKSNNI*SRSPH*ITR NLNNSNMAHKMKFAN
9073	39441	C	9132	170	310	

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9074	39442	A	9133	1	859	MSCGRPPDPVDMITLKVDNL TYRTSPDSLRVFEKYGRVGDV YIPREPHTKAPRGFAFVRFHDR RDAQDAEAAMDGAE*EGRAL RIQVARYGRRDLPRSRQG/PTP RGRSRGGGYGRRSRSYGRRSRS PRRR/HRRNRFPCSCSRRRGR YRGSRYSRSPYSRSPYSRYSR SPYSRYSRYSRSGSHYSSSG YNSRYSRYHSSRSHKPGSSTS SRASSTSKSSARRSKSFSVRS RSRSRSSMTSRPPGVSKRKSK SRISRSKRPPKSPEEQGMSS
9075	39443	A	9134	161	332	SCLNQLN/YLEMWKLFRKAQE DHTLGRDISYVAEVRPGEAGGR AHTGDSLLTMNPSFL
9076	39444	A	9135	1123	1489	LQTLQGHNSQNSMVLVPKQR YRSMEQNRLRNNVTYLQLSD L*QA*EKQAMGKGFPI*MLVG KLASHM*KAESGLPYTLYKN* FKMD*RLKH*T*NHKNPRRKPR HYHSGHRHGQGLHV
9077	39445	A	9136	277	367	
9078	39446	B	9137	1	1136	
9079	39447	A	9138	3	1168	
9080	39448	A	9139	1	1460	ERGLETNCSSEELSSPRGGG GGGRLLLPPELPPVPFPLQD LVPLGRLSRGEQQQQQQQPPP PPPPPGPLRPLAGPSRKGSFKIRL SRLFRTKSCNGSGGGDGTGK RPSGELAASAASLDMGGSAG RELDAGRKPKLTRTQSAFSPVS FSPLFTGETVSLVDVDSIRGLI SPHPPTPPPPRRSLSLDDISGT LPTSVLVAPMGSSLSQSFPLPPP PPHAPDAFPRIAPIRAAESLHSQ PPQHLQCPLYRPDSSSFAASLRE LEKCGWYWGPMNWEDAEMK LKKGKPDGSLVRDSSDPYILSL SFRSQGITHHTRMEHYRGTFSL WCHPKFEDRCQSVVEFIKRAIM HSKNGKFLYFLRSRVPPELPPNS CQLIYPMRSRFSIYESFQHLAKF RIRQLVRIDHIPDLPLPKPLISYI RKFYYYDPQEEVYLSLKEA/QS VSKQKQEVETST*RGAPCWSPP RAFGCQAPALKNQIKLP

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9081	39449	A	9140	2	418	KSPSKYLCYTFIISTAALVLLIM LPHESMPVYLGMACTLGFGAIV FTQRAVFFFAPIGEAKIAENKTG AAMALGSFIGYAPAMFCFSLYG YILDNLNPGIIGYKIVFGIMACFA FSGAVVSVMLVKRISQRKKEM LAAEA
9082	39450	A	9141	26	180	KPAHQCVFFCPVVSAAHQGEV LPYKSGVTSIESFVTHICKVIRR* LLSFLA
9083	39451	A	9142	299	921	FGTAALVL*IVLPPEISPSH*GM ACTLGLGAI/VLTQRAV/FFAPIG EAKIAENKTGAAMALGSFIGYA PAMFCFSLYG YILDNLNPGIIGYK IVFGIMACFAFSGAVVSVMLVK RISQRRIRRLRRIRQFHRRNTSS RYGSGFARGGRKATRGISSQEL GQGLSGEEQDASGGVTAGDI ATGDYFLLTPHLQICTGAKGGL GCVVEGR
9084	39452	A	9143	1	752	MSELPFAIASKRKEYVGIQLPR YTIQKLEENLVFLDRSGHRT KFTNVGRMILLERGRVLLQAAD KLTTDAEALARGWETHLTIVTE ALVPTPAFFPLIDKLAAKANTQ LAIIT*VLAGA WERLEQGRADI VIAPDMHFRSSSEINSRKYLT MNVVYAAPDHPHQEPEPLSEV TRVKYRGIAVADTARERPVLTV QLLDKQPRLT VSTIEDKQALL AGLG VATMPYPMVEKDIAEGR LRVVSPESTS
9085	39453	A	9144	389	760	SWRIDVHPV*YTRLFPFVLVY MQKGT SIRTSSRQLLDKQPRLT V/STIEDKQALLAGLGVA/TMP YPMVEKDIAEGR/LRVVSPESTS EIDHMAWRVTKRTPKN*WTM MPENIGEYTKTHILG

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9086	39454	A	9145	1	941	MTAMERSRILRRVVDILRRND ELAKLETLDTGKAYSETSTVDI VTGADVLEYVYAGLIPALEGSQI PLRETSFVYTRREPLGVVAGIG AWNYPQIALWKSAPALAAAGN AMIFKPSEVITPLTALKLAEIYSE AGLPDGVFNVLPGVGAETGQY LITEHPGIKVSFTGGVAGSKKV MANSAASSLKEVTMELGGKSP LIVFDDADLDAADIAMMANF FSSGQAKR/NGARVLCGGDGVR ARDRPNLRRENLRGKYHS*QR HRRPDAC*YRPL*RCGGRYAD D*VQAGAGSDGL*ATGHGRR EC*PYVTGEAG
9087	39455	A	9146	3	504	DQQQNRQR/LIDCFHPAQWAKE VDVSDKEARCGVRCATRDHLP MVCNVPDYEATLVEYASSAEH KDDAVSAPVFDLFL/GSRGLC SGPLCAEILAT*IS/DEPMPMDA SMLAALIPNRLVWRKLLKGKA VKAGAVHFRRSIYFHPQQANA LDFPSTHIKYCTMLL
9088	39456	A	9147	197	353	YGFRWPD*AHPAIN*ASAAISIF LRWLRLTSITETAPLNAKQAI MPNTIL
9089	39457	C	9148	1	1263	
9090	39458	A	9149	3	726	GAKNAREAIYHIEGDPDHP/EN RLRYPEYRAPGSDKWQRISWEE AFSRIAKLMKADRANFIEKNE QGVTVNRWLSTVNKKKISLRT VGAALVLQVVIGGIMLWLPPG RWVAEKVAFGVHKVMAYSDA GSAFIFGSLVGPKMDTLFDGAG FIFGFRVLPALIFVTALVSILYYI GVMGILIRLGGIFQKALNISKIE SFVAVTTIFLGQNEIPAIVKPFID RLNRNELFTAICSGMASIDG
9091	39459	B	9150	1	1662	
9092	39460	B	9151	1	2658	
9093	39461	C	9152	1	2526	
9094	39462	A	9153	422	585	PYRLKQNIAGA*PIKLPAIAAP VLFSIAFASTIGAKIL/LAVLRSLR PHPSVHA
9095	39463	A	9154	1275	1485	
9096	39464	A	9155	1	439	

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9097	39465	A	9156	1049	2195	NMPKASSCRFSTATTYLRDRSC K*PWAGS*KKNSWR*CRRTTS SHRTRLNATGWGVSVKRRTKAR CSMVCSARGS/SNARGLELVKE GRAQACVSAGNTGALMGLAK LLLKPLEGQNHMRLLRWEAKL AALVRLQENTAQPVPFAPNNA RPLTLEDDRLSCTVRGYNFAITF SKMSGKPTSWQLVASALATKI AHEVNPQNQVGCMLAGGNFYF YSCKPEDVWAALEKDRENLFIF DVQARGTYPAYSARVFREKGV TINKAPGDDEILKNTVDFVSFSY YASRCASAE MNANSSAANVV KSLRNPYLQVSDWGWGIDPLG LRITMNM MYDRYQKPLFLVEN GLGAKDEFAANGEINDYRISY LREHRCNGRSDCRQAFR
9098	39466	B	9157	482	542	
9099	39467	A	9158	115	1662	TPYPDAITTHDIVDTPYVQGG VRVLVFSASLVRVSSVLFSLV WGFVSFCRRFVPCRVCVLLCCL FWCFVFGVWLPRRHMSNHAAL GVGEQQCQRGNINGAPETFAS MANTGT*QW/QRISWEEAFSRI AKLMKADRDANFIEKNEQGV VNRWLSTASLAPTEFRGAMTN HWVDIKNANVVMVMGGNAAE AHPVGRWAMEAKNNNDATLI VVDPRFTRTASVADIYAPISGT DITFLSGVLRyliENNKINAEYV KHYTNASLLVRDDFAFEDGLFS GYDAEKRYDKSSWNYQLDE NGYAKRDETLTHPRCVWLLK EHVSRYTPDVVENICGTPKADF LKVAPDRNTTFLYALGWTQHT VGAQNIRTMAMIQLLLGNMGM AGGGVNALRGHSNIQGLTDLG LLSTSLPGYLTLPSEKQVDLQS YLEANTPKATLADQVNYWSNY PKFFVSLMKSFGDAAQKNN WGYDWLPKWDQTYDVIKYFN MMDEGKVTGYFCQGFNPVASF PDKNKVVSLSKLKYMVVIDP LVTETSTFWQNHEAAVSGGKR PGRKRLNLLPMARLTTTIASAT YANISAQWAKRLQTAFR
9100	39468	A	9159	1	2235	
9101	39469	A	9160	1	1821	



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9102	39470	A	9161	14	1785	FDQVEERVSVIEDQMNMKRE EKFREKRVIRNEQSLQEIWDYV KRLNLHLIGVPESDWENGTKLE NTLQDIIQENFPNLARQANIQQ EIQRMPQRYSSRRITPRHILNA HKRK*ERYKIDTLTSQKLELEK QEQTYSKASRRREITKIRAEI.KE IETQKTLQKINESRSCFEKINKID RLLARLIKKKREKNQTDVIKND KGDITDPTETIQTIREYYKHLY TNKLENLEEMDKFLDTYTLPLRL NQEEVESLNRPTGSEIEAHNSL PTKKSTGPDRTAEFYQRYKEE LVPFLKLFQSEIEGILLNSFYE ASTILJPKAGRDTTKKENFRPISL MNIDAKILNKILANRIQQHIKLL IHYNQVSFIPGIQGFENICKSIN VIQHINRTKDNHTIISDAEKA FDKIQQPFMLKTLNKLGDGTY LKIMTAIYDKPTASTILNGQKLE AFPLKTGTRQGCPLSPLLFNIVL EVLARAIRQEKEIKGILGKEEV KLSLFADDMMIVYLENPVSAQT LLKLISNFSKISGYKINVQKSQV FPYTNNRQTESQIMSELLFTIAS KRKIYVVGQLTRDVKDLFKEN
9103	39471	B	9162	1	2025	
9104	39472	B	9163	67	3156	

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9105	39473	A	9164	1	2019	MDTIKNDKGDTTDPTEIQTTIR EYYKHL YANKLENLEEMDKFL DTYTL PRLNQEEVESLNRPVRG SEIEAIINSLPT/KKSPGPDEFTAE FYQRK\AFDKIQAFTLKTLNK LVIDGTYRKIIRAICDKPTANIIL NGQKLEAFPLKTGTRQGCPLSP LLFNIVLEVL DRAIRQEKEITCIQ LGKEEVKLSLFADDMIVYLENP IISAQNLLKLISNFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKKIKYLGQLTRDVKD LFKENYKPLLNEIKEDTNK WEN IPC SWVGRINIMKMAILPKVIYR FNAIPIKLPVAFTELEKTTLKFI WDQKRAYIAKSILSQKNKAGVI MLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEIMLHIY NYLIFDKPDKDEQWGKDSL FN KWCWENWLDIWRKLLDPFLT PYTKINSRWIKDLNVRPKTIKTL EENLGNLIDIGMGKDFMSKTP KAMATKAKIDNWDLIKLSFC TAKETTIRVNRQPTKWEKIFTT YSSDKGLISRIYKELKQIYKKKT NNPMNKWAKDMNRHFSKEDI YAAKRHMKKCSSLAIREMQIK TTMR YHLTPVRMVIKKSGNNR PPLSKEQPIFRLSILATTRDGN PAAVENVLHIKATLSFQQTHKA FYFQPS
9106	39474	A	9165	1	3477	

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9107	39475	A	9166	1	2460	MGDFNIPLSTSDRSTRQKVNDK TQELNSALHQADLIDYRTLHP KSTEYTFPSAPHHTYSKIDHIVG SKALLSKCRRTEIITNCLSDHSA IKLEIRIKKLTQNCSTTWKLNLL LLNDYWVNNEMKAEIKMFFEI NEDKDTTYQNRWDTFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTTHSKASRRQEI TEIRAELEKETQKTLQKMNES RSWFFKEINNIDRLRLARLIKRR EKNQIDAIAKHNHKGDTTNPTEIQ TTIREYDKHLYANKLENLEETD KFLDTYILPRLNQEQUESLNRPI TGAIEIAIINSLRTKKSPGPGGF TAEFYQRYKEE/HVLEVLARAI RQEKEIKGIQLGKEEVKLSLFA DDMTVYLENPTVSAQNLLKLIIS NFSKVSGYKINVQNPQAFLYTN NRQTESQIMSELPFTIASRKIKY LGQLTRDMKELFKENYKPLLS EIKEDINKWKNIPCSWVGRINVR KMAILPKVIYRFNAIPKLPMTF FTELEKTTFKFIWNQKRARIAK SILSQKNKAGGITLADFKLYYK ATVTKTAWYWYQDRHIDQWN RTESSEIMPHIYNLIFDKPDKN KKWGKDSL FNKWCWENWLAI CRKLKLDPLTPYTKINSRWIK DLNVRPKTIKLEENLGITIQDT GMGKDFMSETPKAMATKDKID KWDLIKLSFCTAKETTIRVNR
9108	39476	A	9167	1	1389	

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9109	39477	A	9168	1	1659	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIRSLH AKSTEYTFSSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRKIKNLTQNRSTTWKLN NLLNDYWIHDEMKAIEIKMFF ETNENKDDTTYQNLWDAFKATA SKTNKEKEKNQIDTIKNDKGDI TTDPTEIQTTIREYYKHLIYANK LENLEEMDKFLDTYTLPRLNQE EVESLNRPIITGAEIVAIINSLPTK KSPGPDGFTAIFYQRYKEELHI NRAKDKNHMIIISIDA EKAFDKI QQPFMLKTLNKLIGDGYFKIIR AIYDKPTANILNGQKLEAFPLK TGTRQGCPLSPLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLF ADDMTVYLENPIVSAQNLLKLI SNFSKVSQYKINVKQSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGQLTRDVKDLFKENYKPLL KEIKEDTNKWKINPCSWVGRIN IMKMAILPKVIYRFNAIPKLP TFFTELEKTTLKFIWNQKIRARI AKAILSQKNEAGGITLP
9110	39478	B	9169	1	1716	
9111	39479	B	9170	1	3171	
9112	39480	A	9171	1	2952	MLLNQGRKLPVFAEETLKFK GTSNKPQTLEQISTSHAQKEAT VMVPGSNQEIPSGAYAIRALGF KHKTGRLFEQTLNVLQEFLLTP QWHLECCQERTVHSPGKAAEA REPSVIDRHLEQESSNWHLVGA ALGQSQRKEQAAIFAVLQPLL VIPRQTGSGVDLQKTPDLOQR GLIVRRKTNKQKGIHVHNSTRE QNWTENEFDKLEGGFKRWVI TNSSELKEHVLQTCKEDKNLEK SAIKLELRKINLIQN
9113	39481	B	9172	1	2406	
9114	39482	A	9173	1	2307	

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9115	39483	A	9174	3	2776	QRDLDSHTLMGDFNTPLSILDR STRQKVNKDTQELNSALHQAD LIDYRTLHPKSTYTFPSAPHH TYSKIDHILGSKALLSKCKRTEII TNCLSDHSAIKLELRITLTQSH STTWKLNNLLNDYVWHNEM KAEIKMFFETNENKDDTTYQNL WDAFKA VCRGKFIALNAHKRK QERSKIDTLTSQLKELEKQEQT HSKASRRQEITKIRAELEKIEITQ KTLQKINESRSWFFERINKIDRP LARLIKKKREK
9116	39484	B	9175	133	3213	
9117	39485	A	9176	284	1689	QNFNGFKDLL*RSW*REKSWI CML*ARNTASRQQRNKAGQR MTLMS*EKKASDDQTSPS*R/Q EVRTHRKEAKNLVKRLDKWLN RITSVEKSLNDLMELKTM/RTR TTT*MHKLQ*PI*SFGKKEIQT IREKHLIYANKLENLEEMDKFL ETYTLPRLNQEEVESLNRPITGS EIEAIINSLPTKNSPGPDRFTAKF YQMYKEELVPFFLKLQFSIEQE GILPNSFYEASIIIPKGRDPTK KENFRPISLMNIDAKIFNKILAN QIQQHKKLIHHDQMGFIPGMQ DWFNIRKSINVIQHINRTKDKN HTIISIDA EKA FDKIQQCFLKKT LNKLGIDGTYVKIIRAIYDKPTA NIILDGQKLEAFPLKTSTIQGCP LSPLLFNIVLEVLARAVRQEKEI KGIQSGKEEVKLSLFADDMTV YLENPIISAQNLKLSNFSKVS GYKINVQKSQAFLYTNNREP
9118	39486	A	9177	1	1515	

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9119	39487	A	9178	3	1601	ESRS*FFEKINKI/D/RLARLIKK KREKNQIDAINKDGDITDPT EIQTITREYYKHLTYNKNLENLEE MDKFLNTYTLPRLNQEEVESLN RLITGSEIAIINSLPTKKSPGLD TFTAIFYQRYKEELVPFLKLF QSIEKEGILPNSFYEAIIILIQKP RDTTKENFRPISLMSINAKILN KILANRIQQHIKKLIHHDQVGS PGMKGWFNICKSINVQMHNRT KYKNHMIISIDEEKAFQKIQKRF MLKTLNKLSDGTLYLKIRAIYD KPTANIILNGQKLEAFPLKNGT RQGCPLSPVLFNIVLEVLARAI/ RLISCFKSVSGYKINVQKSQAFL YTNNRQTESQIMSELPFTIASKR IKYLGQLTRDVKDLFKENYKP LFNEIKEDTNKWSIPCSRVGRI NIVKTAILPKVIYRFNAIPIKLP TFFTELEKTTLKFIWNQKRACIV KTILSKKNKAGGITLPDFKRY KATVTKTA/WSFHELGKTQLAT RTTVSTFQQIPGI*VQLRFDFSR DITLLSLLCR
9120	39488	B	9179	1	2034	
9121	39489	B	9180	1	2088	
9122	39490	A	9181	1	1870	MKAIEKMFETNENKDDTTYQN LWDTFKAVCRGKFIALNAHR KQERSKIDTLTSPKLEKQEQT HSKASRRQEITKIRAEKKEIETQ KTLQKINESRSWIFESINKIDRPL ARLIKKKREKNQIDAINKDGD IITDPTIEQTITREYYKHLTYNKN LENLEEMDKFLDITYTLPRLNKE EVESLNRNPTGAIEIVAIINSLPTK KSPGPDGFTAIFYQRYKEELVP FLIKLFQSIEKDGIILPNSFYEASI ILIPKP
9123	39491	A	9182	1	1410	
9124	39492	A	9183	1	3996	

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9125	39493	A	9184	281	3030	KPRL ENYMKNAEASRADAINW KKG Y/LVMEDKMNMKREGKF REKRIKRNKQSLQEIW DYVKRP NLRLISVPESDRENGTKLENTL QDIHQENFPNLA RQANIQIQEIQ RTPQRYSSRRATPRHIVRFSKV EMKEKMLRAAREKEIQTNIREY YKHYRANKLENLEEMDKFLNI YTLRRLNQEEVESLNRPIRGSEI VAIINSLPTKKSPGPDGFTA EYY QRYKEELVFP LLLKLFQ SIEKEGI LPNSFYEASII
9126	39494	A	9185	1	2250	
9127	39495	A	9186	248	2385	RQWAGVVGRC SHLASVWSST SETGAIRSSTEVDAPDDSM LST CDIDLTAARRAWLGCLPTK KSP GPDGFTA EYFQRCKEELVPFLL KLFQSI/EKEGILPNLFD EASII PKRGRD TT KENFRPISLMNID AKILNKILANRNQQHIKLIHH DQVGFI PMGMQGWFNICKSINVI QHINRTKDKNHNMIISIDAEKAF DKIQQPFMLKTLNKL GIDGTYL KIIRAIYDKPTANIILNGQKLEAF PLKTGTGRGCLP LLFNIVLEV LARAIRQEKEIKGIQLGKEEVKL SLFADDMIVYLENPIVSAQNLL KLISNFSKVSAYKIN VQKSQAF LYTNNRQTESQIMSVFPFTIASK RIKYLGIQLARNAKDLFKENYK PLLNEIKEDTKK WKNIPCSWVG RINIVKMAILPKVIYRFNAIPK L PMTFFTELEKTTLKFIWNQKRA RIAKSILSQKNKAGGITLPDFKL HYKITVTKTAWY WYQNRDIDQ WNRTEPSEITPHIYNYLIFDKPE KNKQWKGKDSL FNKWCWENWL AICRKLKLDPLTPYTKIHPRWI KDLNVRPKTIKLEENLGNTIQ DIGMGKDFMSKTPKAMA AKA KIDKWDLIQLKSFCTAKETTIRV NRQPTKWEKIFATYSSDKGLIS RIYKELKQIYKKKTNNPIKKW AKDMNRHFSKEDIYAANKHM KKCSPSLAIREMQIKT TMRHYL

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9128	39496	A	9187	1	2229	MGKKQNRKTGNSKTQSA SPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTGKGE VQNFENLEECITRITNTEKCLK ELMELKTKARELREECRLSR CDQLEERVSADEMNEMKRE GKFRERIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIHQENFPNLARQANVQI QEIQRTPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKEIQT TIREYYKHLVANKLENLEEMD TFLDTYTLPRLNQEEVESLNRPI TGSEIVAIINSLPTKKSPGPDGFT AEFYQRYKEELVPFLKLFQSI KEGILPNSFYEASIIIPKGRDT TKKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFIPG MQGWFNIRKSINVQHINRAKD KNHMIISIDA EAKFDKIQPFML KTLNKLIGIDGTGYFKIIRAIYDKP TANIILNGQKLEAFPLKTGTTRQ GCPLSPLL FNI VLEVLAIRQE KEIKGIQLGKEEVKLSLFADDM IVYLENPVSAQNLLKLSNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMGELPFTIASKRIKYLGIQ LIRDVKDLFKENYKPLLKEIKE DTNKWKNIPCSWVGRINIVKM AIIPLKVIKGTTLKFIWNKKSRIAK SILSQKN/KAGGITLLTQLYYKA TVTKTAWWYQNRDIDQWNR
9129	39497	A	9188	1	2667	
9130	39498	A	9189	1	3033	MADMLTWESCLEESLQEE SPL VTHCGPSCCISGQSPSSARPSS VSSAISVLMPLPQNRKLPPAWTS PGIFPTDLVVYSMSLPHALARY NCDVCKSMLPPRLYAPEEKAR TSPLCGTWYSPSLPLCGAWCKK NEKKRERERERKRQREDILSGA SSYKDTIHQIRPPPYDVLQIQ TTIREYFKHLVANKLENLEEMD KLLDTYTLPRLNQEEVESLNRPI TGSEIVAIINSLPTKKSPRPGFT AEFYQRYKEE



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9131	39499	A	9190	1	950	MQAICTGQARALICMGGNFAL AMPDREASAVPLTQLDLAVHV ATKLNRSLLTARHSYILPVLG RSEIDMQKNGAQAATVEDSMS MIHASRGVLKPAGVMLKSECA VVAGIAQAALPQSVVAWEYLV EDYDRIRNDIEAVLPEFADYNQ RIRHPGGFHLINAAAERRWMT SEIQTITREYVKHLYTNKLAENL EEMDKFLDTYSLPRLNQEVEES LIRPITGSEIEAVVNSPPTKNSPG PDRFTAKFYQRY/K/EELVPFFL KLFLAAVPAPSSHGPFCCSRKA LRGSKTGSAYPSSSALRRVTVS EVVCLFAEAQLF
9132	39500	A	9191	1	3470	MASVSSATFSGHGARSLLQFLR LVGQLKRVPRTGWVYRNVQRP ESVSDHMYRMAVMAMVIKDD RLNKDRCVRLALVHDMAECIV GDIAPADNIPKEEKHREEGNK CHKQKAMGKHLKEPHVLGGQET KGLESTDVLLPLAAGQDLGRE KKIREEAMKQITQLLPEDLRKE LYELWEDLEFESPCLDSLCLCC SLKPQSESSPVLPEGCETLIQRL CAVGTGVTAAALATRLCRASGL PAPHQWASELQRSRKKE
9133	39501	A	9192	1	3907	MAAWNLLKSYAYWGGLRKE DFHCLDRKTLRTVSFLAALLSY ESIGGKGKLTTRKDIYTENPSV HHHHQRPKVDKTTKMGKKQN RKTGNSKMQSAPPPKERSSSP ATEQSWMENDFEELREEGFRRS NYSELRREDIQTKGEVENFEKN LEECITRITNTEKCLKELMELKT KARELREECRLSRCDQLEER VSAMEDEMNMKREGKFRDK RIKRNEQSLQEIWDYVKRPNLR LIGVPESDVENGTKLENT
9134	39502	A	9193	3	3197	

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9135	39503	A	9194	I	3158	MVKGSIQQEELTILNIYAPNTG APRFIKQLLSDLRDLSDHTLIM GDFNTPLSTLDRSTRQKVNKD QELNSALHQADLIDYRTLHPK STEYTLFSAPHHTYSKIDHILGS KALLSKCKRTEIITNYLSDHSAI KLELRINKLTQSRSTTWKLNLL LLNDYWRKQERSKTDLTLSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERINKIDRPLARLIKKEKNQID TIKNDKGD
9136	39504	A	9195	I	3285	
9137	39505	B	9196	I	1366	
9138	39506	A	9197	735	3541	RSFPRSRSPPFLLLSRYLRIHMV FSVLPGFLQNP KYLLSGSLQEK FRTPGINSHKTLDPNRVIVKVR RLEKEKALRAYVGKSEVRNMH LRERCKL*KKREKNQIDTIKND KGDITDATEIQTITREYVKHLY ANKLENLEEMDKFLDTYILPRL NQEEVESLNRPTGSEIAIINSL PTKRSPGPDGFTAIFYQTYKEE LVFPFLKLFQSTEKEGILPNSFY EASILIPKGRDITTKENFRPIS
9139	39507	A	9198	I	5356	MGKKQNRKTGNSKMQSASPPP KERSSPATDQSWMENDFDEL REEGFRRSNYSELREDIQTGK EVENFEKNLEECITRITNEKCL KELMELKTKARELREECRSLRS RCDQLEERVSA MEDEMNEMK QEGKIKRDKEGHYIMVKGSIQQ EELTILNIYAPNTGAPRFIKQVL SDLQRDLSDHTLIMGDFNTSL TLDRSMRQKVNKDTQELNSSL HQADLIDYRTLHPKSEIYTFFS APHHTYSKIDHIVGS

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9140	39508	A	9199	I	2491	MGDFNTPLSTLDRSTRQEVNK DTQELNSALHQVDLIDIRTLH PKSTEYTFSSAPHYTYSKIDHIV GSKALLSKCKRTEITNCLSDHS AIKLELRICKLTQNHSTTWKLN NLLNDYWVNNEVKAIEKMFF ETNENKDTTYQNLWDTFKAIN KIDRPLARLIKKKREKNQIDA NDKWDITTDPEIQTITIREYYK HLYANKLENLEEMDKFLDTYT LPRLNQEEVESLNRPIGTSEIEAI TNSLTITKKSPPGPDGFTAKFYQR YKEELVPFLKLFLQIEKEGILP NSFYEASIIIPKPGRDTTKQKK NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFIPWQMG LFNICKSINVIHHINRTKDKNYM IIS/I*DAEKAFDKIQPFMLKTL NKLIGDGYTLKIIAIYDKPTAD IILNGQKLEAFSLKTGTROGCP SPLLFNIVLEVLARAVRQEKEIK GIRLGKEEVKLSLADDMIVYL ENPIVSAPNLLKLISNFSKVS KINVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD MKDLFKENYKPLLNEIKEDTNK WKNIPCSWVGRINIMKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRARIASLSQKNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIT PHIINYLIIDKPEKMSIIDTGGW
9141	39509	A	9200	I	3083	MGKKQNRKTGNSKTQSASPPP KERSSPATEQSWMENDFDEL EEGFRRSNYSSELWEDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELREECRLRSR CDQLEERVSAEDEMNEMKRE GKFRERIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGKLE NTLQDIQENFPNLARQANVQI QEIQRTPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKEIQ TIREYYKHLYANKL

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9142	39510	A	9201	1	4201	MRKKQSRKTGNSKKQSTSPPPK ERSSPAMEQSWTENDFDELRE EGFRSNYSKLEIEITKGQEV ENLEKNLDKCITRITNIEKCLKE LMELKAKARELHEECRLSRSC DQLEERVSVMEDEMNMKQKQ GKFREKRIRNEQSLQEIWDYV KRPNLPPIDVPESDRENGTKLE NTLQDVIQENFPNLRQANIQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKAFKQ ASRREDDIAKVTSG
9143	39511	A	9202	715	6193	GQHHIPDTKAWQRHKKKENF RPISLMNIDAKILNKMLANQIQ QHKKLIYHDQVGFIPGMQGW NICKSINVIIHINRTKDKNHMII SIDAAKAFDKIQPFMLKTLNK LGIDGTYLKIRAIYDKPTASIL NGQKLEAFTLKTGTGGCPLSP LLFNIVLEVLARAIQKEIKGI QLGKEEVKLSLFADDMIVYLEN PIISAQNLKLGINFSKVSGYTIN VQKSQAFLYTNNRQTSEQIMSE LPFTIASKR
9144	39512	A	9203	1	3682	KEGHYIMVKGSIQEEILTILNIY APNTGAPRFKQVLSDLQRDL SHTLIMGDFNTPLSTLDRSTRQ KVNKDTQELNSALHQADLIDIY RTLHPKSTEYTFPSAPHTYSK IDHILGSKALLSKCKRTEITNCL SDHSAIKLELRIRKLTQNRSAT WKVNNLPPGMTYVWVHNGNE GQKLKMFETQWE/HKDTAYQ NLWDTFKAGCRGKFIALNAHK RKAGDKPKLTPLTSQKK/LEK QEQTNSKAS
9145	39513	A	9204	1187	1680	DSPCTIASTRSYFCINRPLSVDI QLRCSCRNVRLSTYC/LYLRLQ LRIEGGNFVFTTKADNGPQQIIT *TNSFPVGNNATVKVRHHILT FFINLFGEIGGPDHFNNGFTQP LPSSGTQPQHLSCVTIDGGNVT MRIHRNQPFINRTKQRLLLT ACDLLWLH
9146	39514	A	9205	3	293	ERSWSQLLFSTEQFWQQLPGTG SGRARQNISRKTPREHAGGYRR DNGNNWAVPHIQCNLVPR**K RPPVRAHRAPETLCASKALQE RYWVFELLR
9147	39515	A	9206	1	4509	
9148	39516	A	9207	1	507	

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9149	39517	B	9208	1	3448	
9150	39518	A	9209	1	2652	
9151	39519	A	9210	75	784	
9152	39520	B	9211	1	1968	
9153	39521	A	9212	1	298	LQGHVLVDYVLSCLPFGIMGH GNWPLVWLTAACLVLLC*/WSL RRQ*1QQ*APSDQKRDFLVPHG A/VFDR*ISATCWSSINWPANCS RPSIAGWPKQAS
9154	39522	B	9213	167	362	
9155	39523	A	9214	959	1267	YHWHQLLSMVRQLMVLSSWKK ISSWFMGPPIIRKSILAENSI*KN LV*VILKLTGISTLK*MAPQN TQY*MTVIKLFKWWARQTRLR SIMVCYSSTTTLLT
9156	39524	A	9215	370	555	
9157	39525	A	9216	1	1016	MSHQLTFADSEFSSKRRQTRKE IFLSRMEQILPWQNMVEVIEFPY PKAGNGRRPYPLETMLRIHCM QHWYNLSDGAMEDALYEIASM RLFARLSLDSALPDRTTIMNFR HLLEQHQALARQLFKTINRWLA AGVMMTQGLVDAITIEAPST KNKEQQRDPEMHQTKKGQNW HFGMKAHIGVDAKSLTHSLV TTAANEHDLNQLVQNELETAE RFRRQEDTQSKCLLSSIMLYIKN LSGPDVSELISPLSEGNLCSV VVAVIAA VLRRAPIHMPSGWW RSWNAESGAYNVTRSGDSYI/H G*LLYRSRKLDPDADEGALQK WWSVLPPFKRRLWF
9158	39526	A	9217	408	643	PGCGSGHSWHRHQCGPSCQSA TDCLSWSDASPDRAALCSWS SWVPQ*WHR/HKVP*VIMTP ASASQRLMVLNNWRAS
9159	39527	A	9218	626	760	
9160	39528	A	9219	1	2469	
9161	39529	A	9220	1	756	
9162	39530	A	9221	1738	1913	PTAWSPPRPTSMTSISWVICFME RSNLSPMPATKERHSARSWPR WMWTG*SPSVPAR
9163	39531	A	9222	2403	2760	FRGDGILVSCPLVFSSAFSWRA ADGGKNRNVHPSV/VR*AGAL RPRTQSRQ/SQRLNKVEKGGV KQFEHNQSCRQQVGVITIKVVK QLADILPHGHFQFYAEVIGKLF RQRSARDAIRGSS
9164	39532	B	9223	1	3663	

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9165	39533	A	9224	1	1584	MELIEKHVSFGGWQNMRYRHS QSLKCEMNVGVYLPKAAANEK LPVLYWLSGLTCNEQNFITKSG MQRYAAEHNHIVVAPDTSRGS HVADADRYDLGGQAGFYLA TQAPWNEHYKMYDYIRNELPD LVMHHPATAKKSISGHSMMGG LGALVLA LRNPDEYVSVSAFSP IVSPSQVPWGGQAFAYLAEN KDAWLDYDPVSLISGQQRVAEI MVDQGLSDDFYAEQLRTPNLE KICQEMNIKTIRYQRGACISAD AATRGAKRESCRS CGGLLIAER PAKVEPGTASRQDNATINIEYM KASIRARVEHPFRIJKRQGFVK ARYKGLLKN/ETNWRCSRW/P/ HLFRADQMIRNPHDLYAPEVV HQA KAVTTSGYRFLPCCGFAN TFWGKTTADGTLIEHFGRRCCQ WFEDDDGHREQCDFRFRFKNC PQCN AENDIAARRCRECDTVLV DPDDMLKAALRLKDALVLRCSS GMSLQHGHEKGEWLKITYYD EDGADVSEFRQLTPAQRATAFE QLFIRPHTRTPGI
9166	39534	C	9225	1	2127	
9167	39535	B	9226	1	1917	
9168	39536	A	9227	1671	2198	RAGAWASDPQRGVVRNAALL PPDDRS DGRDAKTQSHRDG/VI SY/RAFDETILASGIVPRTPIDGI DHPKNEADDMRLRMGFIEDVETI /IGADPGRSSDRSVLCNHAGSDS SHYPL YERAAGSAHSVQRDYP SGHQPELLDCLGYARTRSTDTG TPERWSSGHPDCDRRCSPWPGR
9169	39537	A	9228	642	746	
9170	39538	A	9229	1	2031	
9171	39539	A	9230	909	1058	
9172	39540	A	9231	2	268	WRCLLRQLKFIKTVTSWICTG KLMLSTTSPLMMQMMVILLMP VLASKVKPKSTIN*LVSVSGNM NSKATALNLKVPKIKPVLPSL
9173	39541	A	9232	63	463	FPATCWSSINWPANC SRPSIAG WPK/PGVMMTQGT/LVDAITIEA PSSTKNKEQQRDP EMHQTKKG NQWHFGMAHIGVDAKS/A*P TAWSPRPRTSMTSISWVICCME RSNLSQMPMPATKGRHSARSWP RWMWTG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
9174	39542	A	9233	74	247	RNVMIKRRVLSSTSAS*LPPASA FCRLFTSPARWRSTACFTSGNR YRFLTVRLSGYW
9175	39543	A	9234	3	271	ASYWNRSFSPWGTYNRHPR*N RQCASRHCRGLHKQYQWPRJR S/WLNCTPAPHARDVLLWRPSS LPAGNADGPIRWRPCCVFTACS IGTT
9176	39544	A	9235	1	1048	MCSFRSQTCSSSRFTFARVSVI HSANHRVNLNDRSTIMRTRGQD PTLPEMRRVRLLEMAADMDMF CQGLRYGPLPAPVRQQAIIIPC HRVVRGDGTLSGYRWGVSRA QLVREAEENEERPINRGWPKQP SDDPKHFVMPTHIEAPSSTKNKE QQRDPPEMHQTKKGNQWHFGM KAHIGVDAKSLTHSLVTAA NEHDLNQLGNLLHGEKQFVSA DAGYQGAPQREELAEVDVDW LIAERP GKVKTLKQNP RKNTA INIEYMKASIRARVEHPFRIKR QFGFVKARYKGLLKN/ETNWR CYSWPWTCFGWTK*YPSIPTCLL TTRTASLLKPPGVRTSVCWQQL

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9177	39545	A	9236	I	2493	MTQIFTGLVEADPFHAVTLVA NHDQPLQALEAPVEPWFKPL AYALILLRENGVPSVFYPDLYG AHYEDVGGAGQTYPIDMPIEQ LDELILARQRFAGVQTLFFDH PNCIAFSRSGTDEFFPGCVVMS NGDDGEKTIHLGENYGNKTWR DFLGNRQERVVTDENGEATFFC NGGSVSVWVIEAANNRQYDY GAGHKIPVINYTDVHLRIERSCR FRADPRQQHELQLSSKLAVHD VLTNIYNRRYFFNSVESLLSRPV VKDFCVMLVDINQFKRINAQW GHRVGDKVLVSIVDIQQSIRPD DILARLEGEVFGLLFTELNSAQ AKIIAERMKNVELLTGFSNRY DVPEQMTISIGTVFSTGDTNRIS LVMTEADKALREAKSEGKNKH WYNLSDGAMEDALYEIASMRL FARLSLDSALPDRTTIMNFRHL LEQHQLARQLFKTINRWLEA GVMMTQGTLDATIEAPSSTK NKEQQRDPPEMHQTKKGNQWH FGMKAHIGVDAKSGLTHSLVT TAANEHDLNQLGNLLHGEEQF VSADAGYQGAPQREELAEVDV DWLIAERPQKVRTLKQHPKRN KTAINIYMKASIRARVEHPFRII KRQFGFVKARYKGLLKN.ETN WRCYSRWP/HLFRADQMILCPV FVHHIPRFFGTFFGATDQTFTL TESVIHQPLVLTNFIADIGNDFA
9178	39546	B	9237	I	3148	
9179	39547	B	9238	I	1680	
9180	39548	A	9239	191	470	



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9181	39549	A	9240	1	1675	MFARVSTTPVTRYEMYRKTRS TRLEDNNALSQSKPLPFSEVT GSKGKADKEKVG DY VFCLKAQ GRYNGEPLTGTGKIGGMLALR GEGTPEFPVQADFRSGNTRVAFD GVVNDPMKMGVVDLRLKFSG DSLGDLYELTGVLDPDTPPFET DGRLVAKIDTEKSSVFDYRGFN GRIGDSIHGSLVYTTGKPRPK LEGDVESRQLRLADLGPLIGVD SGKGAEKSKRSEQKKGESVQ PAGKVLPHYDRFETDKWDVMD ADVRFKGRRIEHGSSLPISDLST HIILKNADLRLQLKFGMAGGS IAANIHLLEGDKKPMQGRADIQA RRLKLELMPDVLMQKTLGE MNGDAELRSGNSVAALLGNS NGNLKLLMNDGLVSRNLMEIV GLNVGNVYVGAIFGDDEVRYN CAAANLNIANGVARPQIFAFDT ENALINVTGTASFASEQLDLTID PESKGIRIITLRSPLYVRGTFKNP QSG*WS/GTLLSTKAKTIVAI TTLKVTVMASVSLPMNTKDS VSVQLMRNLIVPTLKLMMQGGKF LKYLLPVKMQKFGPQV
9182	39550	A	9241	72	506	GHVAHLQPRAGGRQPAPRLHHP QGTDRVLHGQRGGQPGP/LLPS LSAWRPSTSLKPA SCGLRGPT SKRMSMQDGGPLPHHRAGAQP PVHPGQEA VG* C/EYWSASSRP VTQPGALMWRLWSAGRPRPY LLSHSQHDPHSGQGGGEHP
9183	39551	A	9242	1	447	
9184	39552	A	9243	70	490	CGCDAETIILRINALAFIWKCGT EWICCFCLALRELQQA VHVAG LPQQA KILFDGSGSEIGKIH*LRC AHCPLSSGKPVVPAALMNRPT RGERRFAYWAPGWFFSPVRR ATADCPSPGPERVAASGRPRWF APAGENPV

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9185	39553	A	9244	1097	1841	ANDGDLRSCVTLSCHMASHASE AADPPATTAFTDEHMSVKLRR TVGVACSVCPGWVTSCHPVNP AAS/GAKVLPGDTDIALPGPLPF ILSR\QLRDNTLILSDNGG\RLY FELLFPGEDGYRRCESLWLVRG GVAKL DQGHRLAALWQALSEE LRLTPHRYLATNSPQGPWWLL GWCERVPEADEVLPAPLPPYRV LTGLVDRIWRSEDVSAASGLHH DNRNAPSLSDQTRTDPPIRAH SR\YQRQKPDG
9186	39554	A	9245	456	928	EAATEPKHLHLQRHAALAQHR QAPRPQGRPLARPHQGDQPD RLHHLRGGGRHGARGHLHQA GAGESAPAPKG/VTCPASPLGD VTGKPTSAWNTEKGRWAQHR GYPSGPAAPLVLRSWPIPLFRP PPLLPLSSPAWILPSPLCHSLKA QSLVQATI
9187	39555	A	9246	1	1572	

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9188	39556	A	9247	1	2505	MAWRNSVNWQCKQEPGLHR RHGRRKLTNGTTRRSQNKKE DFYTSQPGFPALALGCCLRVNL LLGHRGISAGSSYRPITSTPCHL CKLGQEVFAKPLNLQDQCQON LVMQVLKLVNLCLNDFIGSSA DESADDLCTVQIPTTWRTMGL VGCDGVCCRTWCQCLATAV VSGVGGGPWLLPACSSGSPMIS KRKKFVHKWAKDLVEPRHGLE NVWDLPRAMAGSYLMYKQQRK WKIMEFGKWALQHKTMTVKDIE RLQLYNKVKEQPVQVEGSGRA STIFVVLKTFKGGKSPCGAPGE CVAWTQCRILGWVQIHFKEHP ADRVVGLIKMPGLDFYFAADV CYAEKVAQEKGLYRLTSRYR HYAAFERATFEQGSTKLMMML TDKQIADFQKHYTEPERFQILP PGIYPDRKYSEQIPNSREIYRQK NGIKEQQNLLQVGSDFGRKG VDRSIEALASLESRLHNTLLFV VGQDKPRKFEALAEKLGSRAS MEFKRYEYNAAGDLTAVITPD GNRSETQYDAWGKAVSTTQG GLTRSMEYDAAGRVISLTNENG SHSVFSYDALDRLEDEGLVIL WYYDESDRITHRTVNGEPAEQ CQYDGHGWLTDSHLSSEHGRV AVHDGYDDKGRLTGECQTVEN PETGELLWQHETKHAYNEQGL ANRVTPDSLPPVEWLTYGSGYL
9189	39557	A	9248	481	857	PLAYLYRDPHVRCVTASGPAP VYGFQPGFSAPTGI/IRKSVHGD HSYCKYAHSCSRQYRAPEPRLS RTSQCLFSHRSARCPDLLMGR RYRRPECRLSPLLPAAPVPGLP WTIYPRRLYRNSPR
9190	39558	A	9249	777	1229	GAGYSSARCGKHHARTGGAGR NILWRQLRRRGCRSTVDRSHH NQPGTWHRHQPGRGPAKPAR PWRAGTHLPTGTASVRHPCLG QPLRAEPRPAVPDAPRNQNLFP PAPQTDSALPGAVRG*RAR*YH *SRITTPPPDEHDSHWARACSP
9191	39559	B	9250	1	2681	

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9192	39560	A	9251	933	1828	VSRHVLVWQPRMPAPPAVDW LTY/GSGIL/SGNKLVGTPLEVEY TRDSLH/RETLRSFASMAGSNA AY/*LTSTDTAPAGQLQSQH/LNS LVYDRDYGWSDNGD/LVRSIGP RQTREYGYSATGRLESVRTLA PDLDI/RIPYATDPAGNRLPDPE/ LHPDMRADGGATGQKVEPEYT PARKAHLHYHWTGDCRWRLSA KTAIRVERGI**MGQPAY*GEPH HVYQPR*TWHRWRWQKGRKS ASGRRYLRPINPNVNGRENQRP TSPDGTHTMAPISLMAWQPIQLR YRGHVRQRLSAVGERIYRYLPP
9193	39561	A	9252	I	1409	MECDASALLRYDSRQFIPLAID GLAKDVLGRRFALEGHPRLEAI ARAGDVVRFPADSELPPDYDG LIPGQESLKVHACVGLPLFAGQ NLIGALTLDGMQPDQFDVFSDE ELRLIAA\LAAGALS\NALLIEQL ESQNMLPGDATPFEA\VKQTQM IGLSFGMTQLKKEIEIVAASDLN VLISGETGTGKELVAKA\HEASP RAVNPLVYLNCAALPESVRKSE LFGHVKGAF\TAISNRSGKFEM ADNGTLFLDEIGELSLVLQAKL LRVGQYGD\IQRVGDDRCLRVD VRVLAATNRDLREEVLA\GRFR ADLFHRLSVFPLSV\PLRERGD DVILLAGYFCEQ\RLRQGLSRV VLSAGARNLLQHYSFPGNVREL EHAIHRAVVLARATRS\GDEVIL EAQHFAFPEVTLTPTEVA\AVPV VKQSLREAT*AFQRETIRQALA QNRKRWACARMLETSVANV HRLGKRLVLKK
9194	39562	A	9253	389	799	PQFLIPSVTPCMFIHPLDAK/AR DLRRGDKVKVVSRRGEV\ISIVE TRGRNRPQGLVYMPFFDAAQ LVNKLTLDATDPLSKETDFKKC AVKLEKACPYDTLKLATLASG LSAGTPYFVARDIPCMECDIPC AKVCPS

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9195	39563	A	9254	588	1500	RHPPIPAKIGLHAVAQDRAWNN MQAGPNINEERMPGWRDPRNF IIVSDPYPTVSALAADL/TPEVSK FPGSELAEDQLNDESRELGFYL QKGLFEEYAWFGRGHGHDLP FDDYHKARGLRWPVNVNGKET QWRYSEGNDPYVKAGEGYKF YGKPDGKAVIFALPFEPAAEAP DEEYDLWLSTGRVLEHWHGTGS MTLRVP*LHRAFPDAGLFIYPL DAKARDLRRGDKVVKVVSRRGE VISIVETRGRNRPPQGLVYMPFF DAAQLVNKLTLDATDPLSKET DWPHFSSTYNGPLLQGANGLIL VQQH
9196	39564	A	9255	1	1698	MEREQDSIIIMDAATTRNLEITQ NLGGAENTLASVLDCTVTPM GSRMLKRWLHMPVRDTRVLLE RQQTIGALQDFTAGLQPLVRQV GDLERILARLARTRARPDLAR MRHAFQQLPELRAQLETVDSA PVQALREKMGFAELRDLLE AIIDTPPVLWSWMSGARWLTA IICNYEVDRTIRHTKMNVGDVQ RLSVAVVVNYKTLDPGKPLPLS NEQMKQIEDLTREAMGFSEKR GDSLNVVNSPFSNDSDESG
9197	39565	A	9256	590	910	SCSIQLSPWILPRTVMCPVGFTC ELLST*WLAKEPKTVSWITIRS FTAETSTFGPTMTASMTFLPTY CSIIASLLSSFKLAAAILNSLPQI GRYITIGSGVRRNA
9198	39566	A	9257	1	854	MANRMLNETAWFGRGAVGA LTDEVKRRGYQKALIVTDKTL VQCGVVAKVTDKMDAAGLAF AIYDGVVANQHYYCRQSSSEDF AEMSLIEGRRGLRRRPLWEFEI DTARQQLNLQFGTRDLVGFV ENAPRGLCAAGCLLQYAKDTQ RTTLPHRSITMEREQDSIIIMDA ATTRNLEITQNLGGAENTLAS VLDCTVTPMGSRMLKRWLHM PVRD/DPRVA*APANYWRIAGF HRRATAGTASGRRPGTYSGTSG FTNCSPTRSGPYAPRPATAGA ACAVRNCR
9199	39567	B	9258	122	868	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
9200	39568	A	9259	2610	2897	PNLYLRFFFFFLRQESHVSTQA GVQWCNLSLQPLPPGFKQFSH LTGALPKCWDRSKRPRPANQT SILDVKEDPY*LHWPRSNRDIK LNLVANP
9201	39569	A	9260	2166	2426	VQPGGCGL*RQHGSYRPESRTA GGRHRG*RRLRRAPIDGGANSS GTGICRDAFNRIHWTGRTGRP DVDSGEHRKTAEQRRDGA VR
9202	39570	A	9261	846	1022	
9203	39571	A	9262	1	1339	MNALSKARQYVEEFDGNIASFI FSGKPGTGKNHLLAAICNELL RERNLGESEIHTTSDHMTATL PGETQTWPEDFRDVEQRQVV FQHLVGCVKVDGKYIQVCTFT VGGNYGGTCLRGDES LVIKKES DIEPLIVTVVQQFHIGNGYVVI TITPSEGERYQGVVGLGRIRRT RRIRHKQSARCYNLRFKPTCAIT QTTPTEVSPVLKKQLVLPNPH YPGNKPNFKRVSVKIIGESASRR LQLSRGDDIADALDRFVSEAI TAKVEAAIKN*LSQYGILPEEW GGESQFVHVSAGKTGIDELLA DAILLQAEVLELKAVRKGMS GAVIEFPPLDKGRGPVVTVLV REGTLHKGDIVLCGFYGRVRA MRNELQGEVLEAGPSIPVEILGL SGVPAAGDEVTVVRDEKKARE VALYRQGGKFREVKLARQQKSK LENMFANMTEGEVHEVNIVLK ADVQGSVEAISDLLKLSTDEV KVKIIGSGVGGITETDATALAAS NAILEGLFTLTSQDEFVIAPGFS TDPLEEQHSVVSGLLHKYIHN ALLLVKGGCAVNCRYCFRRHF PYAENQGNKRNVQTAL EYVA AHPELDEMIFSGGDPLMAKDH ELDWLLTQVVHQHDVGRRVQ RLPFIHDALFHQQFFNQHTTF GQVHLARFFVHREVDSILFRIS VLKMMMSPHRVKDRCYCAQFI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
9204	39572	A	9263	922	2357	GKGNDEKKI.VSDQ*MGTA*RQ RIHPISIIPL.LW/YPEGPSVSRPE AGGYNSLL.MVTHGK.VINGRRG ILIESD.EPGDAR*SSGSCARHGL VFVWLCSCRRCMPQTIEAIQHNP A/VAVNKIDRPEADPDRVKYVL SQYGIL.PEEWWGESQFVHGS AGTGIDELLDAIL.LQAEVLELK AVRKGMA SGAVIESFLDKGRG PVATVLVREGTLHKGDIVLCGF EYGRVRAMRNELQGQEVLEAGP SIPVEILGLSGVPAAGDEVTVVR DEKKAREVALYRQGGKFREVKL ARQKSKLENMFANMTTEGEVH EVNIVLKADVQGSVEAISDSL KLSTDEVKVKIIGSGVGVIEAES LDLRYYSVIYNLIDEVKAAMSG MLSPCLKQIIGLAEVRDVFKSP KFGAIAAGCMVTEGVVKRHNPIR VLRDNVVIYEGELESRRFKDD VNEVRNGMECGIGVKNYNDVR TGDVIEVFEIHEIQRITIA
9205	39573	A	9264	1	748	
9206	39574	A	9265	923	1387	PPNLARCSPSAMARQSPIRSPRR PLAPSPALRAPSPAPPHAARLA VPRQA*GLLLLLALIAVSTHIEMI SNTLAMGWNSPLTTVLALLAC GFACFIEMGKIPFDVAASWIIMI WSQSSTCTAPTLKPLRSVTLMR LTPVSARDLVGYFATAVRLP
9207	39575	A	9266	352	478	CDPTQRKPLYWLQALRRGLPI WRNQRFRKAVR*MAMAPMFS
9208	39576	A	9267	54	811	HTTGGNPLYGI/SRQIAR*QSRV/ GPGFCQDYRDIHKLFKRQEVAP TSSGLMFRMLMPWVLISSMLVLA MALPLFITVSPFAGGGDLITLIY LLALFRFFALSGL.DTGSPFAGV GASRELT.LGILVEPMLILSLVL ALIAGSTHIEMISNTLAMGWNS PLTTVLALLACGFACFIEMGKIP FDVAEAEQELQEGPLTEYSGAG LALAKWGLGLKQVVMASLFV DI.FLPFGRAQELSUAACLLTSLV VTLLKRLL

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9209	39577	A	9268	2	627	CGSIIALVAIFKSFSGHYLGTLE GLNGLVLKFGYKGDKTQVSLG KLNTISMIFIMGSTWVYAYANP NILDLEAMGAPIASLLCLLPM YAIRKAPSLAKYRGRLDNVPH AITRVDLKEDGKGLKIVRQSLP YGTASGTHGLYFCAYCARLHNI EQQLSMFGDTDAIKAYQSFLA RSAFAVSQCIPVNTVYRAYSVI QNWIATIRHV
9210	39578	A	9269	2648	3072	LSRTGTGKTTFAIT/LEYAASIIAL VAIFKSFSGHYLGTLEGLNGLV LKFGYKGDKTQVSLGKLNTIS MIFIMGSTWVYAYANPNILDLI EAMGAPIASLLCLLPMYAIRK APSLAKYRGRLDNVFTVIGLL TILNIVYKLF
9211	39579	A	9270	467	614	VPLAVPYGRLWRTIFSPSSFR STRE*YESMLGRFFERTACLQQ KQF
9212	39580	A	9271	1	846	MSYLVVWPFIASLVLSLIPYW NSAVIDQVDLGSALATGHDGILI TVWGGIMSTKVFPLNFPNVFSF GIVSKIRKK*KKDFGRDFTERKC SQIISRASMLMVAVVMFFAFSC LFTLSPANMAEAKAQNPVLSH LANHFAASMTGKTTFSITLEYA ASIIALVAIFKSFSGHYLGTLE LNGVLKFGYKGDKTQVSLGK LNTISMIFIMGSTWVYAYANPN ILDLEAMGAPIASLLCLLPMY AIRKAPSLAKYRGRLDNVFTV IGLLTILNIVYQLF
9213	39581	A	9272	95	456	RAISMSFRMERPCCLSLPSSLCIS STRVTASSPLSGCSSCTLLWISW GRMVRNCNT/MQI.QDLLRA HLRPPKPPMAKLLLEPAEGFPGTS CLLEAEPSTIRDVVLIASQPASQ PASQQGSQI
9214	39582	A	9273	1	1241	



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9215	39583	A	9274	3	1608	SRGFPRRREFSGPSIKKKVDAPTQ AQWVPVHAVITNSTYDGLLYNT DWIKQTLDPVSIHLDSAWVPYT HFHPIYQKGKSGMSGERGAGKVI FEPQ*AHRLMLAALSQGSLLIKG EYDQEAFAFMHRHSPSSPSYPI GGSVETAAAMLRGNPGKRLIN RSVERALHFRKEVQRLREESDG WFFDIWQPPQVDEAECWPVAP GEQWHGFNDADADHMFDPV KVTLTPGMDEQGNMSEEGIPA ALVAKFLDERGIVVEKTGPYNL LFLSIGIDKTKAMGLRLGLETF KRSYDLNLRKNMPLDLYAEDP DFYRNMRIQDLAQGIHSRRVTA SVSSGSQANQQVNFIGDQSTAA LTLSPVSGDITVTNTAPQYMTA TLQDKNGNPLKDKETFSVPND VASKFSISNGGKGMTDSNGVAI ASLTGTLAGTHMIMARLANSN VSDAQPMTFVADKDRVVVLQ TSKAEIINGVDETTLTATVKD PSNHPVAGITVNTMPQEGVYA MSLEYIILTFIALNGSRMWINS REKRTQRND
9216	39584	A	9275	106	709	LRS AEDNDTREKNKQTNRSDS KLRLVETSGSPPTSSSQTPDPF RYPKKYCVEDCS\YRPE*PRITP DNRLLYGGGVVYGARDPDVVE RLVVPKLLKTFPQLKGVKIDYR WTGNFLLTLRMPQYGRDNTNI YYMQQYSGHGVTCNHLAAGRLI AELLRGDAERFDFANLPHYFP PGGRTLRLVPFTTKSAAYYSLR DRLGV
9217	39585	A	9276	140	558	RKPIHRQGEKAGRNRSVDGCC EKAMSVIIVGGGMAGATLALAI SRLSHGALPVHLIEATAPESHA HPGFDGRAIALAAGTCQQLARI GVWQSLADCATAITTVHVS DR GHAGFGTLSRKITTWGL*QRSW ARWIWYPFKNYHLGALTTVV ELQMGGKRLF
9218	39586	A	9277	3799	4086	
9219	39587	A	9278	3017	3184	
9220	39588	B	9279	1	1050	
9221	39589	B	9280	1	1455	
9222	39590	A	9281	374	506	RCIALIAWLTLPVLRVTLK*RW RVARR*RAACW*S*WHHSALA P
9223	39591	C	9282	47	406	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
9224	39592	A	9283	1	4749	
9225	39593	B	9284	507	3568	
9226	39594	A	9285	101	638	RQKYSWSSALVPTAGEPTRH TQTRAGIAHA/EADFAADILFL LCGKDISTAGGFSFV*LADNKQ HLMPCVCFANHLTVKM/PHQSPV PDH/QALISHRIRSSRGSCSRYS DNSVSRTPLSPTPGRSTMVICS PICRRKRKGSRVQAATSLTGD SPANRALQRLLFPAPVLPMMPI TGS
9227	39595	A	9286	271	532	
9228	39596	A	9287	643	768	
9229	39597	A	9288	1	1948	MCSHAAGCTIPDVEHWTRINR KVPRLVSVLPNGPDYHPTVRAF LAGGVPEVMLHLRDLGLLHLD AMTVTGQTVGENLEWRPEPGA FRQCLREQDGVPPDDVILPPEK AKAKGLTSTVCFTGNIAPEGS VIKATAIDPSVVGEDGVYHHTG RVRVFVSEAQAIIKAKRVVIVA CGFSPTRTAHAASDIDITNTVDL RNRRLRRLRGEIVQF/IPANKYR TSA*GS*LAHPTGSLCD*VGRL DIPLAANFVQR*SPPGISPTPV
9230	39598	A	9289	2166	2426	VQPGGCGL*RQHGSYRPERSTA GGRHRG*RLRRAFIDGGANSS GTGICRDAFNRIJSHWTGRTGRP DVDSGEHRKTAEQRRDGA VR
9231	39599	A	9290	846	1022	

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9232	39600	A	9291	1	1336	MNALSKARQYVEEFDGNIAIFI FSGKPGTGKNHLAAICNELLL RERNLGESEIHSTSDHMTATL PGETQTWPEDFRDVEQRQQVVI FQHLVGCVKVDGKYIQVCTFT VGGNYGGTCLRGDES LVIKES DIEPLIVVTVVQQFHIGNGYVVI TITPSEGERYQGVVGLGRIRRT RRIRHKQSARCYNLRFKPTCAIT QTTPTPEVSPVLKKQLVLPNPH YPGNKPNFKRVSVKIJESASRR LQLSRGDIADALSDRFVSEAI TAKVEAAIKN*LSQYGILPEEW GGESQFVHVSAGAGTGIDELLA DAILLQAEVLELKAVRKGMA GAVIESFLDKGRGPVATVLVRE GTLHKGDIVLCGFYGRVRAM RNELGQEVLEAGPSIPVEILGLS GVPAAGDEVTVVRDEKKAREV ALYRQKGFREVKLARQOKSKL ENMFANMTEGEVHEVNIVLKA DVQGSVEAISDSLKLSTDEVK VKIIGSGVGGITETDATALAASN AILEGLFTLTSQDEFVIAPGFST DPLEEQHSVVSGLLHKYHNRA LLL VKGGCAVNCRYCFRRHFP YAENQGNKRNVQTALEYVAA HPELDEMIFSGGDPLMAKDHEL DWLLTQVVHQHDVGRRVQRL PFIHDALFHQQFFNQHTTFGQ VHLARFFVHREVDSILFRISVL KKMMSPHRVKDRCYCAQFICP
9233	39601	B	9292	1	2890	
9234	39602	A	9293	1	822	ITQYCDSTFICLSKGLGTPVGS LVGNRDYIKRAIRWRKMTGGG MRQSGILAAAGIYALKNNVAR LQEDHDNAAWMAEQILRETG A\DVMRQDTNML\FVRVGEEN AAALGEIT*KPRNVLI\NASPIV RLERDVPQRILVLGASGYIGQH LVRTLSSQGHQILAAARHVDR LAKLQLANVSHKVDLSWPDN LPALLQDIDTVYFLVHSMGEAA IYRSAGVASVSSVERYCLRPSY DPRVFPCLCCRALVLPCLLIY SPLSFALVLSLAPIK
9235	39603	A	9294	1565	1825	SRMCVAIRSNRQSRCEITIAQPG NSSRAFSSARRVSISSLVGSSSS SMLPPTCSSFARCRPRSPPESS PTRLP*STPLKKLRPT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
9236	39604	A	9295	236	742	VATRCRSRSPSLSPSLSLRVMIPTTSAYSFMITAKSSPAVLKLSNASERVNVSGTISVLRICPTLFSA RLWLASTFRSRLST*PMMWS ISSLQTRNLECGCSATLFFRLCSSWRSN/TNDVFTAVTLITERDGI PAQRRFQSARVPVYTRPPAH RLPLPRRCHQK
9237	39605	B	9296	1	951	
9238	39606	B	9297	1	666	
9239	39607	A	9298	761	1162	IILGSMIAIFILPIHEQGMFFHL FVTSFILSSGL*FSLKRSFTSLV SCIPRYFILFVAIVNGSSLV\WLS VFLLFVYRNACDFCTLILYPETL LKLLISLRRFWAETLGFSKYTIM SSANRDNLTSFFPN
9240	39608	A	9299	82	160	
9241	39609	B	9300	64	477	
9242	39610	A	9301	408	507	LLPLFQNL LLYVYSGI*LLPGLVW KGCMPHGIYP
9243	39611	A	9302	1	3141	MLLGLHSLAAFLQRESFGSKQS WGCQLAALLQRRITKMTTEAMK ITLSTQPADARWGEKATYSINN DGITLHLNGADDLGLIQAARK IDGLGIKHVQLSGEGWDADRC WAFWQGYKAPKGRKVVWPD LDDAQRQELDNRLMIIDWVRD TINAPAEELGPSQLAQA VDLIS NVAGDRVITYRITKGEDLREQG YMGLHTVGRGERSPVLLALD YNPTGDKEAPVYACLLGDIITY RNGKKVEVMNTDAEGRVL
9244	39612	A	9303	1	983	MVRASGYLQTLDDFNHIVLKA SENGVPVYL RDVAKVQIGPEM RRGIAELNGEGEVAGGVILRS GKNAREVIAAVKDKLETLKSSL PEGVEIVTTYDRSQLIDRAIDNL SGKLL EEFIVVAVCALFVWHV RSALVAIISLPLGLCIAFIVMHFQ GLNANIMSLGGIAI AVGAMVD AAIVMIENA/R*TAGRVAAPAS* RHAG**NALAGQEGRLFGPLAL HQNVCDGGCGAAGDRSDPD PD GLLDWPQNSAGKQ*PAQSLFDS CLSSAVAESTALAENHAAGG AFGADGSLAAQ*SSPGEFLPQIN EGDLLYMPCDAAQGPQRRR
9245	39613	A	9304	362	436	
9246	39614	A	9305	101	208	
9247	39615	C	9306	1	882	
9248	39616	B	9307	1	822	